Access DB# \_\_\_\_\_

28488

## **SEARCH REQUEST FORM**

Scientific and Technical Information Center

	1		Dr.288 %	DECTRICATION OF THE STATE OF TH	
	Requester's Full Name: S. Devi Art Unit: 16.4. Phone Number 3 Mail Box and Bldg/Room Location: All-	08-9367	aminer #: 5. Devi Serial Number: 09 Format Preferred (circle)	Date: 08 May 00 /240,675 PAPER DISK E-MAIL	
	If more than one search is submitted, ple	· / .	,		
		****		*******	
	Please provide a detailed statement of the search topi Include the elected species or structures, keywords, s utility of the invention. Define any terms that may h known. Please attach a copy of the cover sheet, perti	ynonyms, acronyms, ave a special meaning	and registry numbers, and c Give examples or relevan	ombine with the concept or	
	Title of Invention: Manacloual o			nterseron Receptor	)
	Inventors (please provide full names): Patric	K. Benoit	et al	- good	
	D. F. (D. t. Pills, Date, 03, 3)	.92	Cr	- Lata	
	Earliest Priority Filing Date: 03.31.92  *For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the				
	appeareinte serial number		,	* **	
	Please ask [43. Beve	ly Shew	rs) to perso	in this search	•
	Please perdosur. Search on the SE	a Série	unce 4 au -	Interderence	
	eauch on the SEE	ID NO	· 1 and 2	and portross	
•		A A	and the second of the conference of	Second Historica Street, Second Second	. 4
	claims are enclose	े । े	<i>f</i>	1.6	Ų
		•	CAT POLY	51708	
	Thanks.		oint c Bever mical 12C1	₩ - 32	
	in the second of		A Tel	Paris I	
		•	tact: ears Speci		
			alist <b>4994</b>	The second secon	
			•		
`	×		1 + 1 + 1		
			المراجعة والمنافعة المنافعة ا	day i American inggan paga kanananan inggan kananan	
	STAFF USE ONLY Type o	f Search	Vendors and cost w	here applicable	
21,3	Sembler Bellevin C459 FINASON	ence (#)\$]	N		à
	Searcher Phone #: AA Sequ	ence (#) Di	ialog	The second secon	
	Searcher Location: Structure	(#) Q	uestel/Orbit		13
	Date Searcher Picked Up: Bibliogr	aphic Di	r.Link	The same of the same	
	Date Completed: OC-OS-OO Litigation	n <u> </u>	exis/Nexis		
	Searcher Prep & Review Time: 12 Fulltext	Se	equence Systems	omgadas A. Sa Alagaina a	

PTO-1590 (1-2000)

```
A_Geneseq_36:R37804
A_Geneseq_36:R85911
A_Geneseq_36:R10796
A_Geneseq_36:R10545
A_Geneseq_36:R46233
A_Geneseq_36:R75368
                                                                                                                                                                                                                                                                 A_Geneseq_36:R14642
A_Geneseq_36:R14641
A_Geneseq_36:R55749
A_Geneseq_36:R07469
A_Geneseq_36:R70113
                                                                                                                                                                                                         A_Geneseq_36
A_Geneseq_36
A_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query: US-09-240-675-1_CO
Query length: 401
Database: A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database sequences: 188963
Database length: 23686106
Search time (sec): 60.370000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ક
                                                                                                                                                                                                                                                                                                                                       A_Geneseq_36:W97864
A_Geneseq_36:R71035
A_Geneseq_36:R75783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: May 31,
                   A_Geneseq_3
A_Geneseq_3
                                                                                                                                                   A_Geneseq_3
                                                                                                                                                                              Ceneseq_3
                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search
                                                                                                                                                                  _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MODEL-frame*_n2p.model -DEV-x1p
-Q-/cgn2_1/USPTO_spool/US09240675_runat_30052000_164311_24603/app_query.fasta.1
-Q-/cgn2_1/USPTO_spool/US09240675_runat_30052000_164311_24603/app_query.fasta.1
-DB-A_Geneseq_36 -QFMT-fastan -SUFFIX-modif.rag -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH-0.100 -COOPELT-0.000 -LOOPEXT=0.000
-QGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-GAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-110.000 -YGAPEXT=0.500
-DELOP-6.000 -FGAPEXT=7.000 -YGAPOP-110.000 -YGAPEXT=0.500
-DELOP-6.000 -DELEXT=7.000 -STARTA-DISONMESC
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext :MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                       _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                        _Geneseq_36:W97861
Geneseq_36:R75782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _Geneseq_36:W21805
                                                                                                                                                                                            _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                   _Geneseq_36:W52296
                                                                                                                                                                                                                                                                                                                                                                                                                                  _Geneseq_36:W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                              _Geneseq_36:R75356
_Geneseq_36:W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _Geneseq_36:W21806
_Geneseq_36:R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _Geneseq_36:R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   information block:
US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Results were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1_COPY_27_427
                                                                                                                                                 36: W40099
36: R62023
36: R14643
36: R57138
36: W41804
86: W41803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000 7:05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ere produced by (c) 1993-2000 (
      776.550
                                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8888
                                                                                                                                                                                                                                                                                                                                                                                                                              1512.59
1512.59
1512.59
1512.59
1512.59
1511.30
1510.14
1510.14
1510.14
1510.14
1510.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the GenCore
                                                                                                                                                                                                                                                                                                                           281.30
240.06
244.43
230.08
230.84
209.84
170.47
       140.19
140.19
138.26
137.59
137.59
137.59
137.24
140.06
138.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: A_Geneseq_36:*
                                                                                                                                  9.7e-05
9.7e-05
9.0225
0.0225
0.0237
0.0280
0.0503
0.0469
0.1216
0.2156
0.2156
0.2156
0.3301
0.3430
0.3502
0.3770
0.3770
0.3770
                                                                                                                                                                                                                                                                                                                                                                                                                   1.1e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EScore
2.0e-77
2.0e-77
2.0e-77
                                                                                                                                                                                                                                                                                                                                                                      .2e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2e-77
.2e-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1e-77
.2e-77
.2e-77
                                                                                                                                                                                                                                                                                                                                                                                                                                 2e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      version
Soluble human interferon gamma Gamma interferon receptor. New Interleukin-10 receptor subunit Human IL-10 receptor. Interleuk Mouse IL-10 receptor. Interleuk Human gp130 splice variant. New Human gp130 receptor. Interleuk Human gp130 receptor. Interleuk Human gp130 receptor. Service variant. New Human gp130 receptor. Human gp130 receptor. Service Human gp130 receptor. New splice Human soluble glycoprotein (GP) Human gp130 rotein. New splice Human gp130 rotein. New splice Human gp130 receptor subunit Human interleukin-12 receptor.
                                                                                                                                                                                                                                                                                                                                       2Cytor7 cytokine receptor polyp
CRFB4 protein. New recombinant
Human cytokine receptor 11 (2cy
IFN-gamma receptor beta-subunit
Human cytokine receptor 11 (2cy
Human iFN-gamma accessory facto
IFN-gamma receptor beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              out_format :
                                                                                                                                                                                                                                     Plasmid pBABLUE human interfero
Gamma-IFN-R-GBP 130 fusion prot
Arabidopsis thaliana ferulate-5
Arabidopsis ferulate-5 hydroxyl
                                                                                                                                                                                                                                                                                              Gamma interferon receptor. New Gamma interferon receptor. New Extracellular domain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of a soulble form of t
Human interferon receptor. Mono
Human IFN receptor. Compsn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human alpha-interferon receptor Complete interferon-alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soluble interferon-alpha/beta t
Sequence of a soulble form of
IFN receptor extracellular doma
Spliced-deleted interferon alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spliced-deleted interferon Soluble interferon-alpha/bo
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human IFN receptor. Compsn. of
Transmembranal interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpi
```

```
seq_documentation_block:
ID W21805 standard; Prot
AC W21805;
DT 23-SEP-1997 (first e
DE Spliced-deleted inter
KW Interferon alpha-rece
OS Homo sapiens.
FH Key I Alabe
FT domain Alabe
FT AU947597-A.
PR 24-OCT-1993; II-10737
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_36:W12772
A_Geneseq_36:W93941
A_Geneseq_36:W17859
A_Geneseq_36:W70799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: A_Geneseq_36:W21805
PT New mammalian Soluble interferon alpha-receptor forms - used for prinhibiting, modulating or modifying the activities of interferon(s) PS Example 2; Fig 7; 46pp; English.

CC (W21805) Is characterised by a new domain (S) which follows an CC end-deleted extracellular domain when compared to transmembraneal CC IFNAR (W21804). There is no transmembrane domain. The amino acid CC sequence is predicted from a cDNA clone (see also T73520) obtd.

CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR CC splice-deleted forms 1 and 2 (see also W21806) probably regulate CC the response of human cells to IFNS, either by acting as IFN CC antagonists or by regulating the activity of the multiple IFN CC subtypes. They can be expressed in host cells and used to inhibit, CC modulate or modify the activities of IFNS alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA) YEDA RES 6 DEV C. (ABRA/) ABRAMOVICH C. Abramovich C, Partiller C, WPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novich C, Ratovitski E, 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Extracellular_dc
/note= "comprises amino
transmembranal IFNAR"
428. .434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75
73
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ၀
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha-receptor form IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138.65
129.83
141.20
141.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.4569
0.6556
0.6623
0.6640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acids 1-427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662
1429
329
332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interleukin-12 beta-1

Human brx protein. Breast C

Rheumatoid arthritis auto-an

Human gp130-delta-3fibro ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ę,
```

```
alignment_scores:
                                                                                                                                                                                   alignment_block:
                                                                                                                                                                        US-09-240-675-1_COPY_27_427 x W21805
                                                                                                                                                                                                      Percent Similarity:
                                                101
        151
                                                                   17
                            34
                                                                                       51
                                                                  AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                          lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                    1
                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                    to: W21805
                                                                                                                                                                                                       100.000
                                                                                                                                                                                                                692.00
5.203
                                                                                                                                                    from: 1 to: 434
                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                Length:
Gaps:
                                                                                                                                                                                                       100.000
                                                                                                                                                                                                                133
```

ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy

```
seq_name: A_Geneseq_36:R14487
                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-240-675-1_COPY_27_427 x R14487
                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                   Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                               Align seg 1/1 to: R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 91-319778/44.

WPI: 91-319778/44.

N-PSDB; Q14239.

New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 2; Page 45; Szpp; French.

The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFN; autoimmune
Homo sapiens.
FR2657881-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soluble interferon-alpha/beta receptor. IFN; autoimmune disease; graft rejection; histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tovey MG, Uze G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EUBI-) LAB EURO BIOTECHNO.
Eid P, Gresser I, Lutfalla G, Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                      101
                                                                                                                                                                           51
                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                               MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 436
                                                                                                                                                                                                                                                                                   from: 1 to: 436
                                                                                                                                                                                                                                                                                                                                                                         Percent
                                                                                                                                                                                                                                                                                                                                                                  Length: 133
Gaps: 0
: Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F, Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                         150
                                                                        50
                                                                                                                                            34
                                                                                                                                                                               100
                                                                                                                                                                                                                 17
```

```
seq_documentation_block:
ID R28495 standard; Prot
AC R28495;
DT 31-MAR-1993 (first e
DE Sequence of a soulble
DE with a high affinity
Interferon receptor;
OS Synthetic.
PN W09218626-A.
PD 29-OCT-1992.
PP 17-APR-1991; WO-F0031
(EUBI-) LAB EURO BIOT
PI Eid P, Gresser I, Lut
PI Tovey M, UZe G;
DR WPI; 92-382110/46.
DR N-PSDB; Q30532.
PT diseases and transplane
PS Claim 2; Fig 1; 58pp;
CC DNA encoding the wate
CC IFN-alpha and -beta i
CC oligonucleotides as p
DC bacteriophage lambda
CC the IFN-alpha and -be
CC 030534 and Q30535.
CC 1FN in the same way a
CC treating autoimmune d
CC treating autoimmune d
CC Sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: A_Geneseq_36:R28495
                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            water soluble polypeptide(s) strongly bind interferon(s) alpha pr and beta - useful as immunosuppressants, for treating auto:immune pr diseases and transplant rejection claim 2; Fig 1; 58pp; English.

SC Claim 2; Fig 1; 58pp; English.

SC Claim 2; Fig 1; 58pp; English.

SC Claim 2; Fig 1; 58pp; English.

Claim 2; Fig 1; 58pp; English.

SC Claim 2; Fig 1; 58pp; English.

Claim 2; Fig 1; 58pp; English.

SC Claim 2; Fig 1; 58pp; English.

Claim 2; Fig 1; 58pp; English.

SC Camana and -beta is isolated by PCR, using appropriate

SC Camana claim 2; Fig 1; 58pp; English.

SC Camana and -beta is isolated by PCR, using appropriate of complete control of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Claim 2; Fig 1; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AAATTGCGTATAAGAGCAGAAAAAGAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
EId P, Gresser I, Lutfalla G, Meyer F, Mogensen
Tovey M, UZe G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1993 (first entry)
Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R28495 standard; Protein; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                17
                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS}
                                                                                                                                                                                                                        ATGATGGTCGTCCTGGGCGGCGACGACCCTAGTGCTCGTCGCCGTGGG
AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                          .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F00318.
WO-F00318
                                                                                                                                                                                                                                                                                                                                                           R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 692.00
: 5.203
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                          x R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                           to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                      17
                                                                                                       34
                                           150
```

```
alignment_scores:
Quality:
                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_27_427 x R71723
                                                                                                                                                                                                                            Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: A_Geneseq_36:R71723
                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 documentation_block:
                                                                                                                                                                                                                                                                                                                         Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; Epglish.

A recombinant soluble form of the human interferon class I receptor protein extracellular domain, given in R71723, was expressed in either E. coli or COS cell hosts. The protein was used to raise
                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo saplens.
WO9507716-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q86457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-1995 (first entry)
IFN receptor extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                 101
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulator; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-1995
                                                                         17
                                                                                                                                                                                                                                                                                                                 mmunomodulatory monoclonal antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                       CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                     LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTGCGTATAAGAGCAGAAAAAGAAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                       436
                                                                                                                                                                                                                                                                                                       <u>Α</u>
                                                                                                                                                                        R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 436
                                                                                                                                                                        from: 1
                                                                                                                                                                                                                            Length: 133
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
                                                                                                                                                                     to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                       SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
  200
                                                150
                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                          50
                                                                        34
                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                 alignment_block:
US-09-240-675-1_COPY_27_427 x W21806
                                                                                             alignment_scores:
Align seg
```

Ratio: Similarity:

5.203 100.000

Percent Identity:

Gaps:

133

Quality:

7

.. 6

W21806

from: 1

6 496

```
seq_name:
New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 3; Fig 7; 46pp; English.

C (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain in transment in the extracellular domain. The amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a conductor (see also T73521) obtd. From human myeloma U266 cells. Soluble, non-membrane bound IFNAR police deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed activities of IFNs alpha and beta in cells, tissues and organisms, Sequence 495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _documentation_block:
W21806 standard; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                 Abramovich C, Ratovitski E, WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W21806;
23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spliced-deleted interferon Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                       ABRA/) ABRAMOVICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_36:W21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- Extracellular_domain
/note- "comprises amino acid residues 1-413
422-427 of transmembranal IFNAR"
420-496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "comprises amino
transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abel-
                                                                                                                                                                                                                                                                                                                                                                                                          DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-receptor form IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                    Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids 481-557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
```

```
seq_name: A_Geneseq_36:R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                        18-JUL-1991 (first entry)
Human alpha-interferon receptor protein
Human alpha IFN; IFN agonists; antiviral; anti tumour
                                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis pisclosure; fig 4; 30pp; French.

Disclosure: fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are eg where overexpression of alpha-IFN is harmful. The Abs are halso useful for eg drug targetting. Variants of the protein, having residues 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA;
                                                                                                                                             (CNRS ) CNRS CENT NAT RECH SCI.
MOGENSON KE, UZE G, Lutfalla G,
WPI; 91-148740/20.
N-PSDB; Q11701.
                                                                                                                                                                                                          WO9105862-A.
02-MAY-1991.
19-OCT-1990; F00758
                                                                                                                                                                                                                                                                                                                                                          R11958 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \vdash
                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                               20-OCT-1989; FR-013770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAGTAGAGGTCGACATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                    TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                 targetting.
                                                                                                                                                                                                                                                              Location/Qualifiers
1. .27
                                                                                                                                                                                                                                                /label- signal peptide
                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                              557
                                                                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                                             Gresser I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                    agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
```

alignment\_scores:

Percent

Ratio: Similarity:

692.00 5.203 100.000

Percent

Length: Gaps: Identity:

100.000

Quality:

```
alignment_block:
US-09-240-675-1_COPY_27_427 x R11958
Align seg 1/1 to: R11958
                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
                                                                                                                                                                                   FR2657881-A.
09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
E1d P. Gresser I, Lutfalla G
                                                                                                                                                                                                                                                                                                                                                                                                  _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                   New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, beta - used to treat e.g. lupus erythematosus, Behcet's disease, beta - used to treat e.g. lupus erythematosid arthritis, etc. aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. pisclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from epitopes are eliminated and the deriv. Block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    кеу
                                                                                                                                                                                                                                                                                                                                     Complete interferon-alpha/beta receptor. IFN; autoimmune disease; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                           R14488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                       R14488 standard;
                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                              16-JAN-1992 (first entry)
                                                                                                                                                   WPI; 91-319778/44.
N-PSDB; Q14240.
                                                                                                                                                             Tovey MG, Uze G; WPI; 91-319778/4
             rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_36:R14488
  See also Q14239.
557 AA;
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                           /label- transmembrane
458. .557
                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                 /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                           557
                                                                                                                                                                                          G, Meyer
                                                                                                                                                                                                                                                                                                                                                                                           ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            с
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             557
                                                                                                                                                                                           '
                                                                                                                                                                                           Mogensen
                                                                                                                                                                                                                                                                                                                                             histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
```

```
alignment_block:
US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune diseases and transplant rejection
Claim 3; Fig 2; 58pp; English.
DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind
                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                                                                                                     17-APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
EId P, Gresser I, Lutfalla G, Me
                                                                                                                                                                                                                                                                                                                                      31-MAR-1993 (first entry)
Sequence of a soubble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                      R28496;
31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                              Tovey M, Uze G;
                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                               N-PSDB; Q30533.
                                                                                                                                                                                                                                                                                                                                                                                                                   R28496 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                               92-382110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_36:R28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                                                                                                                                                                                                                                                                                                                                                                      557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                             Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             557
                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                             Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
: 0
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ន្តន្តន
                                                                                                                                                                                                                                                                                                                         seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
         EP-563487-A.
06-0CT-1993;
31-MAR-1992; 400902.
31-MAR-1992; EP-400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE S.
Benoit P, Maguire D, Meyer F, I
WPI; 93-312951/40.
P-PSDB; R42635.
                                                                                                                                                                                                                                                                                  __documentation_block:
R42635 standard; Pro
                                                                                                                                                                                Human interferon receptor. IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFN in the same way as antibodies so are immunosuppressants etreating autoimmune diseases and graft rejection. They lack toxic side-effects of known immunosuppressants such as steroid Sequence 557 AA;
                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                          Ното
                                                                                                                                                                                                                                                         20-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                              TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                        LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                                                                                                                                                                                                                                                                                                                                                    lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                         A_Geneseq_36:R42635
                                                                                                                                                                                                                                                                                                                                                                  to: R28496
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      692.00
5.203
100.000
                                                                                                              1. .436
/label- extracellular_domain
/_---- "soluble, immunogenic
                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                  Protein;
 ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 557
 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ×
                                                                                                                                                                                                                                                                                   557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
 interteron
                                                                                                                                                                                                                                                                                  ₿
                                       SA.
Plavec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identity:
                                       ŗ,
type-I
                                        Tovey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.000
                                                                                                                       form
                                        ត្ត
                                                                                                                       of IFN-R
                                                                                                                                                                                                                                                                                                                                                    133
                                                                                                                                                                                                                                                                                                                                                                                                                                    350
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   steroids
 having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
```

```
£ £ & S S S S S S S S
alignment_block:
                                                                                                                                                                                                                            seq_name: A_Geneseq_36:R75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-240-675-1_COPY_27_427 x R42635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                       _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibodies produced against soluble forms of the hu interferon alpha-beta receptor based on the full-length human sequence are claimed. The antibodies are useful for treatment prophylaxis of disorders involving cell proliferation and/or vinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neutralising activity against human type I interferon, therapy and diagnosis Disclosure; Fig 3; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                    23-MAR-1995.
16-SEP-1994;
17-SEP-1993;
                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                        251
                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
 16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizari EJ, Tovey MG;
WPI; 95-131187/17.
                                                                      W09507716-A.
                                                                                                                                                                                          R75356 standard;
                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                      Homo sapiens.
                                                                                                                                                       Human IFN receptor
                                                                                                                                                                  16-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFN receptor; int
interferon-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                         GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                          AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                             sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557
                                                                                                                                interferon receptor; interferon-alpha;
ta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R42635
                                                                                Location/Qualifiers
1. .436
/label= Extracellul
                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to:
                                                                                   Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 133
: 0
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used
                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
```

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
 seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: R75356 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compsn. of monocional acceptor, eg. for treating new useful as immuno:modulator, eg. for treating new useful as immuno:modulator, eg. for treating new useful as immuno:modulator, Engilsh.

The amino acid sequence of human interferon class I receptor is given in R75356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monocional antibodies.

Sequence 557 AA;
                                                                                                                                                                              documentation_block:
W21804 standard; Pr
AU9475977-A.
11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 AAAAAGTAGAAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                              201
                                                        domain
                                                                             domain
                                                                                                   domain
                                                                                                             Key
                                                                                                                                             Transmembranal
                                                                                                                        Homo sapiens.
                                                                                                                                  rransmembranal interferon alpha-receptor.
Interferon alpha-receptor; IFNAR.
                                                                                                                                                     23-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 692.00
Ratio: 5.203
Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                     TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                              erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                       GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                    lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal
                                                                                                                                                                                                                A_Geneseq_36:W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q86458.

of monoclonal antibodies against interferon receptor
                               __el= Extracellular_domain
437. 457
/label= Transmembrane /
458. 557
/label= In+
075977.
IL-107378.
                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
                                                                                                                                                                                557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
                                                                                                                                                                                $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.000
                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
                                                                                                                                                                                                                                                                                                                                                                                                250
```

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FH CON THE SECTION OF THE SECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                   seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1_COPY_27_427 x W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abramovich C, Ratovitski E, Revel M;
WPI; 95-200634/27.
New manmalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Disclosure; Fig 7; 46pp; English.
Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polyapptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                      20-NOV 1998 (first entry)

20-NOV 1998 (first entry)

20-NOV 1998 (first entry)

20-YOT7 cytokine receptor; polypeptide, polypeptide; kidney; pancreas;

20-YOT7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;

type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;

agonist; cell proliferation; cell differentiation; renal disease; human;

neural disease; pancreatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            purposes.
                                                                                                                                                                                                                                                                                                     W79159 standard; Protein; 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ) YEDA RES & DEV CO
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_36:W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W21804
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PT Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful for treating renal, neural, pancreatic and prostatic diseases Claim 1; Pages 55-59; 72pp; English.

CC This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-binding receptor polypeptide and is a novel member of the type 2 cytokine receptor family (CRF2). An expression vector containing the Zcytor colynucleotide, operably linked to transcription promoter, a sequence encoding a transmembrane and intracellular domain, or both, and a transcriptional terminator can be used to transcription production of the polypeptide. The sequences can be used to study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Agonists of Zcytor7 can be used to stimulate proliferation and 2C differentiation of cell in these organs. The antagonists and agonists can also be used in the treatment of renal, neural, pancreatic and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9837193-A1.
27-AUG-1998.
18-FEB-1998; UO3029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams RL, Fai
Whitmore TE;
WPI; 98-48079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                           WPI; 98-480798/41.
N-PSDB; V57515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC.
Adams RL, Farrah TM, Jelmberg
                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 CTAGTGCTCGCCGTGGGCCCCATGG.....GTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                            34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe
                                                                                                                                                                                                                                                                                                                                                                                ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG...
                                                                                                                                                                                          uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA
                                  TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh
                                                                                                                                                                                                                                                                   :::||||||:::: :::|||
LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe
TCGCAMAGCTCAGATTGGTCCTCCAGAAGTA
                                                                                                                                                     CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA...
                                                                                                                                                                                                                                                                                                                                                 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal
                                                                        GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                               laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30. .250 /note= "extracellular (ligand-binding) domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146.00
1.848
62.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
4
29.921
                                      132
                                                                                                                                                     318
                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                271
```

```
seq_name: A_Geneseq_36:W52296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS Claim 2; Page -; 79pp; English.

PS Claim 2; Page -; 79pp; English.

CC rimis sequence is the human CRFB4 sequence, DNA encoding it is used in the CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1) CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2) CC encoding CRFB4, both operably linked to expression control sequences. CC cells containing (I) may be used to identify agonists/antagonist of CC cells containing (I) may be used to identify agonists/antagonists of inflammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, cc potentially useful for increasing immune responses against tumours, and criminal repetution. A vector containing (I) is used to compreventing organ rejection. A vector containing (I) is used to compreventing and is able to bind IL-10 but not to transduce a dysfunctional IL10R and is able to bind IL-10 but not to transduce a signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit compression of activity in cells. Antibodies specific for CRFB4 are used to reasure and localise CRBF4, for diagnosis of defective IL-10 activity. Can inhibit compression of the compression of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_27_427 x w52296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1997; U12455.
17-JUL-1996; US-663743.
(UYNE-) UNIV NEW JERSEY.
Kotenko SV, Pestka S;
WPI; 98-110590/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection; CRFB4; interleukin-10; IL-10; IL-10 autoimmune disease; vaccine; photosensitivity; inflammation; autoimmune disease; septic shock; immune response; organ rejection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w52296 standard; Protein; 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA - comprises sequences encoding interleukin-10 and CRFB4 linked to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V19874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1998
                        184
                                                                                                                           134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTITT 183
                                                                                                                                                                                                                                                                                                                                       55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT.....
                                                                                                                                                                                  19
                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                   TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG
                                                                          snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA
                                                                                                                                                                                                                              .....cctcaaaaagtagaggtcgacatcatagatgacaact 133
                                                                                                                                                                                                                                                                                                                                                                                                 to: W52296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136.50
1.896
59.504
                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 121
Gaps: 5
Percent Identity: 33.058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
                                                                                                                                                                                                                                                                                                                                                                                                         325
                                                                                                                                                                                                36
                                         233
                                                                                             52
```

```
seq_name: A_Geneseq_36:W97861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 ATGITTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1999 (first entry)
Human cytokine receptor 11 (Zcytor11).
Cytokine receptor 11; Zcytor11; human; pancreas; small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W97861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W97861 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                    Protein
                                                                                           (ZYMO) ZYMOGENETICS INC. Adams RL, Farrah TM, Jelmberg AC, WPI; 99-167425/14.
                                                                                                                             18-FEB-1999.
30-JUL-1998; U15847.
05-AUG-1997; US-906713
This is the amino acid sequence of human cytokine receptor 11 (2cytor11), a novel class II cytokine receptor that appears to be receptor for a helical cytokine of the interferon/interleukin-10
                                Novel human cytokine receptor Zcytoril - use ligands to modulate or promote proliferation of e.g. pancreatic or colon tissue Claim 27; Page 54-56; 62pp; English.
                                                                                N-PSDB; X24379
                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                  Protein
                                                                                                                                                                WO9907848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATTGGTCCTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTICITCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eIleGlyProPro 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HisserAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sCysMetAsnThrThrLeuThrGluCysAspPheSerSer.....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrAlaGlnTyr...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                        2. .574
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                             /note= "this polypeptide in Claim 27"
                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                      /note-
                                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                         . 228
                                                                                                                                                                                                                                                                                                                                          . 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 574
                                                                                                                                                                                                     . 574
                                                                                                                                                                                                                                       . 551
                                                                                                                                                                                                                                                                                                                                                                                               . 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....LeuSerTyrArgIlePheGlnAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                         . 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 228
                                                                                                                                                                                                                                                                                                                                                                                     "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "mature protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                 extracellular domain, the specifically claimed in
                                                                                                                                                                                                                                                "this polypeptide is in Claim 27"
                                                                                                                                                                                                                                                                                  "this polypeptide in Claim 27"
                                                                                                                                                                                                                                                                                                                   "this polypeptide is in Claim 27"
                                                                                                                                                                                                                                                                                                                                                                                                            "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                   "this polypeptide is specifically claimed in Claim 27"
                                                                                                                                                                             "this polypeptide is specifically claimed in Claim 27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574 AA
                                                                                                            Lok S, Whitemore
                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                               is
                                                               useful for screening for ion and/or differentiation
                                                                                                                                                                                                                                                                                                                                specifically claimed
                                                                                                                                                                                                                                                                                               specifically claimed
                                                                                                                                                                                                                                                               specifically claimed
                                                                                                                                                                                                                            specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                        this region
in Claim 20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
```

```
ទួទ្ធទទួទ្ធ ទទួទ្ធ ទទួទ្ធ ទ
        TETTER OK KEEP OK KEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-240-675-1_COPY_27_427 x w97861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: A_Geneseq_36:R75782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       class. The sequence was deduced from the nucleotide sequence (see (x24379) of a cDNA clone obtained from pancreatic islet cDNA (library. Ccytoril is a cell surface receptor that is expressed in cpancreas, small intestine, colon and thymus. Novel Ccytoril (polypeptides, especially an extracellular domain (see W97864) of czytoril, can be used to detect ligands that promote the proliferation and/or differentiation of these organs. The invention provides claimed expression vectors and transformed or transfected cells, as well as an antibody that specifically binds to the extracellular domain of Ccytoril, and an anti-idiotyptic antibody. The vectors include a promoter, a terminator and DNA encoding the extracellular domain, signal sequence, transmembrane domain or intracellular domain of Ccytoril.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: W97861 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                               documentation_block:
R75782 standard; Protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 rLeuGlnHisThrThrLeuLysProProAspVal 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 ATGACAACTTT.....ATCCTGAGGTGGAACAGGAGCGATGAGTCTGTC 168
                                                                                                                                                                                                                                                                                                                                                                                                   R75782;
                                            domain
                                                                                                                     peptide
                                                                                                                                                                                                 Mus sp.
                                                                                                                                                                                                                                 Interferon-gamma receptor beta subunit; interferon-gamma-antagonist.
                                                                                                                                                                                                                                                                                                          IFN-gamma receptor beta-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
                                                                                                                                                                                                                                                                                                                                                      13-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 hrValGluThrGlyAsnLeuThrGluLeuTyrTyrAlaArgValThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValSerAlaGlyGlyArgSerAlaThrLysMetThrAspArgPheSerSe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt ProAspThrValTyrSerIleGluTyrLysThrTyrGlyGluArgAspTr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erSerAsnPheGluAsnIleLeuThrTrpAspSerGlyProGluGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aHisAlaProGluAspProSerAspLeuLeuGlnHisValLysPheGlnS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrLeuLeuThrIleLeuThrValGly......SerLeuAlaAl 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGACCCTAGTGCTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120.50
1.586
59.375
                                    /label Sig_peptide
                                                                                                                                                         Location/Qualifiers
/label= Extracelular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                              muIFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128
3
28.125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x R75782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage Claim 3; Fig.2A; 86pp; English.

The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be used to treat pathological conditions associated with endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AGUE/) AGUET M.
(BOEH/) BOEHNI P
                                                                                             310 ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC
                                                                                                                                                                                                                                    228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HEMM/) HEMMI S.
Aguet M, Boehni R
WPI: 95-224321/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-1995.
07-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                               357 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA 396
                                                                                                                                                                                                                                                                                                181 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT
                                                                                                                                                                                                                                                                                                                                                                   149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q90808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9516036-A
                                                                                                                                                              IFN-gamma production.
Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                   93
                                                                                                                                                                                                                                                                 66 TyrSerPhe......IleAspGlySerTrpHisArgLe
                                                                                                                                                                                                                                                                                                                                                                                                    32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TTGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCC
                                                              ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr
                                                                                                                                                                                                                                                                                                                                                                                                  oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
oPheGlnHisTyrGluAsnValThrValGlyProProLys
                                                                                                                                                                                                 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG
                                                                                                                                                                                                                                G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                 luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu
                                                                                                                                                                                                                                                                                                                                                                TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 148
                                                                                                                                 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boehni R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: R75782 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120.00
1.500
61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267. .332
/label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 ...266
/label- Transmembrane_anchoring_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hemmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 130
Gaps: 8
Percent Identity: 30.769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332
                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32
                                                                                                                                                                                                 93
                                                                                                                                                                                                                                  271
                                                                                                                                                                                                                                                                   76
```

Š

US-09-240-675-1\_COPY\_27\_427

to: Issued\_Patents\_AA:\*

out\_format :

pfs

```
Database sequences: 145308
Database length: 14437401
Search time (sec): 65.1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: May 31, 2000 7:06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query length: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
Query: US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL-frame+_n2p.model -DEV-xlp
-Q-/cgn2_1/USPT0_spool/US09240675/runat_30052000_164312_24612/app_query.fasta.1
-DB-ISSued_Patents_AA -QFMT-fastan -SUFFIX-modif.rai
-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-COOPEXT-0.000 -QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000
-XGAPEXT-0.500 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -START-1
-MATRIX-blosum62 -TRANS-human40.cdi -LIST-45 -DCALIGN-200
-THR_SCORE-pct -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext
-MINLEN-0 -MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3
-NO_XLPXY -WAII -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by Copyright (c) 1993-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y the GenCore
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 software, version
     .8e-07 574
2 1.7e-07
6 9.0e-07
2 1.8e-05
8 0.0025
4 0.0063
                                                                                                                                                                                                                                                                                                                                                      3e-27
                                                                   alignment_scores:
Quality:
                                                                                                                                                                                                                                            ; MOLECULE TYPE: US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                          Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                        Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11,
Patent No. 5
                                                                                                                                                                                                                                                                                              TELEFAX: 202-737-3528
TILEX: 24853
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 419 Sever CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                  TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                    NAME: BROWDY, Roger L. REGISTRATION NUMBER: F
                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5643749
                                                                                                                                                                                                                                                                                               434 amino acids
                                                                                                                                                                                                                                                               ESS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                      protein
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Ggn2_6/ptodata/1/iaa/backfiles1.pep:5221789-1 + 
/Cgn2_6/ptodata/1/iaa/5a_COMB.pep:US-09-091-432-2 + 
/Cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-424-788-5 + 
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-110-683-2 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

ADDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION BATA:
APPLICATION NUMBER: II 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
ABMONT BEGOMY BOGGET I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: REVEL, Michet
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE

TO SEQUENCES: 12
101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: BROWDY AND NEIMARK 419 Seventh Street, N.W.,
                                                                                                                                                                                         US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ication US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVEL-13
                                                                                                                                                                                                                                                                           Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25,618
                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite
                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                         133
0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.50 17
+ 83.00
+ 78.00
+ 78.00
                                                                                                                                                                                          434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170.
                                                 34
                                                                                   100
                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.54 0.
164.03
151.19
151.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.063
0.0633
0.0633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            520
578
578
```

AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn

```
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-2
; MOLECULE TYPE: US-08-307-588-2
                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION NUMBER: EP 92400902.0
APPLICATION NUMBER: EP 92400902.0
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
APPLICATION NUMBER: EP 92400902.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                  TELEPHONE: (202)672-1
TELEFAX: (202)672-539
INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                   REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
ZIP: 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08307588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BENOIT, Patrick
MEYER, Francois
MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
AVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
NVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
                                                                             436 amino acids
                                                                                                                                     (202)672-5399
                                                                                                                                                           (202)672-5300
                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERFERON
                                                                                                                    2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12,
Patent No. !
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: IL 107378
FILING DATE: 24-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: REVEL, Michel
APPLICANT: ABRAHOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCCTC 100
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGATGGTCGTCCTGCGTGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                          COUNTRY: UZIP: 20004
                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Application US/08328256
5643749
                                                                                                                                                                                                                                                                                                    E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          692.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                            Version
                                                                                                                                                                                                                                                                                                          Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-256-12
                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-328-256-12 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-240-675-1_COPY_27_427 x US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
                                                                                                                                                                                  Sequence 10, Application US/08328256 Patent No. 5643749
                           GENERAL INFORMATION: APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                              301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAspLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                           LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
  AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-77,
TELEX: 248633
TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE SEQUENCE CHARACTERISTICS:
TENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                     101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                        251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                       201 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATAFTACTA 250
                                                                                 84
                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                               17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 557 amino aci
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Sever CITY: Washington STATE: D.C.
LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                      AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                               erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                          sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVEL=13
ER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                 34
```

TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399

```
; STRANDEDNESS:
; TOPOLOGY: lin:
; MOLECULE TYPE: |
US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                        Align seg 1/1 to: US-08-471-454-2 from: 1 to: 557
                                                                                                                                                                                                                 US-09-240-675-1_COPY_27_427 x US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: FR 89/13770
FILING DATE: 15-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GRESSER, ION
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                        ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                    MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08471454
5731169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOGENSEN, Knud E. UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUTFALLA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss: single
linear
                                                                                                                                                                                                                                                                                  100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                       692.00
5.203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges
                                                                                                                                                                                                                                                                                Percent Identity: 100,000
                                                                                    17
34
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-466-974-2
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                 TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MOGENSEN, Knu APPLICANT: UZE, Gilles APPLICANT: LUTFALLA, Gec APPLICANT: GRESSER, ION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 AACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 AGGAGCGATGAGTCTGTCGGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                      REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                       FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FITLE OF INVENTION:
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Application US/08466974 5861258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIXON & VANDERHYE P.C.
                   amino acids
acid
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA FRAGMENT CODING FOR THE GENE FOR THE THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREPARATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knud E
                                                                                                                                                                                         960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
```

; TOPOLOGY: 11; ; MOLECULE TYPE: US-08-466-974-2

linear

protein

```
alignment_scores;
Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-466-974-2 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08471453 Patent No. 5886153
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR THE TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGATGGTCGTCCTCGGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                             COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                     ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                           E: VIRGINIA
TRY: U.S.A.
                                                                                                                                                                     1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                    LUTFALLA, Georges
GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                            MOGENSEN, Knud E. UZE, Gilles
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
```

```
seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-471-453-2 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
                                     117
                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
                                                                                                                                           301
                                                                                                                                                                                                                                                                 201 AACTGGGATGGATAATTGGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                            101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                            34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGATGGTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                      TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                     AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                            erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                               GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                        AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/471,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                100
                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                                               150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                      84
```

seq\_documentation\_block:
; Sequence 4, Application US/08307588

```
alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein
US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-5339
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/EP
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 924
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, MICHAEL G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D. 2007
                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
                                                                                                                                                                                                                                                  yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
                                                                                                                                                                                       CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                             ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                  lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BENOIT, Patrick
MEYER, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGUIRE, Deborah
PLAVEC, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               692.00
5.203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP 92400902.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 500
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x PCT-US94-14277-3
                                                                                                                          alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-3
                                                                                                                                                                                                  ; TOPOLOGY: PCT-US94-14277-3
                                                                                      Ratio:
Percent Similarity:
Align seg 1/1 to: PCT-US94-14277-3 from: 1 to: 202
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Aguet, M
APPLICANT: Bohni, R
APPLICANT: Hemmi, S
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER
                                                                                                                                                                                                                                                                                                                                                          NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/164596 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                             910/371-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bohni, Ruth
Hemmi, Silvio
                                                                                                                                                                                                                                                     202 amino acids
                                                                                                                                                                                                                                                                                                                              415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                     linear
                                                                                      273.50
3.552
71.963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US94/14277
                                                                                      Percent Identity: 48.598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 Kb floppy
                                                                                                                                                                                                                                                                                                                                                                                 866PCT
                                                                                                                            Length:
                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08943087 Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                            INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 HisMetSerProProGluVal 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 ..ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 GGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 181
                SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803/305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GAATGTTTATGAAGAAATTAAAT%GCGTATAAGAGCAGAAAAAGAAAAAC. 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 TTTCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                  REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1201 E:
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 erThrSerSerTrpAsnGluValAspProPheIleProPheTyrThrAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 rAsn***TyrIleLysThrGlnPheArgValArgAlaGluGluGlyAsnS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GluCysGlnHisThrThrThrThrLysCysGluPheSerLeuLeuAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 heSerAlaGluTyrArgThrLysAspGluArgLysTrpLeuLys***Pro 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GluAsnLeuLysProProGluAsnIleAsp***TyrIleIleAspAspAs
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             je
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r: Whitmore, Theodore E.
T: Farrah, Theresa M.
INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                            206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jelmberg, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lok, Si
Kho, Choon J.
  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/943,087
                                                                                                                                                                                                                                  96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-943-087-2 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 eLeuGluThrGlnIleGlyProProGluVal 142
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG...
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                   APPLICANT: Farrah, Theresa M. TITLE OF INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                          STREET: 1201 E.
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 CTAGTGCTCGTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 AGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                              COUNTRY: UZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1, Application US/08943087 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                      Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                               Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                              Whitmore,
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146.00
1.848
62.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                   Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 29.921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
  2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087

CLASSIFICATION: 536

```
seq_documentation_block:
; Sequence 16, Application US/08943087
; Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-943-087-14
                                                                                                seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-240-675-1_COPY_27_427 x US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  132 eLeuGluThrGlnIleGlyProProGluVal 142
                                                                                                                                                                                                                                                                                                                                                                                                272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
                                                                                                                                                                                                                                                  116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                    319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 LysvalThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 553 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                   TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                      laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146.00
1.848
62.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 29,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
```

```
; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: p
; FRAGMENT TYPE: 1
US-08-943-087-16
                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-943-087-16 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                           125 ATGACAACTITATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fairah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                  34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe
                                                                        49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                  75 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                     18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                       31 CTAGTGCTCGTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 200-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 553 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                   146.00
1.848
62.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16:
                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 29.921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                               553
                                                                                                                                                                                                                                                                                                                                                                                                                           127
   82
```

```
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-18
                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
FELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA
                      nt Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 206-442-66
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICANT: Whitmore, Theodore E.
LICANT: Farrah, Theresa M.
LE OF INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eLeuGluThrGlnIleGlyProProGluVal 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08943087
                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jelmberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, Robyn L.
                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZymoGenetics, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                     protein
internal
                                                                                                                                                                                                                                 single
                                          146.00
1.848
                      62.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anna C.
                                                                                                                                                                                                                                                                                                                         18:
                    Percent Identity: 29.921
                                                                                                                                                                                                                                                                                                                                                                                                                                96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-943-087-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equence
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lok, S1
APPLICANT: Kho, Choon J
APPLICANT: Jelmberg, An
                                   ATTORNEY/AGENT INFORMATION:
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l16 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                             COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                           FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION
                                                                                                                                                                                                                                                                                                                      98102
                                                                                                                                                                                                                                                                                                                                                                                   Seattle
                                                                                                                                                                                                                                                                                                                                                                 WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08943087
                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                     1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jelmberg, Anna
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                ZymoGenetics,
Paul G
NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anna C.
                                                                                                                                                                     US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                         East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to:
```

96-24C1

```
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-240-675-1_COPY_27_427 x US-08-943-087-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-22
                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-943-087-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                         Patent No.
APPLICANT: LOK, S1
APPLICANT: KhO, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 553 amino acid
                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELLEPHONE: 206-442-6627
TELLEPAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                eLeuGluThrGlnIleGlyProProGluVal 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA
                                                                                                                                                                                                                                                                                                                                                                                                                             TCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                         2, Application US/08943087
5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146.00
1.848
62.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 29.921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-943-087-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1_COPY_27_427 x US-08-943-087-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/9
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
319 GAAAAAGAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 368
                                                                                                                                                                                                                                                                      125 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 171
                                                                                                                                                                                      222 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 271
                                                                                                      272 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 318
                                                         99 laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                              82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe
                                                                                                                                                                                                                                                                                                                 49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                     34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                             75 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 CTAGTGCTCGTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 206-442-66
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/943,087 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1201 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146.00
1.848
62.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/803,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 29.921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
                                                                                                                                                                                                                                   82
```

116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132

```
pir2:S61405
pir2:A41734
pir2:T34345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pir2:A25698
pir2:T04591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
Ouery: US-09-240-675-1_COPY_27_427
Ouery length: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000
                                                                                                                                                                                  pir2:S36638
                                                                                                                                                                                                                                                           P1r2:A36337
P1r2:T22836
                                                                                                                                                                                                                                                                                                  pir1:S14222
pir2:A49667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P1r2:S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pir2:A47003
pir2:JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pir2:G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p1r2:A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pir2:A32694
pir2:S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database: PIR_63:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                          pir2:T04240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MODEL-frame+_n2p.model -DEV-xlp
-0-/cgn2_1/USPT0_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-0-/cgn2_1/USPT0_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-DB-PIR_63 -QFMT-fastan -SUFFIX-modif.rpr -GAPOP-12.000
-GAPEXT-4.000 -MIMANCH-0.100 -LOOPEXT-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -EDEEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALION-200 -THR_SCORE-pct
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1r2:A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -THREADS-1
                                                                                                                                                                                                                                                                                                                                                        :T23031
                                                                                                                                                                                                                                                                                                                                                                                                 ::S61165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :T04239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :T27935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :A49947
                                                                                 : A32034
                                                                                                                                                                                                    : $40027
                                                                                                                                                                                                                    : $20901
                                                                                                                                                                                                                                                                                                                                        :T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                       : A44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : $20106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d Orig
692.00
454.00
366.50
136.50
127.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ş
    104.50
84.00
84.00
84.00
84.00
84.00
84.00
84.00
84.00
85.50
86.50
87.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
77.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2Score
1366.81
890.28
                                                                                                                                                                                                                                                         108.46
143.82
143.6.29
137.24
137.25
130.56
139.42
139.42
139.42
139.42
139.42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153.68
148.15
149.87
138.36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239.65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: PIR_63:*
  4.4e-07

5.2e-06

3.1e-05

0.4261

0.4261

0.4261

0.4361

0.4761

0.4761

1.136

1.136

1.137

1.157

1.157

1.157

1.167

1.167

1.167

1.167

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179

1.179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESCOTE
5.3e-69
1.8e-42
1.1e-32
    out_format : pfs
                                                                                                                                                                    interferon alpha/beta receptor 73 cytokine receptor family II, me cytokine receptor family II, me cytokine receptor family class i cytokine receptor family class i cytokine receptor class II cy interferon gamma receptor beta interferon gamma receptor access interferon gamma receptor precular hypothetical protein ZK617.1b interferon gamma receptor precular hypothetical protein ZK617.1b interferon gamma receptor class in hypothetical protein F14M19.13 interferon gamma receptor class in hypothetical protein F14M19.13 interferon ground from the first protein F14M19.14 interferon grotein F14M19.14 interferon grotein F14M19.14 interferon grotein F14M19.14 interferon grotein g
hypothetical protein C56A3.3 - hypothetical protein T1P17.150 subtilisin-like proteinse home hypothetical protein F23K16.40 choline kinase (EC 2.7.1.32) - trp3 protein rat peroxidase (EC 1.11.7) 1 pred beta-galactoside alpha-2,6-sial hypothetical protein T12A2.15 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon alpha/beta receptor interferon alpha receptor type interferon alpha/beta receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pir1:164231
pir2:A48584
pir2:A45731
pir2:JC2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality: 692.00
Ratio: 5.203
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_427 x A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: A32694 from: 1 to: 557
                                        251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                       201
                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                  101
                                                                                                 67
                                                                                                                                                                              51
                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                 \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGATEGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                              AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                     AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                            ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                               erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
```

Percent Identity:

: 133 : 0 : 100.000

100

84

67

50 150 100 17

```
A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Gross-references: GDB:120078; OMIM:107450
A;Gross-references: GDB:120078; OMIM:107450
A;Gross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein; transmembrane prodicted crRN1>
F;1-21/Domain: transmembrane #status predicted crRN2>
F;437-455/Domain: transmembrane #status predicted crRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interferon alpha/Seta receptor precursor - human
(Species: Homo sapiens (man)
C;Date: 22-Jun-1990 *sequence_revision 22-Jun-1990 *text_change 22-Oct-1999
C;Accession: A32694; S17112
R;Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor into mou.
A;Reference number: A32694; MUID:90124632
A;Accession: A32694
                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-16,'A', 18-329,'V', 343-557 <LUT>
A; Cross-references: EMBL: X60459; NID: g32671
                                                                                                                                                                                                                                                                                                                                                                                A;Description: The structuree of the human interferon alpha/beta receptor gene. A;Reference number: S17112
A;Accession: S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-557 <UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.00
70.00
69.50
69.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
106
132
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.76
14.41
12.21
12.61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368
3135
141
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! high affinity transport s:
! transmission blocking ta:
! comC-alpha protein - phag:
! neutrophil gelatinase-ass:
```

```
interferon alpha receptor type 1 precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Species: Bos primigenius taurus (cattle) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: S27387; S33770 R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G. FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-421,'Y',423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lim, J.K.; Langer, J.A.
Biochin. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a
A;Reference number: S33770; MUID:93305725
A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Specific antiviral activities of A; Reference number: S27387; MUID:93076908 A; Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: lung C;Keywords: antiviral; cytokine receptor; transmembrane protein C;Keywords: antiviral; cytokine receptor; transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG>F;25-560/Product: interferon alpha receptor type 1 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_427 x S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: S27387 from: 1 to: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                               204
                                                                                                                                                                                                                                                                                                            254 CCAAATGCAACTTTTCTTCACTCAAGCTG...AATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                         154 AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                             16 gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACTCATTTACACCATTTCGCAAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluVal 133
                                                                                                              uGlyThrAspAsnTrpLysLysLeuSerGlyCysGlnHisIleThrSerT
                                                                                                                                                            TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 253
                                                                                                                                                                                                               SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGlnIleLe
hrLysCysAsnPheSerSerValGluLeuGluAsnValPheGluLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor type 1 precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _block :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454.00
3.914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identity: 69.403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the human alpha interferons are determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bovine alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID: 9432
                       98
                                                                                                                   82
                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                                                                                                32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 118-125 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: I48426
                                                                                                                                                                                                                                                                                                                                           A; Accession: I48428
                         ;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 al 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 TA 399
```

```
interferon alpha/Teta receptor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 25-Mar-1993 *sequence_revision 18-Nov-1994 *text_change 05-Nov-1999 C;Accession: A4528; 148423; 148424; 148425; 148426; 148427; 148428; 148429 R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A;Title: Behavior of a cloned murine interferon alpha/Deta receptor expressed A;Reference number: A45283; MUID:92262522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: A;Reference number: I48423; MUID:95047447
A;Accession: I48423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone R;Lutfalla, G.; Uze, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-590 <UZE>
                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 425-445 <RE6>
A;Cross-references: embL:U06242; NID:g497112; PIDN:AAA65007.1;
A;Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 265-375 < RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 148, 343-346, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:102354,
                      A; Gene: IFNAR
A; Introns: 177/3; 331/1
                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1;
A;Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810
                                                                                                                A;Residues: 473-590 <RE7>
A;Residues: 473-590 <RE7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AAATTGCGTATAAGAGCAGAAAAA...GAAAACACTTCTTCATGGTATGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 GluLeuArgIleArgAlaGluGluGlyAsnAsnThrSerThrTrpTyrGl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118-125 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                block:
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID: 9194112
NCBIP: 102357)
                                                                                                                          PID:g510265
                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g755812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID:g510262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:9510261
                                                                                                                                                                                                                                                                             PID: 9755813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
```

ថ្ន

```
seq_documentation_block:
cytokine receptor family II, member 4 - human
c;Species: Homo saniane 'man'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_427 x A45283
                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                            A;Gene: GDB:CRFB4; CRF2-4
A;Cross-reterences: GDB:138168; OMIM:123889
A;Map position: 21922.1-21922.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-273 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: G06935
A; Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lutfalla, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
'ignment_block:
'-09-240-675-1_COPY_27_427 x G01418
                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: A45283 from: 1 to: 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: G01418
                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                        Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheArgValArgAlaGluGluGlyAsnSerThrSerSerTrpAsnGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCGTATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hrLysCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sAspGluAlaLysTrpLeuLysValProGluCysGlnHisThrThrThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArgThrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oTrpValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lAspProPheIleProPheTyrThrAlaHisMetSerProProGluVal 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                              Quality:
                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                     EMBL: U08988; NID: g571295; PID: g571296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366.50
3.524
78.195
                                                                              136.50
1.896
59.504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
Percent Identity:
                                                                                 Percent Identity:
                                                                                                                              Length:
                                                                                 33.058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
```

```
alignment_block:
US-09-240-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 21q
C; Keywords: transmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: A new member of the cytokine receptor gene family maps on chromosome A; Reference number: A47003; MUID:93300510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 16, 366-373, 1993
A;Title: A new member of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:A47003
                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Z17227; NID:g393378; PID:g393379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Lutfalla, G.; Gardiner, K.; Uze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A47003
                                                                                                                                                                                 Align seg 1/1 to: A47003
                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             okine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 eIleGlyProPro 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 GATTGGTCCTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 snileLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                          97 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTICITCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 380
yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                       TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                                    TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sCysMetAsnThrThrLeuThrGluCysAspPheSerSer.....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane proțein
                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ф
6
                                                                                                                                                                                                                           _COPY_27_427 x A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family class II protein CRF2-4 precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G01418
                                                                                                                                                                                                                                                                                                136.50
1.896
59.504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (man
                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                   to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273
                                                                                                                                                                                                                                                                                                  33.058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
```

21 a:

Ţ

```
A; Reference number: JC6311
A; Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: JC6311
R;Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A;Title: CRF2-4:isolation of cDNA clones encoding the human and mouse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: pir2:JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_27_427 x JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:U53696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-349 <GIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: JC6311 from: 1 to: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 GATTGGTCCTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
146 GGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAT 195
                                                                                                                                                                                                                                                                                               57 GluSerTyrArgSerPheGlnAspHis
                                                                                                                                                                                              40 rpGluValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr 56
                                                                                                                                                                                                                                                                                                                                               96 TCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                           46 GTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||:::||| :::::: :::|| ||| |||
| HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eIleGlyProPro 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sCysMetAsnThrThrLeuThrGluCysAspPheSerSer.....LeuS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG 233
                                                                                                                                                                                                                                                                                                                                                                                        LeuGlyGlyPheLeuLeuValProAlaLeuGly.....MetIleProPr 23
                                                                                                                                                 CAA.....AAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127.00
1.693
61.983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                   .....CysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.579
       82
                                                       289
                                                                                                     67
```

```
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M. Cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functionality A;Reference number: A49947; MUID:94170381
A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: preliminary
A:Molecule type: mRNA
A:Rollecule type: mRNA
A:Residues: 1-332 < KEMY
A:Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A:Cxperimental source: early B-cell line Y16
A:Experimental source: early B-cell backbone (NCBIN:145654, NCBIP:145656)
A:Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C:Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon gamma receptor beta subunit - mouse
N;Alternate names: IrN-gamma R beta chain; IrN-gamma R species-specific cofactor;
C;Species: Mus musculius (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: pir2:A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-240-675-1_COPY_27_427 x A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: A49947 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 yProProGluMet 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 TCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 ATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAACACTTCT 336
                                                                                                                                                                                                                                                                                                                                   228
                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 ACAGGAGCGATGAGTCT......GTCGGGAATGTGACT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 GluTrpValAsnVal...ThrPheCysProValGluAspThrIleIleGl 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 yrGlyAspTyrThrValArgValArgAlaGluLeuAlaAspGluHisSer
                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LeuGlyAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TTGTCCGCAGCCGCAGGTGGA.....AAAAATCTAAAATCTCC 98
                                                                                                                                                                 93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                     ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu 65
ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA 396
                                                 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                                        G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                       TyrSerPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120.00
1.500
61.538
                                                                                                                                                                                                                                                                                                                                                                                       .....IleAspGlySerTrpHisArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
30.769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
                                                                                                                                                                                                                                                                                                                                         271
                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                          76
```

```
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 *sequence_revision 16-Feb-1996 *text_change 05-Nov-1999
C;Accession: 138500; 138501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S cell 76, 793-802, 1994
A;Title: Identification and sequence of an accessory factor required for activation of A;Reference number: A49946; MUID:94170380
A;Accession: 138500
A;Molecule type: mRNA
A;Residues: 1-337 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 21
C; Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-63,'Q',65-337 <RE2>
A;Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
A;Experimental source: clone pJS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone pSKl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: p1r2:138500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon gamma receptor accessory factor-1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1_COPY_27_427 x I38500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                          104 GlyPheProMetAspPheAsnVal.....ThrLeuArgLeuAr 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 AGAATATTACTAGTACCAAATGCAACTTTTCTTCA........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 ATGACAACTTTATCCTGAGGTGG.........AACAGGAGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ArgProValValTyrArgValGlnPheLysTyrThrAspSerLys.... 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaAlaProProAs
   CACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA
                                                         gAlaGluLeuGlyAlaLeuHisSerAlaTrpValThrMetProTrpPheG
                                                                                                                   AGCAGAAAAAGAAAACACT...TCTTCATGGTATGAGGTTGACTCATTTA 361
                                                                                                                                                                                                                                                                                           hrGlnIleThrAlaThrGluCysAspPheThrAlaAlaSerProSerAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt snAlaGluGlnValLeuSerTrpGluProValAlaLeuSerAsnSerThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuTyrA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG
                                                                                                                                                                                                                                    .....CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAG 314
                                                                                                                                                                                                                                                                                                                                                                                                            ......TrpPheThrAlaAspIleMetSerIleGlyValAsnCysT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I38501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 138500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104.50
1.393
51.724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 7
Percent Identity: 25.517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 337
                                                                                                                                                                                                                                                                                                                                                     273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-
C;Accession: A31555
R;Aguet, M; Dembic, Z; Merlin, G.
Cell 55, 273-280, 1988
A;Title: Molecular cloning and expression of t
A;Reference number: A31555; MUID:89003065
A;Accession: A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superitamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein
seq_name: pir2:T27934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_27_427 x A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-489 <AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: A31555 from: 1 to: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                         130
                                                                                                                392 CAGAAGTA 399
                                                                                                                                                                       113 rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP
                                                                                                                                                                                                                                 342 GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                        99 TrpValArgValLysAlaArgValGlyGlnLysGlu.....SerAlaTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 GTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATG
                                                                                                                                                                                                                                                                                                                                               AAATTGCGTATAAGAGCA......GAAAAAGAAAACACTTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                         isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
                                                   roLysLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....GlnIleMetProGlnValProValPheThrValGluValLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lnHisTyrArgAsnValThrValGlyProProGlu 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.50
1.018
61.765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-Feb-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human interferon-gamma receptor
```

113

86

65

130 391 Genetics:

```
submitted to the EMBL Data Library, May 1996
A;Reference number: 220458
A;Accession: T28030
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, May 1996 A;Reference number: Z20442 A;Accession: T27934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Map position: 4
A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59
144/3; 6683/3; 6768/1; 6800/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-6831 <WIZ>
A; Cross-references: EMBL: Z73899;
A; Experimental source: clone ZK8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-6831 <WIL>
A;Cross-references: EMBL:273897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.la
A;Experimental source: clone ZK617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T27934; T28030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ZK617.1a - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_27_427 x T27934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:ZK617.la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Harris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
seq_name: pir2:S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: T27934 from: 1 to: 6831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics
                                                                                                                                                                                                                                                                                                                                                                                           1919
                                                            1967 1 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1906 TrpValPro......CysAlaLysValLysAspThrLysAlaHisIl 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1856 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh
                                                                                                                                                                     1951 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1889 luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg 1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 ATGTGACTTTTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 CTAAAATCTCCTCAAAAA......GTAGAGGTC...GACATCAT 122
                                                                                                                                                                                                                .....ccattt...cgcaaagctcagattggtcctccagaagt
                                                                                                                                                                                                                                                                                laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr
                                                                                                                                                                                                                                                                                                                                 CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                           eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG
                                                                                                                   399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.00
1.151
62.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 117
Gaps: 8
Percent Identity: 26.496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
                                                                                                                                                                          1967
                                                                                                                                                                                                                              398
                                                                                                                                                                                                                                                                                   1950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1872
```

```
A; Map position: IV
A; Anap position: IV
A; Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/.
A; Introns: 18/3; 69/3; 6808/3
C; Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homolog; Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homolog; Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homolog; serilog; Rof-98, 809-990, 991-1083,1084-1175.1178-1273,1474-1157,170-1864,2065-2158-2358-2.
96-5790, 6263-6356,6386-6478,6541-6633,6649-6742,6745-6838/Kegion: motif 2
F; 1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2.
23,4215-4313,4314-4415,4416-4516,4612-4710,4711-4811,4908-5009,5010-5109,5110-5210, F; 5940-6197/Domain: protein kinase homology < KINP
F; 5948-5956/Region: protein kinase ATP-binding motif
F; 5971/Active site: Lys *status predicted*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898
A;Experimental source: var. Bristol
R;Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 45-50, 1989
A;Title: Sequence of an unusually large protein implicated in regulation of myosin {
A;Accession: S06797; MUID:90044042
A;Accession: S06797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: myosin-regulating protein
N;Contains: protein kinase (EC 2.7.1.-)
C;Species: Caenorhabditis elegans
C;Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 18-Jun-1999
C;Accession: S57242; S07571; S06797; S57218
C;R:Benian, G.M.; L'Hernault, S.M.; Morris, M.E.
submitted to the EMBL Data Library, February 1993
A;Description: Additional sequence complexity within twitching of Caenorhabditis ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: var. Bristol R;Benlan, G.M.; L'Hernault, S.W.; Morris, M.E. Genetics 134, 1097-1104, 1993 Genetics 134,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   twitchin - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_427 x S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Experimental source: var. Bristol
C;Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,
A; Cross_references: EMBL:X1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 792-6839 <BEN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: S07571
A; Accession: S07571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: var. Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-6839 <BEN1>
A;Cross-references: EMBL:L10351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: unc-22
                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
1864 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh
                                                                                                    88 CTAAAATCTCCTCAAAAA......GTAGAGGTC...GACATCAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S57242
                                                                                                                                                                                                                                       to: S57242 from: 1 to: 6839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.00
1.151
62.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
8
26.496
                  1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded
```

2248

2296

2279 363 2263 2218

```
hypothetical protein ZK617.1b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #sext_change C;Accession: T27935; T28031
                                                                                                                            alignment_block:
US-09-240-675-1_COPY_27_427 x T27935
                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, May 1996 A; Reference number: Z20458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-7160 <WIL>
A; Cross-references: EMBL: 273897;
A; Experimental source: clone ZK61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: p1r2:T27935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z20442
A; Accession: T27935
                                                                                                                                                                                                                                                                                                                                                                             h;Map position: 4
h;Introns: 10/3; 61/3; 1
3067/1; 3141/3; 3269/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Nolecule type: DNA; Molecule type: DNA; Residues: 1-7160 <WI2>; Residues: 1-7160 <WI2>; Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
                                                                                   Align seg 1/1
                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: CESP: ZK617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number:
Accession: T28031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1959 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                        88 CTAAAATCTCCTCAAAAA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpValPro.....CysAlaLysValLysAspThrLysAlaHisIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTGACTTTTCATTCGATTATCAAAAA....ACTGGGATGGATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                           Ratio:
                                                                                   to: T27935
                                                                                                                                                                                                               84.00
1.151
62.393
                                                                                                                                                                                                                                                                                                                                                                             135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 6473/3; 7012/3; 7097/1; 7129/3
                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        997; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b
ZK617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1
                                                                                                                                                                                                                  Percent Identity:
                                                                                   to: 7160
.GTAGAGGTC..
                                                                                                                                                                                                                  26.496
                           GACATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266
                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                      542/3; 574/3;
                      A;Cross-references: EMBL:X95644; NID:gl199535; PIDN:CAA64904.1; PID:e223186; PID:g
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain $288C

R;BosKovic, J.; Saiz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.;
submitted to the EMBL Data Library, February 1996
A;Reference number: $67406
A;Accession: $67410
                                                                                                                                                                                               Yeast 12, 1077-1084, 1996
A;Title: The sequence of a 20.3 kb DNA fragment from the left arm A;Reference number: $72094; MUID:97051597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the Protein Sequence A; Reference number: S67629 A; Accession: S67650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X04423; NID:g3848; PIDN:CAA28019.1; PID:g3849 R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-306 <BAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Saccharomyces cerevisiae
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988
C;Accession: A25698; S67650; S67410; S72098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable protein kinase KIN28 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D2330; protein YDL108w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:A25698
                                                                                                      A; Molecule type: DNA
A; Residues: 1-306 <SAI>
                                                                                                                                                             A; Status: nucleic acid sequence
                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                   R;Saiz,
                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-306 < BOS>
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z74156; NID:g1431153; PIDN:CAA98675.1; PID:e253036; PID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-306 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: A25698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: KIN28, a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 5,
                                                                                                                                                                                                                                                            Cross-references: EMBL:x95644; NID:g1199535; PIDN:CAA64904.1; PID:e223186; Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F. east 12, 1077-1084, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simon, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2280 LysalaLysasnProTyraspGluProGlyLysThrGlyThrProAspVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGTGACTTTTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpValPro.....CysAlaLysValLysAspThrLysAlaHisIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; Seraphin, B.; 2697-2701, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                east split gene coding A25698; MUID:87053839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Faye,
                                                                                                                                                             not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a putative protein kinase homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change
```

18-Jun-1999

Ö.

Saccharomyces

PID:9

Revuelta, J.L.;

Length:

```
C:Superfamily: kinase-related transforming protein; protein kinase C:Keywords: ATP; phosphottansferase; serine/threonine-specific prot F:5-259/Domain: protein kinase homology KIN> F:13-21/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_427 x A25698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: MIPS:YDL108w; SGD:S0002266 A;Map position: 4L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position:
A; Introns: 10/1
C; Superfamily: human cytc
C; Keywords: heme; iron; c
F; 458/Binding site: heme
                                                                                                                                                                                                                                                                                           R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; submitted to the Protein Sequence Database, March 1998 A;Reference number: 215378 A;Reference number: 215378
                                                                                                                                                                                                                                                                                                                                                                                             ferulate-5-hydroxylase (EC 1....) - Arabidopsis thaliana
N;Alternate names: cytochrome P450-dependent monooxygenase; protein F23E13.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 29-Sep-1999
C;Accession: T04591
                     A;Map position: 4
A;Introns: 171/1: 314/3
A;Introns: 171/1: 314/3
A;Note: F732B13.110
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Superfamily: heme; iron; oxidoreductase
C;Keywords: heme; iron; oxidoreductase
                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-520 <BEV>
A; Cross-references: EMBL: AL022141
                                                                                                                                                               A;Experimental source: cultivar Columbia;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:T04591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: A25698 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 GACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 CCTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 spTrpProGluValSerSerPheMetThrTyrAsnLysLeuGlnIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 CATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 PheAlaGluLeuMetLeuArgIleProTyrLeuProGlyGlnAsnAspVa 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 TTTTCTTCACTCAAGCTG.............AATGTTTA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 leTrp......serValGlyValIle 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAAC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lAspGlnMetGluValThrPheArgAlaLeuGlyThrProThrAspArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCT...T 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluIleLeuThrSerAsnValValThrArgTrpTyrArgAlaProGlu..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......LeuLeuPheGlyAlaLysHisTyrThrSerAlaIleAspI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProPro 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.50
1.606
50.980
             iron
        (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 102
Gaps: 4
Percent Identity: 26.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306
                                                                                                                                                                                             BAC
                                                                                                                                                                                             clone F23E13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology
tein kinase
                                                                                                                                                                                                                                                                                                                                                                               Jesse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
```

alignment\_scores:

```
A; Experimental source: cultivar Columbia; C; Genetics:
A; Map position: 4
A; Introns: 47/3; 130/3; 163/1; 262/2
A; Note: F14M19.130
                                                                                                                                                                                                                                                                               R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Hoheisel, submitted to the Protein Sequence Database, March 1999
A;Reference number: 215262
A;Accession: T04239
A;Molecule type: DNA
A;Residues: 1-378 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F14M19.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T04239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:T04239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                alignment_scores:
                                                                                                                                                                                                                                                      A; Cross-references: EMBL: AL049480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: T04591 from: 1 to: 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-675-1_COPY_27_427 x T04591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 IleMetAspValMetPheGlyGlyThrGluThrValAlaSerAlaIle..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 CAGATTGGTCCTCCAGAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCT........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 luAspLeuLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .GluTrpAlaLeuThr.........GluLeuLeuArgSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluProGlyValProAsp 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spProThrSerTrpThrAspProAspThrPheArgProSerArgPheLeu 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eIleProLysLysSerArgValMetIleAsnAlaPheAlaIleGlyArgA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProLeuLeuHisGluThrAlaGluAspThrSerIleAspGlyPhePh 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yrLeuLysCysThrLeuLysGlu...ThrLeuArgMetHisproProIle 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .ValGlyLeuAspArgArgValGluGluSerAspIleGluLysLeuThrT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgValGlnGlnGluLeuAlaGluVal.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.00
1.137
46.795
82.50
1.269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
  Length:
Gaps:
                                                                                                                                                                                                                                      BAC
                                                                                                                                                                                                                                   clone F14M19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156
6
21.154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x T04239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: T04239 from: 1 to: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity: 58.559
                                                                                                                                                                                                                                                                                                                                     300 GluSerGluSerThrMetValTrpSerGluVal 310
                    319 GAAAAAGAAAACACTTCTTCATGGTATGAGGTT 351
                                                             288 ysProProThrValLysAsnLeuGluGluVal.....
                                                                                   278 AG......CTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA 318
                                                                                                                                   271 rGlyGluLeuGluValIleTyrAsnAlaLysGluAsnIleThrGlyLeuL 288
                                                                                                                                                                  228 GTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCA 277
                                                                                                                                                                                                  255 AsnIlePheGlyHisTrpAspArgThrValMetAlaLysAsnIleLysTh 271
                                                                                                                                                                                                                       184 TCATTC......GATTATCAAAAAACTGGGATGGATAAATTGGATAAAATT 227
                                                                                                                                                                                                                                                                    Percent Identity: 29.730
                                                                    .....Thr 299
```

. 08 . 91 . 79 . 99

23 24 25

.31

i P49792 homo sapiens i P43560 saccharomyces i P36418 dictyostelium i P49790 homo sapiens

C P 2 C

557

⋧

```
Swissprot_38:110R_MOUSE + Swissprot_38:110R_MOUSE + Swissprot_38:112R_HUMAN + Swissprot_38:NN53_ROTHW + Swissprot_38:NN53_ROTHW + Swissprot_38:P37_MYCGE + Swissprot_38:P37_MARPO + Swissprot_38:P37_MARPO + Swissprot_38:P37_MOUSE + Swissprot_38:P37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search
Query:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SwissProt_38:IL6B_RAT +
SwissProt_38:I10R_HUMAN
SwissProt_38:6DCS_SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database sequences:
Database length: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SwissProt_38:CRF4_HUMAN
SwissProt_38:INGS_HUMAN
SwissProt_38:INGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_38:KI28_YEAST
SwissProt_38:CP84_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_38: INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SwissProt_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SwissProt_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SwissProt_38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database: SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MODEL-frame+n2p.model -DEV-xlp -Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24686/app_guery.fasta.1 -Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24686/app_guery.fasta.1 -DB-Sw1sSProt_38 -OFMT=fastan -SUFFIX=modif.rsp -GAPCP=10.000 -GAPCP-0.000 -COPCL-0.000 -LOOPCL-0.000 -LOOPCL-0.000 -COPCL-0.000 -QAPCXT-0.000 -QAPCXT-0.000 -QAPCXT-0.000 -QAPCXT-0.500 -FGAPCP-10.000 -YGAPCXT-0.500 -FGAPCP-10.000 -YGAPCXT-0.500 -DELCOP-6.000 -FGAPCXT-7.000 -YGAPCP-10.000 -YGAPCXT-0.500 -DELCOP-6.000 -DELCOP-45 -DOCALION-200 -THR_SCORE-PCT -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0 -MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        information block:
US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Results were produced by Copyright (c) 1993-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quences: 83857
ngth: 30454973
(sec): 45.030000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Orig
N + 692.
N + 454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                         79.50 136.24 0.5854
78.50 137.32 0.8091
76.50 139.68 1.10
76.50 139.68 1.27
76.50 130.23 1.27
77.50 127.83 3.25
77.50 127.83 3.25
77.00 125.41 5.31
70.00 125.28 5.95
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 6.23
69.50 129.76 5.96
69.50 129.76 5.96
69.50 129.76 129.76
68.50 121.58 8.85
67.50 121.58 8.85
67.50 121.59 13.15
67.50 121.59 13.15
67.50 121.95 13.15
67.50 121.95 13.15
67.50 121.95 13.15
68.50 121.95 13.15
68.50 121.95 13.15
68.50 121.95 13.15
68.50 121.95 13.15
68.50 121.95 13.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104.50
85.50
83.50
                                                                                                                                       66.50
66.00
66.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the GenCore
Compugen Ltd
                                                                                                                                          112.03
                                                                                                                                  117.46 14.82

108.85 16.88

119.16 16.18

114.12 17.46

112.03 18.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     software, version
  out_format :
ID INRI_HUMAN STANDA AC PIT181;
DT 01-AUG-1990 (Rel. 15, DT 01-AUG-1990 (Rel. 139, DETA AUG-1990) (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:N358_HUMAN
SwissProt_38:YFE2_YEAST
SwissProt_38:VILI_DICDI
SwissProt_38:N153_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: SwissProt_38:INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colamonici O., Yan H., Domanski P., Handa R., Smalley D., Mullersman J., Witte M., Krishnan K., Krolewski J.; "Direct binding to and tyrosine phosphorylation of the alpha subunit of the type I interferon receptor by p135tyk2 tyrosine kinase."; Mol. Cell. B131-8133-8142(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE; 92129376.

Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;

"The structure of the human interferon alpha/beta receptor gene.";

J. Biol. Chem. 267:2802-2809(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          EMBL; J03171; AAA52730.1;
EMBL; X60459; CAA42992.1;
PIR; A32694; A32694.
PIR; S17112; S17112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uze G., Lutfalla G., Gresser I.; "Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERPERON ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION BY TYK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell 60:225-234(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IRNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND
EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
          436
457
557
220
                                                                                                                                                             27
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.00
65.00
65.00
                                                                                                                                                                                                                                            Glycoprotein; Signal; Polymorphism;
        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
109
106
102
```

EMBL outstation a collaboration -

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                        os os seq.
                                                                           seq_name:
                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                 US-09-240-675-1_COPY_27_427 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
MOD_RES
CARBOHYD
                                                             _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
     INR1_BOVIN STANDARD; PRT; 560 AA.

004790;
01-0CT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR
IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                           101
                                                                                                                                          301
                                                                                                                                                                        251
                                                                                                                                                                                                        201
                                                                                                                                                         84
                                                                                                                                                                                        67
                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                   ш
                                                                                                                                                                                                                                                                                   Quality: 692.00
Ratio: 5.203
Similarity: 100.000
                                                                                                                                                                                       AACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                         AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                              AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                   ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                         GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                      \verb|lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn|
                                                                                                                                                                                                                        ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
taurus
                                                                           SwissProt_38:INR1_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       17
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                               $
                                                                                                                                                                                                                                                                                                                                                                                                                                                              466
481
50
58
81
110
110
117
254
254
313
314
416
433
                                                                                                                                                                                                                                                                                                                                                                                                                                       17
63525
                                                                                                                                                                                                                                                                                                                                                                  INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                         Œ.
                                                                                                                                                                                                                                                                                                                                                                                         Percent
                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_002717.

G -> A (IN REF. 2).

; 0F6744C8A1ADBE73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY TYK2) PHOSPHORYLATION (BY TYK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ţ
                                                                                                                                                                                                                                                                                                                                                                                        Length: 133
Gaps: 0
Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                    .
6
                                                                                                                                                                                                                                                                                                                                                    557
                (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PROBABLE).
                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                          100
                                                                                                                                                                          300
                                                                                                                                                                                          84
                                                                                                                                                                                                         250
                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                         200
                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                       150
                                                                                                                                                                                                                                                                                      34
```

```
alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X68443; CAA48484.1; -
EMBL; L06320; AAA02571.1; -
PIR; S33770; S33770.
PIR; S27387; S27387.
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 93076908.

Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;

Mouchel-orantiviral activities of the human alpha inte

determined at the level of receptor (IFNAR) structure.

FEBS Lett. 313:255-259(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 93305725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae; Bos.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                           seg
ATGGTCGTCCTGCGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC 53
                                                           1/1
                                                             .
6
                                                                                                                                                                                                                                                                                    8
                                                             INR1_BOVIN
                                                                                                                                                         454.00
3.914
86.567
                                                                                                                                                                                                                                                                                                         437
458
560
220
220
254
172
254
434
422
                                                                                                                                                                                                                                                                                    63818
                                                                                                   ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                      MW.
                                                                                                     INR1_BOVIN
                                                                                                                                                                Percent
                                                           from: 1
                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

POTENTIAL.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                            Length:
Gaps:
Identity:
                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D
O
```

MetLeuAlaLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr

ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 103

```
seq_name: SwissProt_38:INR1_SHEEP
                                                                 Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;

Molecular cloning of ovine and botine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and pregnancy.";

Endocrinology 138:4757-4767(1997).

-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO INFORMATION OF A NUMBER OF PROTE: INCLUDING JAKS, TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTE: SUBUNITS THEMSELVES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eurheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERCERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
(INTERFERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INR1_SHEEP
Q28589; Q95206;
01-NOV-1997 (Re
                               <del>+</del> +
                                                                                                                                                                                                                                                                MEDLINE; 98006426.
Han C.-S., Mathial
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                          endometrium.";
J. Mol. Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-ENDOMETRIUM;
MEDLINE; 97135690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 al 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaluz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of an ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES CONCEPTUS AT DAY 15 OF PREGNANCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTGCGTATAAGAGCAGAAAAA...GAAAACACTTCTTCATGGTATGA
:::|||||||||||||||:::
GluLeuArgIleArgAlaGluGluGlyAsnAsnThrSerThrTrpTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAAATGCAACTITTCTTCACTCAAGCTG...AATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uGlyThrAspAsnTrpLysLysLeuSerGlyCysGlnHisIleThrSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGlnIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                         S., Fisher P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          17:207-215(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                  Kaluzova M., Sheldrick E.L., Flint A.P. interferon receptor and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                           TISSUES EXAMINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                           EXCEPT
                                                                                                            PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                  TYPE
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_427 x INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                      254
                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            154
                                                                                                                                                       104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U65978; / PFAM; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X95939;
                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                            65
                                                                                       49
                                                                                                                                  32
                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor;
                                                                                                                                                                                                 54
                                                                                                                                                                                                                          Ļ
                                                                                                                                                                                                                                              4
           CCAAATGCAACTTTTCTTCACTCAAGCTG...AATGTTTATGAAGAAATT
                                                                                                                                AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                              ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                        uGlyThrAspAsnTrpLysLysLeuProGlyCysGlnHisileThrSerS
                                                                 TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA
                                                                                                  AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC
                                                                                                                                                                           gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLysSer...GluA
                                                                                                                                                                                                                        erLysCysAsnPheSerSerValGluLeuLysAspValPheGluLysIle
                                                                                     SerSerGluSerValArgAsnValThrPheSerAlaAspTyrGlnIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                    to: INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                              560
                                                                                                                                                                                                                                                                                                                                                                                                        108
108
108
109
172
222
222
235
313
313
313
313
313
313
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB84231.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAA65183.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            A.
                                                                                                                                                                                                                                                                                                                                      439.00
3.851
                                                                                                                                                                                                                                                                                                                            85.075
                                                                                                                                                                                                                                                                                                                                                                                              63918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                                                            Percent Identity:
                                                                                                                                                                                                                                                                    from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                        Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                          -> G (IN REF. 2).
-> D (IN REF. 2).
E7198A1905D4805C CRC64;
                                                                                                                                                                                                                                                                                                                                      Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ormatics and the EMBL outstat
There are no restrictions on
ong as its content is in no
                                                                                                                                                                                                                                                                    560
                                                                                                                                                                                                                                                                                                                            67.910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                           82
                                                                                                                                 48
                                                                                                                                                                                                   103
98
                                                                                       65
                                                                                                                                                       153
                                                                                                                                                                              32
                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
```

```
seq_name: SwissProt_38:INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
                          CARBOHYD
CARBOHYD
CARBOHYD
                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                            TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
"Behavior of a cloned murine interferon alpha/beta receptor exp
in homospecific or heterospecific bactond.";
in homospecific or National Control Control
Proc. Nati. Acad. Sci. U.S.A. 89:4774-4778(1992).
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PRO
INCLUDING JAKS, TYRA, STAT PROTEINS AND IFN-R ALPHA-AND BET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P33896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFNAR1 OR IFNAR OR IFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INR1_MOUSE
                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>a</u>1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uValGluProPheValProPheLeuLysAlaGlnIleGlyProProAspV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŦΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABATTGCGTATAAGAGCAGAAAAA...GAAAACACTTCTTCATGGTATGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNITS THEMSELVES
                                                                                                                                                                                                                                                       A45283; A45;
MGI:107658;
                                                                                                                                                                                                                                                                                   M89641; AAA37890.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92262522
                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                         IFNAR
 413
65776
                                         590
590
220
220
109
181
214
314
                                                                                                                                                                                                                                          Glycoprotein;
  ₹
                            POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                    POTENTIAL.
POTENTIAL.
                                                                                                                            CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
 POTENTIAL.
7EC6DFF370185D3A CRC64;
                                                                                                               POTENTIAL
                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                               INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590
                                                                                                                                                                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF PROTEINS
O BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed
```

alignment\_scores:

```
alignment_block:
US-09-240-675-1_COPY_27_427
 seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
                                                                                                                                                                                                                                                                                                   Q08334;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
SEQUENCE FROM N.A.
MEDLINE; 96054036.
Lutfalla G., McInnis M.
                                                                                                                                                                                                                                                                                             CRFB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                             "A new member of the cytokine receptor gene family maps on chromosome 21 at less than 35 kb from IFNAR."; Genomics 16:366-373(1993).
                                                                                                                                                                                   TISSUE-FETAL BRAIN;
MEDLINE; 93300510.
Lutfalla G., Gardiner K.,
                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                      DUNO SAPARIS (AUMAN).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Entheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                             CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                              "Structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrLysCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGTCGTCCTGGGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheArgValArgAlaGluGluGlyAsnSerThrSerSerTrpAsnGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGCGTATAAGAGAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oTrpValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArgThrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                            lAspProPheIleProPheTyrThrAlaHisMetSerProProGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sAspGluAlaLysTrpLeuLysValProGluCysGlnHisThrThrT
                                                                                                                                                                                                                                                                                                                                                                                                                    SwissProt_38:CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366.50
3.524
78.195
                                                                             .G., Antonarakis S.E., Uz
n CRFB4 gene: comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×
                                                                                                                                                                                      Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                              325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590
                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.
                                                                               Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 632
                                                                                 its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
    OF RECEPTORS
                                                                                 IFNAR
```

\$\frac{1}{2} \frac{1}{2} \frac

```
alignment_block:
US-09-240-675-1_COPY_27_427 x CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A47003; A47003.
HSSP; P13726; 1DAN.
MIM; 123889; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 217227; CAA78933.1; -. EMBL; U08988; AAA86872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor;
                                                                                                                                                                                                                                                                                   184 TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
381 GATTGGTCCTCCA 393
                                                                                                                                        284 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 330
                                                                                                                                                                                                              234 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 283
                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                    ACTICITCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 380
                                                                                                                                                                                                                                                                                                                    {\tt snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe}
                                                                                                                                                                                                                                                                                                                                                       TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                            yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT.....
                                                                                                       erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                               ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy
                               HisSerAspTrpValAsnIle...
                                                                                                                                                                             sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: CRF4_HUMAN from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
20
221
250
66
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
102
161
124
269
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136.50
1.896
59.504
                                                                                                                                                                                                                                                                                                                                                                                                                             .CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 121
Gaps: 5
Percent Identity: 33.058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
A -> D (IN REF. 2).
FLGHP -> VGRME (IN REF. 2).
MISSING (IN REF. 2).
M: 66706C79F8514B23 CRC64;
                               ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOKINE RECEPTOR CLASS-II CRE2-4.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2)
                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                    52
                                                                                                         96
                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                    233
```

```
Seq_documentation_block:
ID INGS_HHMAN STANDA
AC P34848;
DT 01-OCT-1994 (Rel. 30,
DT 01-OCT-1994 (Ruman):
OC Eutheria; Primates; Carbon sepiens (Human):
CC INTERACT WITH GAR
CC -!- SUBCELLULAR LOCAT
CC -!- SUBCELLULAR LOCAT
CC -!- SUBCELLULAR CONTA
CC -!- SIMILARITY: EBLON
CC -!- SUBCELLULAR CONTA
CC -!-
                                          alignment_block:
US-09-240-875-1_COPY_27_427 x INGS_HUMAN
                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name:
Align seg 1/1 to: INGS_HUMAN
                                                                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1997 (Rel. 35, Last annotation update)
1NTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U05875; AAA16955.1; -. EMBL; U05877; AAA16956.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LUNG FIBROBLAST;
MEDLINE; 94170380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SwissProt_38:INGS_HUMAN
                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                   104.50
1.393
51.724
                                                                                                                                                                                                                                                                                                   37834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                   3
                                                                                                                                      Percent Identity:
  from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                   /FTId=VAR_002718.
18C61B10AD90E509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERFERON-GAMMA RECEPTOR BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                         o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Repeat.
337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                         25
                                                                                                                                                                                         145
```

34 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA...

::

81

:::==:::

LeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaAlaProProAs

```
seq_name: SwissProt_38:INGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            P15260;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
                                                                                                                                                                      Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gar "Alignment of disulfide bonds of the extracellular domain interferon gamma receptor and investigation of their role biological activity.";
Biochemistry 32:2423-2430(1993).
                                           Walter M.R., Windsor W.T., Nagabhushan T.L., Zauodny P.J., Narula S.K.; "Crystal structure of a complex between inter soluble high-affinity receptor."; Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                  Aguet M., Dembic Z., Me
"Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE: 89003065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                         MEDLINE; 95342235.
                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF
                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                    DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                X-RAY CRYSTALLOGRAPHY (2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGACAACTTTATCCTGAGGTGG......AACAGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgProValValTyrArgValGlnPheLysTyrThrAspSerLys....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \verb|snAlaGluGlnValLeuSerTrpGluProValAlaLeuSerAsnSerThr|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gAlaGluLeuGlyAlaLeuHisSerAlaTrpValThrMetProTrpPheG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyPheProMetAspPheAsnVal.....ThrLeuArgLeuAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrGlnIleThrAlaThrGluCysAspPheThrAlaAlaSerProSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pProLeuSerGlnLeuProAlaProGlnHisProLysIleArgLeuTyrA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lnH1sTyrArgAsnValThrValGlyProProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCAGAAAAAGAAAACACT...TCTTCATGGTATGAGGTTGACTCATTTA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAATATTACTAGTACCAAATGCAACTTTTCTTCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....TrpPheThrAlaAspIleMetSerIleGlyValAsnCysT
                                                                                                                                                                                                                                                                                                    55:273-280(1988).
                                                                                                                                                                                                                                                     93183911
 98035727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                  Merlin
                                                                                                                                                                                                                                                                                                                                     expression
                ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                    <u>ဂ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                     of.
                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                              interferon-gamma
                                                                                                                                                                                                                                                                                                                                     human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                  28-122 COMPLEX WITH ANTIBODY
                                                                                                                                           26-248
                                                                                                           Lundell D.J., Lunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CDW119).
                                                                                                                                                                                                       Garotta G.;
nain of the
ole in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                               and
                                                                               148
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x INGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Neutralizing epitopes on the extracellular interferon gamma receptor (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex."; J. MOl. Biol. 273:882-897(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- PIM: PHOSPHORYLARED AT SER/THR RESIDUES.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sogabe S., Stuart F., Henke Winkler F.K., Robinson J.A.;
                                                                                           104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                              154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .mmunoglobulin
                                                              34
                                                                                                                           17
                                                                                                                                                             57
                                                                                                                                                                                            \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERFERON-GAMMA DIMER.
                           AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                             MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl
                                                                                                                                                                                                                         GTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A31555; A31555.
                                                              snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr
                                                                                                                             aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA
                                                                                                                                                            GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1JRH; 25-MAR-98.
.GlnIleMetProGlnValProValPheThrValGluValLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein; Signal; Phosphorylation
                                                                                                                                                                                                                                                          .
С
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stuart F., Henke C., Bridges A., Williams G.,
                                                                                                                                                                                                                                                          INGR_HUMAN from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain;
                                                                                                                                                                                                                                                                                                                                        85.50
1.018
61.765
                                                                                                                                                                                                                                                                                                                                                                                                                                           54404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                           ME.
                                                                                                                                                                                                                                                                                                                                            Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERFERON-GAMMA RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                            to: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                              24.265
   65
                                                                  50
                                                                                              153
                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birch A.,
```

```
seq_name: SwissProt_38:KI28_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saiz J.E., Buitrago M.J., Garcia R., Revuelta J.L., del Rey F "The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevisiae chromosome IV contains the KIN28, MS: PHO2, POL3 and DUN1 genes, and six new open reading frames."; Yeast 12:1077-1084(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIN28 OR YDL108W OR D2330.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
SERINE/THREONINE-PROTEIN KINASE KIN28 (EC 2
EMBL; X04423; CAA28019.1; -.
EMBL; X95644; CAA64904.1; -.
EMBL; Z74156; CAA98675.1; -.
PIR; A25698; A25698.
                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: PROTEIN KINASE ESSENTIAL FOR CELL PROLIFERATION.
FUNCTION IN ASSOCIATION WITH CYCLIN CCL1.
-!- SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY OF SER/THE
                                                                                                                                                                                                                                                                                                                                                                                                                              J. Mol. Biol. 234:307-310(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 94047081.
Valay J.G., Simon M., Faye G.;
"The kin28 protein kinase is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 87053839.
Simon M., Seraphin B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / FY1679;
MEDLINE; 97051597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 5:2697-2701(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "KIN28, a yeast split gene coding homologous to CDC28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 CAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASSOCIATION WITH CCL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KI28_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 TrpValArgValLysAlaArgValGlyGlnLysGlu.....SerAlaTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATTGCGTATAAGAGCA......GAAAAAGAAAACACTTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                              PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roLysLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
(EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            putative protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
                                                                                                                                                                                                                                                      a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSS2,
                                                                                                                                                 .ch/announce/
```

```
seq_documentation_block:
ID CP84_ARATH STANDA
AC Q42600;
DT 15-DEC-1998 (Rel. 37,
DE CYTOCHROME P450 84A1
GN CYTOCHROME P450 84A1
GN CYP84A1 OR FAH1 OR F20
OS Arabidopsis thaliana
OC Eukaryota; Viridiplan
OC euphyllophytes; Sperm
OC core eudicots; Rosida
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RX MEDLINE; 96293440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                       seq_name: SwissProt_38:CP84_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-240-675-1_COPY_27_427 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOTTT TENEDRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                       Q42600;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 84A1 (FERULATE-5-HYDROXYLASE) (EC 1.14.-.-) (F5H).
CYP84A1 OR FAH1 OR F23E13.110.
Arabidopsis thallana (Mouse ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P24941; 1.
TRANSFAC; T0219
SGD; L0000905;
PROSITE; PS0010
PROSITE; PS0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          245
                                                                                                                                                                                                                                                                                                                                                                                             388
                                                                                                                                                                                                                                                                                                                                                                                                                                228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; L0000905; KIN28.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 GACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leTrp.....SerValGlyValIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluIleLeuThrSerAsnValValThrArgTrpTyrArgAlaProGlu..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l division.
AIN 7
BIND 13
BING 36
DING 36
SITE 129
                                                                                                                                                                                                                                                                                                                                                          ProPro 246
                                                                                                                                                                                                                                                                                                                                                                                             CCTCCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCT...T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITTCTTCACTCAAGCTG......AATGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spTrpProGluValSerSerPheMetThrTyrAsnLysLeuGlnIleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt lAspGlnMetGluValThrPheArgAlaLeuGlyThrProThrAspArgA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheAlaGluLeuMetLeuArgIleProTyrLeuProGlyGlnAsnAspVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....LeuLeuPheGlyAlaLysHisTyrThrSerAlaIleAspI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: KI28_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą,
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.50
1.606
50.980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290
21
36
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KI28_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
GF; 763A5720A1D9ACF3 CRC64;
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Gaps:
                                                                                                                                                                                                                                                                     520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102
4
26.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264
```

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SO TENERS OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_427 x CP84_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: CP84_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1998) to the EMBL/GenBank/DDBJ database --- PATHWAY: GENERAL PHENYLPROPANOID PATHWAY. --- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. COLUMBIA;
Bevan M., Hilbert H., Braun M., Holzer E.,
Hohelsel J., Jesse T., Heijnen L., Vos P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase: Monooxygenase; Membrane; Heme.
BINDING 458 458 HEME (BY SIMILARITY).
SEQUENCE 520 AA; 58720 MW; E812779AF5BF01BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL022141; CAA18128.1; -.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450;
PFAM; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U38416; AAC49389.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meyer K., Cusumano J.C., Somerville C.R., Chapple C.C.S.; "Ferulate-5-hydroxylase from Arabidopsis thaliana defines a family of cytochrome P450-dependent monooxygenases."; Proc. Natl. Acad. Sci. U.S.A. 93:6869-6874(1996).
   401
                                                                                                                                                                                                                                                                                                                                                                                                                                    353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGATGGTCGTCCTGGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                     AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleMetAspValMetPheGlyGlyThrGluThrValAlaSerAlaIle..
eIleProLysLysSerArgValMetIleAsnAlaPheAlaIleGlyArgA
                                                                                                                                          ProLeuLeuHisGluThrAlaGluAspThrSerIleAspGlyPhePh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         luAspLeuLys........
                                                                                                                                                                                                                     AAATTGCGTATAAGAGCAGAAAAAAGAAAACACTTCT........
                                                                                                                                                                                                                                                                                                                                                            GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgValGlnGlnGluLeuAlaGluVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                    .ValGlyLeuAspArgArgValGluGluSerAspIleGluLysLeuThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .GluTrpAlaLeuThr.................GluLeuLeuArgSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.00
1.137
46.795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brandt A., Do
Mewes H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156
6
21.154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duesterhoeft
       418
                                                                                                                                                                                                                                                                                                                                                                                                                                       369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                           336
                                                                                                                                              401
                                                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                             384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mayer
Seq_documentation_block:
ID I16B_RAT STANDARD;
AC P4190;
DT 01-FEB-1995 (Rel. 31, Last
DT 11-JUL-1999 (Rel. 38, Last
DT 11-JUL-1999 (Rel. 38, Last
DE 115-JUL-1999 (Rel. 38, Last
DE 15-JUL-1999 (Rel. 38, Last
DE 15-JUL-199 (Rel. 38, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: SwissProt_38:IL6B_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT transducing molecule, 9p130.";

RI Genomics 14.666-672(1992).

C: I--6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION, BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, CRESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, CAND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).

C: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C: ISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS AND ENDOTHELIAL CELLS.

C: SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

C: SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

C: SIMILARITY: BELONGS TO THE CYTONINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M92340; -; NOT_ANNOTATED_CDS
PIR; A44257; A44257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, LAST Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wang Y., Nesbitt J.E., Fuentes N.L., Fuence Mand Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGATTGGTCCTCCAGAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluProGlyValProAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spProThrSerTrpThrAspProAspThrPheArgProSerArgPheLeu 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                       CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN-6 RECEPTOR BETA CHAIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuller G.M.;
lon of the rat liver IL-6 signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
```

domain; Signal;

Rattus Mammalia;

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID I10R_HUMAN STAN
                           seq_name: SwissProt_38:I10R_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: IL6B_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-240-675-1_COPY_27_427 x IL6B_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                       279
                                                                                                                                                                                                                                           263
                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                           113 TCGACATCATAGATGAC.....
                                                                                                                                                                                                                                                                                                                                                                                                198 uAlaGluAsnAlaLeuGlyAsn.....ValSerSerGluProIleAsnP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                     182 MetMetGlyTyrThrProIleTyrPheValAsnIleGluValTrpValGl 198
                                                                                                       331 ACTTCTTCATGGTATGAGGTTGACTCATTTACACCA.....TTTCGCAA 374
                                                                                                                                                                295
                                                                                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                               246 rGlyLeuAspSerIleLeuArgLeuLysSerAspIleGlnTyrArgThrL
                                                                 375 AGCTCAGATT 384
                                                                                                                                                              lPheArgIleArgSerIleLysGluAsnGlyLysGlyTyrTrpSerAspT 312
                                                                                                                                                                                 ProArgThrSerPheThrValGlnAspLeuLysProPheThrGluTyrVa 295
                                                                                                                                                                                                                                           ysAspAlaSerThrTrpIleGlnValPro...LeuGluAspThrValSer
                                                                                                                                                                                                                                                             CTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGT 252
                                                                                                                                                                                                                                                                                                  GAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAA 202
                                                                                                                                                                                                                                                                                                                    ThrAsnSerGluGluLeuSerSerIleLeuLysLeuAlaTrpValAsnSe
                                                                                                                                                                                                                                                                                                                                                          heAspProValAspLysValLysProSerProProHisAsnLeuSerVal 229
                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTT 62
                                                                                                                        rpSerGluGluAlaSerGlyThrThrTyrGluAspArgProSerLysAla 328
                                                                                                                                                                                                                       ACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTATGAAGAAATTAA 302
                                                                                    ProSerPheTrpTyrLysValAsnAlaAsnHisProGlnGluTyrArgSe 345
                                                                                                                                                                                                                                                                                                                                    .....AACTTTATCCTGAGG.....TGG...AACAG 152
                                               rAlaArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
61
83
131
157
226
226
382
389
                                               348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.50
1.019
45.882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
43
61
131
131
131
131
131
131
131
205
226
389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9E18B6FECFF087F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            918
 Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170
                                                                                                                                                                                                                                                                                , 263
                                                                                                                                                                                  330
                                                                                                                                                                                                                                           278
                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                               19
                                                                                     v
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: I10R_HUMAN from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                          US-09-240-675-1_COPY_27_427 x IIOR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE; 94165477.

Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;

"Expression cloning and characterization of a human IL-10 receptor.

J. Immunol. 152:1821-1829(1994).

J. Immunol. 152:1821-1829(1994).

J. IMMUNOL. RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         013651;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PEMC. FAINT EXPRESSION
IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENT
LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U00672; AAA17896.1; -. MIM; 146933; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                    104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL10RA OR IL10R
                                                                                                                                                         54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                     4 ATGGTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
erValTrpPheGluAlaGluPhePheHisHisIleLeuHisTrpThrPro
                                                                                                                                                                                                              LeuValValLeuLeuAlaAla....LeuLeuSerLeuArgLeuGly..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
236
257
257
202
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.00
1.026
58.915
                                                                                                         .SerAspAlaHisGlyThrGluLeuProSerProProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189
62903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERLEUKIN-10 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EE1B29064338157C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                          578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
6
24.031
                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ë
```

AGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAAAAC

Quality:

```
seq_name: SwissProt_38:6DCS_SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
01-AUG-1992 (Rel. 26, Last annotation update)
NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
                                                                                                                                                                                                                                                                                                                                                                                                         the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Induced plant responses to pathogen attack. Analysis and heterologous expression of the key enzyme in the biosynthesis of phytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63)."; Eur. J. Blochem. 196:423-430(1991).

-i- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF 4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF GLYCEOLLIN TYPE PHYTOALEXINS.

-i- PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycine max (Soybean)
PFAM; PF00248; aldo_ket_red; 1.
Flavonoid biosynthesis; Oxidoreductase; NADP.
SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;
                                                                                                            PRINTS; PR00069; ALDKETRDTASE
PROSITE; PS00062; ALDCKETO_REDUCTASE_3;
PROSITE; PS00063; ALDCKETO_REDUCTASE_1;
PROSITE; PS00798; ALDCKETO_REDUCTASE_1;
                                                                                                                                                                                                                                                                                                 EMBL; X55730; CAA39261.1; -. PIR; S14222; S14222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Fundamental statement of the fundament of the fundamental statement of the fundament of the fundamental statement of the fundame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- INDUCTION: BY PATHOGEN ATTACK.
-1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rValThrAsnThrArgPheSerValAspGluValThr 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrArgAlaArgValArgAlaValAspGlySerArgHisSerAsnTrpTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTAAATTGCGTATAAGAGCA...GAAAAAGAAAACACTTCTTCATGG..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt rGlyIleGluSerTrpAsnSerIleSerAsnCysSerGlnThrLeuSer.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleProAsnGlnSerGluSerThrCysTyrGluValAlaLeuLeuArgTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHYTOALEXINS IN SOYBEAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....TyrAspLeuThrAlaValThrLeuAspLeuTyrHisSerAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schroeder G., Schiltz E., Grisebach H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315
                                                                                                                       느무느
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schroeder J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
```

alignment\_scores:

```
alignment_block:
US-09-240-675-1_COPY_27_427 x 6DCS_SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: SwissProt_38:I10R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: 6DCS_SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       MEDLINE; 94068585.

HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;

"A receptor for interleukin 10 is related to interferon receptors.";

Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).

-!- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: TYPE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O61727:
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 LysSerLeuLysThrLeuGlnLeuGluTyrLeuAspLeu.......
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC; MEDLINE; 94068585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IL10RA OR IL10R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 aPheSerProLeuArgLysGlyAlaSerArgGlyProAsnGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I 10R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGAAAACACTTCTTCATGGTATGAG...........GTTGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laThrIleArgProValValAspGlnValGluMetAsnLeuAlaTrpGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTTACACCATTTCGCAAA...GCTCAGATTGGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnLysLysLeuArgGluPheCysLysGluAsnGlyIleIleValThrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heProIleGluValGluAspLeuLeuProPheAspValLysGlyVal...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCATTCGAT......TATCAAAAACTGGGATGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .TyrLeuIleHisTrpProLeuSerSerGlnPro...GlyLysPheSerP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eGlyValSerAsnPheSerValLysLysLeuGlnAsnLeuLeuSerValA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AACTTTTCTTCACTCAAGCTGAAT.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......GTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .TrpGluSerMetGluGluCysGlnLysLeuGlyLeuThrLysAlaIl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.50
1.048
55.303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
```

```
alignment_scores:
Quality:
Ratio:
Percent Similarity:
          alignment_block:
US-09-240-675-1_COPY_27_427 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SO STATE TO SECOND
                                                                                                                                                            seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: I10R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                    documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
SIGNAL
                                         P40189:
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA)
6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130)
RECEPTOR) (CDW130) (CD130 ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGD;
                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TCCTGAGGTGG.....AACAGGAGCGATGAGTCTGTCGGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                    Homo sapiens
                                 IL6ST.
                                                                                                                          IL6B_HUMAN
                                                                                                                                                                                                                               105 AlaValAspAsnSerGlnTyrSerAsnTrpThrThrThrGluThrArgPh
                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                           71
                                                                                                                                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                                                                                                                                                                                                                                       42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 CTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                 ) TACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTA
                                                                                                                                                                                   eThr 122
                                                                                                                                                                                                                                                     GCA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCA...TT
                                                                                                                                                                                                                                                                            heThrLeuAspLeuTyrHisArgSerTyrGlyTyrArgAlaArgValArg
                                                                                                                                                                                                                                                                                                   TCAAGCTGAATGTTTATGAAGAA.....ATTAAATTGCGTATAAGA
                                                                                                                                                                                                                                                                                                                          pIleHisIleCysArgLysAlaGlnAlaLeuSerCysAspLeuThrThrP
                                                                                                                                                                                                                                                                                                                                                 ATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                       ValAlaLeu.....LysGlnTyrGlyAsnSerThrTrpAsnAs
                                                                                                                                                                                                                                                                                                                                                                                              GTGACTTTTTCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                      leLeuHisTrpLysProIleProAsnGlnSerGluSerThrTyrTyrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uLeuProSerProSerTyrValTrpPheGluAlaArgPhePheGlnHisI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuValThrIleSerSerLeuSerLeuGluPheIleAlaTyrGlyThrGl
                                                                                                                                                            SwissProt_38: IL6B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:96538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
263
204
50
66
113
182
238
(Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA16156.1;
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.50
1.062
61.017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL10RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
64248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 575
241
262
262
575
225
20
50
66
113
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal.
POTENTIAL.
INTERLEUKIN-10 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I10R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
POTENTIAL.
          Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          820B9CD576F686B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                          918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575
          Vertebrata; Mammalia
                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
5
23.729
                                                                                                                                                                                                                                                                                                    315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                      359
                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                 274
                                                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                                                                               224
                                                                                                                                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
                                                                  (INTERLEUKIN
                                                      (ONCOSTATIN
          A Bravo J. Staunton D., Heath J.K., Jones E.Y.;

A Bravo J. Staunton D., Heath J.K., Jones E.Y.;

A Proposed Structure of a cytokine-binding region of gp130.*;

EMBO J. 17:1665-1674(1998).

C -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6. LIF. OSM. CNTF. AND IL-61L-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN CHAPTACH CONTROL EXCEPTION: TYPE INDUIT HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C -1- SUBGELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -1- SINGLARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

WWW-"http://www.nobi.nlm.nlh.gov/prow/cd/cdd30.htm".
                                                                                                                                                                                                                                                                                       PFAM; PF00041; fn3;
Receptor; Transmembr
Repeat; 3D-structure
SIGNAL 1
                                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                   DOMAIN
                   CARBOHYD
CARBOHYD
                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91084844.
Hibi M., Murakami M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Primates; Catarrhini; [1]
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M57230; AAA59155.1; -. PIR; A36337; A36337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                      TRANSMEN
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63:1149-1157(1990).
                                                                                                                                                                                                                                                                                                    3D-structure
                                                                                                                                                                                                                                                                                                                                     PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98169383.
                                                                                                                                                                                                                                                                                                              Transmembrane;
      564
918
                                                                                                                                                                                                                                                                                                                                                                        26-AUG-98
                                43
131
157
227
227
379
383
383
553
         ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND PLACENTA;
                                103522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression
                                                                                                                                                                                                                                                                                                               Glycoprotein;
          ₹.
                   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                 FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                           SER-RICH
                                                                                                                                                                     FIBRONECTIN
FIBRONECTIN
                                                                                                                                                                                                                    FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                INTERLEUKIN-6
EXTRACELLULAR
                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hirano T., Taga T.,
on of an IL-6 signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo
          D813F3672DD10D53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 122-325
                                                                                                                                                                                                                                                                                                               Immunoglobulin domain;
                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                            RECEPTOR BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kishimoto T
transducer,
                                                                                                                                                                                                                                                                                                              Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T : ;
```

```
seq_documentation_block:
ID I12r_HUMAN STANDA
AC P42701:
DT 01-NOV-1995 (Rel. 32,
DT 01-NOV-1995 (Rel. 32,
DT 15-JUL-1999 (Rel. 38,
DT 15-JUL-1999 (Rel. 38,
DT 15-JUL-1999 (Rel. 38,
DE INTERLEUKIN-12 RECEPT
GN IL12RB OR IL12RB OR
GN IL12RB1 OR IL12RB OR
GN Eukaryota; Metazoa; C
CC Eutherla; Primates;
CC Eutherla; Primates;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94267217.
RA Chua A.O., Chizzonite
RA Gubler U;
RT "Expression cloning of the cytokine recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-240-675-1_COPY_27_427 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: SwissProt_38:I12R_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253
                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN PRECURSOR
IL12RB1 OR IL12RB OR IL12R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 TAGAG.....GTCGACATCATAGATGACAACTTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 SerThrValTyrPheValAsnIleGluValTrpValGluAlaGluAsnAl
                                                                 SEQUENCE FROM N.A.
MEDLINE; 94267217.
Chua A.O., Chizzonite R., De
Minetti L.J., Warrier R.R.,
                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 IleAsp 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 GTTGAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
    "Expression cloning of a human IL-12 receptor component. A new member of the cytokine receptor superfamily with strong homology to gpl30.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerIleLeuLysLeuThrTrpThrAsnProSerIleLysSerValIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....CTGAGGTGG...AACAGGAGCGATGAGTCTGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alLysProAsnProProHisAsnLeuSerVallleAsnSerGluGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aLeuGlyLysValThrSerAspHisIleAsnPheAspProValTyrLysV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTGGAAAA......AATCTAAAATCTCCTCAAAAAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAGAAAAC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValGlnAspLeuLysProPheThrGluTyrValPheArgIleArgCysMe 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erGlnIleProPro...GluAspThrAlaSerThrArgSerSerPheThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eIleLeuLysTyrAsnIleGlnTyrArgThrLysAspAlaSerThrTrpS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lylleThrTyrGluAspArgProSerLysAlaProSerPheTrpTyrLys 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....ACTTCTTCATGGTATGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tLysGluAspGlyLysGlyTyrTrpSerAspTrpSerGluGluAlaSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL6B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.50
1.077
46.711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL6B_HUMAN
                                                                   Desai B.B., Truitt T.P., Nunes
., Presky D.H., Levine J.F., Gai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                            662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       918
                                                                                                                                                                                                                                                                                                                                                                            ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
6
21.711
                                                                                                                                                                                                                                                                  (IL-12R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                     Gately M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x I12R_HUMAN
                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                          Align seg 1/1 to: I12R_HUMAN
                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat.
SIGNAL
                                                                                                                                                            107 ValLeuTyrThrValThrLeuTrpValGluSerTrpAlaArg...AsnGl 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00340; RECEPTOR_CYTOKINES_2; PFAM; PF00041; fn3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U03187; AAA21340.1; -.
MIM; 601604; -.
 183
                        156
                                                                                                                 122
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                      84 AAATCTAAAATCTCCTCAA.....
                                                                                                                                                                                     34 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAA
                    ArgMetGluTrpGluThrProAspAsnGlnValGlyAlaGluValGlnPh
                                                                                                               {\tt nThrGluLysSerProGluValThrLeuGlnLeuTyrAsnSerValLysT}
TTCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTG
                                            ATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG...AATGTGACTTT
                                                                  yrGluProProLeuGlyAspIleLysValSerLysLeuAlaGlyGlnLeu
                                                                                       Quality:
                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                  75.50
1.020
52.857
                                                                                                                                                                                                                                                                                                                                      442 P
456 P
662 K
73108 MW;
                                                                                                                                                                                                                                                                                                                                                                                   3444
3459
3444
3469
                                                                                                                                                                                                            from: 1 to:
                                                                                                                                                                                                                                                                    Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
KAKM -> DE
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN
                                                                                                                                                                                                                                                                                                                                      KM -> DE (IN A SHORTER FORM).
541ADA60F62DA1EF CRC64;
                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                            662
                                                                                                                                                                                                                                                                 27.143
                                                                                                                                                                                                                                                                                           140
                                                                      155
                                                                                                                    139
                                                                                                                                         102
                                               182
```

```
sp_nammal:018966
sp_plant:09XFM2
sp_rodent:007313
sp_rodent:007313
sp_rodent:007280
sp_rodent:007311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
Query: US-09-240-675-1_COPY_27_427
Query length: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database sequences: 225878
Database length: 69334122
Search time (sec): 89.94000
                                          sp_virus:039225
sp_invertebrate:002424 +
sp_invertebrate:023047 +
sp_bacteria:034739 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_invertebrate:045604
sp_virus:065525
+
sp_fungi:008773 +
                                                                                                                                                                                           sp_invertebrate:061210
                                                                                                                                                                                                                                 sp_invertebrate:Q25994
sp_plant:Q92Q67 +
                                                                                                                                                                                                                                                                                                      sp_rodent:007310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_invertebrate:076835
sp_mammal:018965 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_bacteria:085940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:Q18876
sp_plant:Q41577 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rodent:Q62478
sp_plant:Q39688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_invertebrate:076514 + sp_human:Q9Y5T6 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_invertebrate:Q20930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_fung1:Q06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_human:Q10466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_vertebrate:013048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:Q23020 +
sp_invertebrate:Q23550 +
sp_invertebrate:Q23551 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_human:Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_vertebrate:Q9YGC8 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_rodent: Q63953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rodent:Q61190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_vertebrate:Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score_list:
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_mammal:Q28733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MODEL-frame+_n2p.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/USO9240675/runat_30052000_164313_24664/app_query.fasta.l
-DB-SPTREMBL_12 -QFMT-fastan -SUFFIX-modif.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINANCH-0.100 -LOOPEL-0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Results were produced by Copyright (c) 1993-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strd Orig

100 + 248.50

+ 127.00

+ 120.00

100 + 104.50

100 + 104.50
+
                                                                                                                                                                                           +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y the Gent
Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e GenCore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 i Ogygce gallus (chicken).

484 i Ol4936 homo sapiens (human). in

6048 i Ol23020 caenorhabditis elegan

66 6831 i O23550 caenorhabditis elegan

7160 i O23551 caenorhabditis elegan

402 i Ol3048 xenopus laevis (african

26926 i Ol3046 homo sapiens (human).

442 i O06349 saccharomyces cerevisiae

1083 i O45604 caenorhabditis elegan

733 i O45604 caenorhabditis elegan

733 i O4570 bovine group c rotavirus

1120 i O08773 saccharomyces cerevisia

1120 i O08773 saccharomyces cuniculus (
365 i O20930 caenorhabditis elegan

6875 i O20930 caenorhabditis elegan

6875 i O20931 caenorhabditis elegan

6875 i O39586 homo sapiens (human). b

212 i O995t6 homo sapiens (human). b

213 i O39688 daucus carrota (carrot).

426 i O18876 caenorhabditis elegans

316 i O2677 triticum aestivum (wheat
           3168 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 | 368 |
                                                                                                                                                                                                                  1 085940 sphingomonas aromaticivo (1076835 caenorhabditis elegans (108965 bos taurus (bovine). eag (108966 bos taurus (bovine). eag (108967 arattus norvegicus (rat) (107313 rattus norvegicus (rat) (107313 rattus norvegicus (rat) (107312 rattus norvegicus norvegicus norvegicus (107312 rattus n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     out_format :
                                                                            1 061210 caenorhabditis elegan
039225 murine hepatitis virus
1 002424 caenorhabditis elegans
1 023047 caenorhabditis elegans
           34739 bacillus
Q23552 caenor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 gallus gallus
0 mus musculus
3 mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_plant:023357
sp_plant:041442
sp_plant:039658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-09-240-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQUETTE RAPPOCO OF THE RESERVE OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name:
       seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                    124
                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                         304
                                                                                                                                                                                                                                                                                                                                                                                                                                                       254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFNAR1.
                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID Q9YHW0 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_vertebrate:Q9W669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-240-675-1_COPY_27_427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REBOUL J., GARULMER A., "Comparative genomic analysis receptor gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9YHW0;
01-MAY-1999 (TrEMBLrel. 10, Creat
01-MAY-1999 (TrEMBLrel. 10, Last
01-MAY-1999 (TrEMBLrel. 10, Last
INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 0:0-0(1999).
EMBL; AF082664; AAD13669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                           TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAATGTGACTTTTTCATTCGATTATCAA......AAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAAATGCAACTTTTCATCAACTCAAGCTGAATGTTTATGAAGAAATTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laValAsnThrAsnPheThrLeuMetTrpAsnTyrThrGlyAspGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sCysAlaGlyGlnThrAsnLeuLysSerProGlnAspIleGlnValTyrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
                          TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTA
                                                                                                                       TTGCGTATAAGAGCAGAA....AAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                             {\tt rSerGluProGluTrpLysGluLeuSerGlyCysGlnAsnValSerHisTlumberGluProGluTrpLysGluLeuSerGlyCysGlnAsnValSerHisTlumberGluProGluTrpLysGluLeuSerGlyCysGlnAsnValSerHisTlumberGluProGluTrpLysGluLeuSerGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlnAsnValSerHisTlumberGlyCysGlyCysGlnAsnValSerHisTlumberGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCysGlyCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...AsnValThrPheSerAlaGlnTyrGlnCysPheAspAspLeuGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyArgLeuAlaAlaValLeuLeuCysValLeuValValValSerArgCy
ePheGluMetIleProTyrGluIleAlaGlnIleGlyProProGluIle
                                                                                                                                                                                                                                                     hrGluCysAspPheSerSerAlaIleThrAlaTyrTyrAspThrHisHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_vertebrate:Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GARDINER K., MONNERON ve genomic analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMHA60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248.50
2.824
66.165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.50
68.00
68.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            x Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
122
120
119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ç
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F99BC099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
17
17
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 74
. 96
. 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687
407
509
568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           023357
Q41442
Q39658
Q9w669
                                                                                                                              124
                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                    303
                                                                                                                                                                                                                                                                                                                                                                                                                                                  253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cucumis sativus (carassius auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thalia
```

\_documentation\_block:

PRELIMINARY;

PRT;

349

₽

```
SOO SOOR THE TRACE OF THE TRACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_427 x Q61190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
seq_name: sp_rodent:Q63953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q61190 from: 1 to: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O61190:
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
IL10RB OR CREB4 OR CRF2-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins.";
Gene 186:97-101(1997).
EMBL; U53696; AAC53062.1; -.
MGD; MGI:109380; Illorb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIBBS V.C., PENNICA D.;
"CRF2-4: isolation of cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00041; fn3; 1.
SEQUENCE 349 AA; 39774 MW;
                                                                                                                                                                                                                                                                                                                               387 TCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 ATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAACACTTCT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 GGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 oProGluLysValArgMetAsnSerValAsnPheLysAsnIleLeuGlnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 GTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sArgThrAlaSerThrGlnCysAspPheSer.....HisLeuSerLysT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA....AAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||:::
rpGluValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluSerTyrArgSerPheGlnAspHis......CysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGlyGlyPheLeuLeuValProAlaLeuGly.....MetIleProPr
                                                                                                                                                                                                                                                            yProProGluMet 118
                                                                                                                                                                                                                                                                                                                                                                                                       GluTrpValAsnVal...ThrPheCysProValGluAspThrIleIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yrGlyAspTyrThrValArgValArgAlaGluLeuAlaAspGluHisSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127.00
1.693
61.983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 30.579
       Created)
                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4AC1802A CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding the human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                  332
                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
```

```
alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PESTKA S., DEMBIC Z.;

Trenomic organization and promoter analysis of the gene lingr2 encoding the second chain of the mouse interferon-gamma receptor.";

L Scand. J. Immunol. 44:599-606(1996).

R EMBL; U69599; AAC52938.1; JOINED.

R EMBL; U69595; AAC52938.1; JOINED.

R EMBL; U69596; AAC52938.1; JOINED.

R EMBL; U69596; AAC52938.1; JOINED.

R EMBL; U69597; AAC52938.1; JOINED.

R EMBL; U69598; AAC52938.1; JOINED.

R EMBL; U69597; AAC52938.1; JOINED.

R EMBL; U69598; AAC52938.1; JOINED.

R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-675-1_COPY_27_427 x Q63953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: Q63953 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 94170381.
HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
"A novel member of the interferon receptor family complements functionality of the murine interferon gamma receptor in human cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-129SV/J;
MEDLINE; 97128072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFNGR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBENSPERGER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 76:803-810(1994).
                                                              310 ATRAGAGCAGAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 356
                                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 ACAGGAGCGATGAGTCT......GTCGGGAATGTGACT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TTGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                               lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                               G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHEE S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120.00
1.500
61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTHUKUMARAN G., LEMBO D., DONNELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 8
Percent Identity: 30.769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76
```

ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA 396

```
SO SEE THE SECTION OF THE SECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_27_427 x Q9YGC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_vertebrate:Q9YGC8
seq_documentation_block:
ID Q14936 PRELIMI
AC Q14936;
                                                                                                                                       seq_name: sp_human:Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q9YGC8 from: 1 to: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 GAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGAT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor gene cluster.";
Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1; -.
EMBL; AF082666; AAD13671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REBOUL J., GARDINER K., MONNERON D., "Comparative genomic analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
INTERLEUKIN-10 RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....TATCAAAAACTGGGATGGATAATTGGATAAAATTGTCTGGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pAspProProGlyValArgLysGlyAsnLeuSerTyrThrValGlnAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProArgAsnAlaArgIleSerSerValAsnPheArgSerValLeuLeuTr 40
                                                                                                                                                                                                                   GlyProProSerVal 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysSerIlePheProLysGlnAsnPheAsnAsn......val 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oPheGlnHisTyrGluAsnValThrValGlyProProLys 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrThrAsnLeuAsnValThrGluCysAspValSerSer....LeuSe
                                                                                                                                                                                                                                                                                                                                                              isSerAspTrpAlaValValArgPheLysProMetAlaAspThrValIle
                                                                                                                                                                                                                                                                                          GGTCCTCCAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 AA;
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104.50
1.713
58.095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7433D364 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 105
Gaps: 3
Identity: 27.619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UZE G., LUTFALLA G.; interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341
                                     484
                                     ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEMBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
```

```
SQRRAD DRAFT ARAXX OCCURATE TO THE CONTRACT OCCURATE OCCURATE TO THE CONTRACT OCCURATE TO THE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_427 x Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1994)
EMBL; U19247; AAC520
EMBL; U19241; AAC520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEMBIC Z.;
"The gene for the ligand binding chain receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MERLIN G., VAN DER LEEDE B.-J.M., MCKUNE K., KNEZEVIC N., BANNWARTH W., ROMQUIN N., VIEGAS-PEQUIGNOT E., KIEFER H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE FROM N.A. MEDLINE; 97246734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor.";
Cell 55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89003065.
AGUET M., DEMBIC Z., MERLIN G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 45:413-421(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MERLIN G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
AAATTGCGTATAAGAGCA......GAAAAAGAAAACACTTCTTCATG
                                                                 isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu
                                                                                                                                                                                                                                                                           AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                 AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATG
                                                                                                                                     GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                   nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH
                                                                                                                                                                                                                                                                                                                                                .....GlnIleMetProGlnValProValPheThrValGluValLysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U19244;
U19245;
U19246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; AAC52064.1; JOINED.
2; AAC52064.1; JOINED.
3; AAC52064.1; JOINED.
4; AAC52064.1; JOINED.
5; AAC52064.1; JOINED.
5; AAC52064.1; JOINED.
6; AAC52064.1; JOINED.
6; AAC52064.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.50
1.018
61.765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EBC99D1F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the human interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136
5
24.265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGUET M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma
```

```
seq_name: sp_invertebrate:Q23020
                                                                                                                                                                                                               alignment_block:
US-09-240-675-1_COPY_27_427 x Q23020
                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                         Align seg 1/1 to: Q23020 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block:
                                                                                      1073
                                                                                                                                                                                                                                                                                                                                                                                                    PKinase; 1.
...ars; pRO0014; FNTYPEIII.
MYOSin; Kinase.
SEQUENCE 6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q23020; Q27232;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X15423; CAA33463.1; -
EMBL; Z7389; CAA98081.1; ALT_INIT.
EMBL; Z73897; CAA98081.1; JOINED.
HSSP; O63450; 1A06.
PFAM; PF00041; fn3; 31.
PFAM; PF00041; fn3; 31.
PFAM; PF00047; 1g; 13.
PFAM; PF00067; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNC-22 OR ZK617.1.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BENIAN G.M., L'HERNAULT S.W., MORRIS M.E.;
"Additional sequence complexity in the muscle gene, unc-22, encoded protein, twitchin, of Caenorhabditis elegans.";
Genetics 134:1097-1104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 93387664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BENIAN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G., WATERSON "Sequence of an unusually large protein implicated in regulati myosin activity in C. elegans.";
Nature 342:45-50(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE; 90044042.
                    123 AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA 172 :::::|||||||::: ||| ||||::: ||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HARRIS B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAAGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roLysLeu 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TrpValArgValLysAlaArgValGlyGlnLysGlu....SerAlaTy
                                                                                 CTAAAATCTCCTCAAAAA......GTAGAGGTC...GACATCAT 122
eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                    84.00
1.151
62.393
                                                                                                                                                                                                                                                                                                                                                                                                                       668449 MW;
                                                                                                                                                                                                                                                                  vaps: 8
Percent Identity: 26.496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
                                                                                                                                                                            to: 6048
                                                                                                                                                                                                                                                                                                                                                                                                                       1977C602 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6048
                                                                                                                                                                                                                                                                                                              Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ያ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WATERSON R.H.; regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                        1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
```

```
seq_documentation_block:
ID Q23550
AC Q23550;
AC Q23550;
DT 01-NOV-1996 (TIEMBLTel. 01.
DT 01-NOV-1998 (TIEMBLTel. 02.
DT 01-NOV-1999 (TIEMBLTel. 12.
DE UNC-22 PROTEIN.
GN UNC-22.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoo.
OC Rhabditina; Rhabditoidea; 1
RN [1]
RP SEQUENCE FROM N. A.
RA WHITE S.;
RR WHITE S.;
RR SEMBL; Z73897; CAA98064-1; 1
DR EMBL; Z73897; CAA98064-1; 1
DR EMBL; Z73897; CAA98064-1; 1
DR PFAM; PF00041; fn3; 31.
DR PFAM; PF00041; fn3; 31.
DR PFAM; PF00047; phinase; 1.
DR PFAM; PF00064; FNTYPEIII
SQ SEQUENCE 6831 AA; 75257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_invertebrate:Q23550
                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_427 x Q23550
                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality:
                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02/51; 1:....

PFAM; PF00041; fn3; 31.

PFAM; PF00047; 19; 17.

PFAM; PF00069; pkinase; 1.

PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1184 1 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1106 luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg
                                                                                      1872
                                                                                                                                                                 1856 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 A 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 273897; CAA98064.1; -.
EMBL; 273899; CAA98064.1; JOINED.
HSSP; P02751; 1FNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                    88 CTAAAATCTCCTCAAAAA.......GTAGAGGTC...GACATCAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpValPro.....CysAlaLysValLysAspThrLysAlaHisIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTGACTTTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                                                      AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA 172
{\tt luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg}
                                      ATGTGACTTTTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                   eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG
                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                   to: Q23550 from: 1 to: 6831
                                                                                                                                                                                                                                                                                                                                                    84.00
1.151
62.393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oda; Secernentea; Rhabditia; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0A66C338
                                                                                                                                                                                                                                                                                                                                                                           Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
                                                                                                                                                                                                                                                                                                                                                        : 117
: 8
: 26.496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1122
        1905
                                                                                      1889
```

```
A CONTRACTOR AND THE PROPERTY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_invertebrate:Q23551
                                                                                                                                                                                alignment_scores:
                                  Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                               Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 273899; CAA98082.1; -.

REMBL; 273897; CAA98082.1; JOINED.
EMBL; 273897; CAA98065.1; -.

EMBL; 273899; CAA98065.1; JOINED.

REMBL; 273899; CAA98065.1; JOINED.

REMBL; 273899; CAA98065.1; JOINED.

REMBL; 273899; CAA98065.1; JOINED.

RESSP; PO20751; IFNA.

RESSP; PO20761; FO3; 31.

RESSP; PO20761; FO3; A1.

RESSP; PO20761; FO3; A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1967 1 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1951 LysAlaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., KEMEN T., AMOSTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Ehabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZK617.1B PROTEIN.
ZK617.1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q23551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HARRIS B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHITE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eAspGlyLeuLysLysGly......GlnThrTyrGlnPheArgValLysA 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpValPro.....CysAlaLysValLysAspThrLysAlaHisIl 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA...GAAAAAGAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                  84.00
1.151
62.393
eaps: 8
Percent Identity: 26.496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7160
                                                                                        Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis.
```

```
alignment_block:
SEE CHARLES SEE CH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: sp_vertebrate:013048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: Q23551 from: 1 to: 7160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1_COPY_27_427 x Q23551
                         organizer.";
Dev. Biol. 184:367-372(1997).
1- SIMILARITY: TO OTHER GROWTH FACTORS OF EMBL; U79162; AAC60127.1; -.
HSSP: P18075; 1BMP.
PROSITE; P500250; TGF_BETA; 1.
PFAM; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2185 LeuAspArgProSerLysProAsnGlyProLeuGluValSerAspValPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2280 LysalaLysAsnProTyrAspGluProGlyLysThrGlyThrProAspVa 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2296 1 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XNR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399 A 399
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 97278865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XNR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 CTAAAATCTCCTCAAAAA.....GTAGAGGTC...GACATCAT 122
                                                                                                                                                                                                                                                                                                                                              JOSEPH E.M., MELTON D.A.;
"Xnr4: a Xenopus nodal-related gene expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eGluAspAsnLeuAsnLeuSerTrpLysProProAspAspAspGlyGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA...GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eAspGlyLeuLysLysGly.....GlnThrTyrGlnPheArgValLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TrpValPro......CysAlaLysValLysAspThrLysAlaHisIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luProIleGluTyrTyrGluValGluLysLeuAspThrAlaThrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTGACTITTTCATTCGATTATCAAAAA.....ACTGGGATGGATAAT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laValAsnLysGluGlyAlaSerAspAlaLeuSerThrAspLysAspThr
   402 AA; 46271 MW;
   039E7186 CRC32;
                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                               THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amphibia;
                                                                                                                                                                                                                                                                                                                                                         Spemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2201
```

alignment\_scores:

Quality:

80.00 1.404 50.893

Gaps: Percent Identity:

23.214

Ratio: Percent Similarity:

```
alignment_block:
US-09-240-675-1_COPY_27_427 x 013048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: 013048
                                                                                                                                                                                                                                                                                                                                                                               Q10466;
01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-NOV-1996 (TrembLrel. 02, Last sequence update)
01-NOV-1999 (TrembLrel. 12, Last annotation update)
TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Eukheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
Q10466 PRELIMI
                           MEDLINE; 95331314.

GAUTEL M., CASTIGLIONE-MORELLI M.A., F
"A calmodulin-binding sequence in the titin kinase.";

Eur. J. Biochem. 230:752-759(1995).
                                                                                                                                                                                   SEQUENCE OF 22277-25376 FROM N.A. MEDLINE; 92258380.

LABEIT S., GAUTEL M., LAKEY A., TRI "Towards a molecular understanding EMBO J. 11:1711-1716(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295
                                                                                                                                              SEQUENCE OF 1976-2014 FROM N.A. LABEIT S.;
                                                                                                                                                                                                                                                                                                                    MEDLINE; 96026330.
LABEIT S., KOLMER B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 TGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTA 194
                                                                                                  CHARACTERIZATION.
                                                                                                                              Submitted (DEC-1994)
                                                                                                                                                                                                                                                                                            elasticity
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 eLysGluHisValMetGlyMetLysHis......valProProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 GlyIleGlnThrIleAlaHisThrArgArgHisArgArgSerHisIlePh
                                                                                                                                                                                                                                                                           Science 270:293-296(1995).
                                                                                                                                                                                                                                                                                                     "Titins: giant proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 CTCAAAAAGT...AGAGGTCGACATCATAGATGACAACTTTATCCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTC
                                                                                                                                                                                                                                                                                                                                                    SSUE-HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysGluGlyGluCysProSerProValAsnGluSerValLysProAsnAs
 FUNCTION: THIS GIANT MUSCLE ASSEMBLY AND IN MAINTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nHisAlaTyrMetGlnSerLeuLeuAsnTyrTyr 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eLysGlnIleGlyTrpAspSerTrpIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAGCAGAAAAAGAAAACACTTCTTCATGGTAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTAT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....GAAGAAATTAAATTGCGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laAspSerSerArgThrLeuCysArgArgValAspPhePheVal.AspPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_human:010466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 402
                                                                                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                      charge of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
PROTEIN MAY BE
THE STRUCTURAL
                                                                                                                                                                                                      TRINICK J.;
ing of titin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26926
                                                       PFUHL M., MO
e C-terminus
                                                                                                                                                                                                                                                                                                        muscle ultrastructure
                                                                                                                                                                                                                                                                                                                                                                                                                                     ation update) (CONNECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ζ
                                                      MOTTA A.,
 INVOLVED
                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144
               Z
                                                                    PASTORE A.;
                                                         cardiac
               MUSCLE
                                                                                                                                                                                                                                                                                                        and
                                                                                                  10955
                                          10969
                                                                                                                                                           10938
```

GGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTACTACCC | | ::::::|||||||:::

AAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATT lyThrGlnAspTrpIleLysPhe....LysThrValThrAsnLeu

305

10968 255 gAspGlyGlySerProIleThrGlyTyrLeuValGluTyrGlnGluGluG

10955

306

GCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACT GluCysValValThrGlyLeuGln......GlnGlyLysThrTy 10981

```
alignment_block:
US-09-240-675-1_COPY_27_427 x Q10466
                                                                                                                                                                                             alignment_scores:
                                                                 Align seg 1/1 to: Q10466
                                                                                                                          Percent
                      10922 ValAspValAspLysThrGluValSerLeuValTrpAsnLysProAspAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X64698; CAA45939.1; EMBL; X63270; CAA5828.1; EMBL; X64697; CAA45938.1; EMBL; X90568; CAA62188.1; EMBL; X64699; CAA45940.1; EMBL; X64699; CAA45940.1; FEAM; FF00047; fn3; 132. FFAM; FF00047; fn3; 132.
162
                                                                                                                                                                                           MOD_RES
MOD_RES
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                       MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                          112 GTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>+</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                  Muscle protein; Cytoskeleton; Structural protein; Calmodulin-binding;
Serine/threonine-protein kinase; Alternative splicing; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRODO14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
-1- SIMILARITY: TO THE CATALYTIC DOMAINS
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00726; LEXASERPTASE.
                                                                                                                                                                                                                                                                                                                                                                                         [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE
PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE
DISTRIBUTION, DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN AND ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
                                                                                                                        Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112 IMMUNOGLOBULIN C2-LIKE DOMAINS AND 132 FIBRONECTIN TYPE III-LIKE
GTCTGTCGGGAAT.....GTGACTTTTTCATTCGATTATCAAAAAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINASES
                                                                                                                                              Quality:
                                                                                                                                    Ratio:
                                                                                                                                                                                                                             26171
26178
26184
26190
26190
22277
222449
                                                                                                                                                                                                                                                                                               1382
1387
                                                                                                                                                                                                                                                                                                                                                                                                                                     pkinase; 1.
4; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                         domain;
                                                                                                                         80.00
1.379
58.586
                                                                                                                                                                                                                             4614
25070
25056
1377
1387
1387
1387
26178
26178
26178
26190
222277
                                                                 from: 1 to: 26926
                                                                                                                                                                                            2993428
                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . . . . . .
                                                                                                                         Percent
                                                                                                                                                                                                                           PHOSPHORYLATION
T -> P (IN REF. :
E -> G (IN REF. :
                                                                                                                                                                                                                                                                                              PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                      , , , ,
, , , ,
                                                                                                                                                                                                                                                                                                                                                       GLU/LYS/PRO/VAL-RICH. CATALYTIC.
                                                                                                                                                                                                                                                               PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                      PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                              CALMODULIN-BINDING.
                                                                                                                                                                                            ž
                                                                                                                       Length:
Gaps:
Identity:
                                                                                                                                                                                                                                                                                                                                                                              5 AA TANDEM REPEATS OF R-M-S-P-A.
                                                                                                                                                                                                       ro o
                                                                                                                                                                                            0214E3A3
                                                                                                                                                                                                       Ë
                                                                                                                                                                                                                  (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဝှု
                                                                                                                                                                                            CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER SERINE/THREONINE
                                                                                                                         25
                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                              (BY PDPK)(POTENTIAL).
(BY PDPK)(POTENTIAL).
(BY PDPK)(POTENTIAL).
(BY PDPK)(POTENTIAL).
                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                         99
4
. 253
                                             161
205
                      10938
```

10981 rArgPheArgValLysAlaGluAsnIleValGlyLeuGlyLeuProAspT 10998

```
SARLE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_27_427 x Q06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: sp_fung1:Q06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
Q06349 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    006349;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
CHROMOSOME IV COSMID 9481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T.,
HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MADIN S., MENEZES S.,
MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
WILSON R., WATERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JIA Y., CHERRY J.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U28373; AAB64806.1; -.
SEQUENCE 442 AA; 50492 MW; 5073BCOA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOHNSTON M., ANDREWS S., BRINKMAN R.,
175 GTGACTTTTTCA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                              25 ACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrThrIleProIleGluCysGlnGluLysLeuValProProSerVal 11013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATTTACACCATTTCGC...AAAGCTCAGATTGGTCCTCCAGAAGTA
                                                               yrSerAsn.....AspProAsnMetLysLys
                                                                                                                                       ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAAT 174
                                                                                                                                                                                                                                                                          AGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                          ThrSerLeuIleValThrTyrMetGlyAlaGlyLeuLeuSerPheCys..
                                                                                                                                                                                                   .....ArgAsnValLysLysAspSerGlnMetSerLysGluGlyIleT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: Q06349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.00
1.162
58.120
   .TTCGATTATCAAAAAACTGGGATGGATAATTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COOPER J., DING H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                       246
                                                                                                                                                                                                          238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

alignment\_block: US-09-240-675-1

Align seg

7

to: 045604

from: 1

ë

\_COPY\_27\_427 x 045604

Ratio: Percent Similarity:

Percent

Identity: 24.219

```
SOD DRAFACTION OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_invertebrate:045604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU 2., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN F
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275
                                                                                                                                                                                                                                         Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z92811; CAB07274.1; -
EMBL; Z92789; CAB07274.1; JOINED.
EMBL; Z92789; CAB07273.1; JOINED.
EMBL; Z92881; CAB07233.1; JOINED.
PFAM; PF00400; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           045604; 045724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 A 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lThrGluAsnSerLysValAlaAspLeuThrGlySerLysCysProIleP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A...AAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAAC...T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleCysTyrSerGlyPheGluPhe..
                                                                                                                                                                                                             1083 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
78.00
1.068
57.031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                     1.
119604 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                23EC3C85 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .GluMetAspAlaPheAsnPr
                                       Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....GluAsnTrpVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHOWNKEEN R.,
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x Q65525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: sp_virus:Q65525
                                                                                                                                                                                       Align seg 1/1 to: Q65525 from: 1 to:
                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCT......TCATG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 spGlnValLysLeuLeuArgTrpAsnLeuLysAsnGluSerValPheAla 182
                                                                                                                                                                                                                                                                                                                                                                                                   JIANG B., GENTSCH J.R., TSUNEMITSU H., SAIF L.J., GLASS R.I.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U26551; AAB01672.1; -. PFAM; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 GTATGAGGTTGACTCATTTACACCATTTCGCAAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 SerIleSerSerArgArgValSexPhe...TrpAspLeuArgArgAsnGl 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133
                                                109
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SHINTOKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine group C rotavirus.
Viruses; dsRNA viruses; Reoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last anno
ROTAVIRUS C VP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q65525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 300
                                                                      63 GTCCGCAGCCGCA......GGTGGAAAAAAT.........
                                                                                                                   93
                                                                                                                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnLeuIleValSerSerGlnSerGlnHisAlaSerValIleGlnLysTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ySerProValLeuGluPheAlaGluIleProGly......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTC.... 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....AATCTAAAATCTCCT...CAAAAAGTAGAGGTCGACATCATAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyArgTrpMetAlaSerGlyGlyGlySerGlyGlnIleLeuLeuTrpAs 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGGAT.....AATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....GGGAATGTGACTTTTTCATTCGATTATCAAAAAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAA......
                                            uAlaAlaPheGluLeuTrpTyrGlyLysAlaAsnThrThrValThrSerA 126
                                                                                                                   SerThrValLysLeuLeuLysAsnGlyProGluSerTyrSerTrpAsnLe
                                                                                                                                                  ACGACCCTAGTGCTCGCCGTGGGCCCA.....rGGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pAspSerArgPheThrSerThrProValLysGlu 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ........CysAspTrpSerSerLeuSerTrpAsnProSerAspAlaSer 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
.....CTAAAATCTCCTCAAAAAGTAGAGGTCGACATC
                                                                                                                                                                                                                                                                                                                                                                                      Α
                                                                                                                                                                                                                                                                         77.50
0.934
49.405
                                                                                                                                                                                                                                                                                                                                                                           82494 MW;
                                                                                                                                                                                                                                                                         Length: 168
Gaps: 8
Percent Identity: 23.810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                     93174D55 CRC32;
                                                                                                                                                                                         733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ⋛
            120
                                                                               87
                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
```

```
seq_documentation_block: ID Q08773 PRELIMI
                                                                                alignment_block:
US-09-240-675-1_COPY_27_427 x Q08773
                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                             SOUTH TENTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_fung1:Q08773
                                                                                                                                      Ratio:
Percent Similarity:
                                                  Align seg 1/1 to: Q08773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               008773;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CHROMOSOME XV READING FRAME ORF YOR304W.
                                                                                                                                                                                                                                        Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases EMBL; Z75212; CAA99622.1; -. PFAM; PF00271; helicase_C; 1. PFAM; PF00176; SNF2_N; 1. SEQUENCE 1120 AA; 130326 MW; 51FC7F47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189
                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
CZIEPLUCH C., JAUNIAUX J.C., KORDES E., POIREY R., PUJOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 uVal 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 AGTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 rAsnLysVallleAsnPheSerTrpAsnValGlyGlyVal....LeuI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
                                                                                                                                                                                                                                                                                                                                                                                                  IOBIASCH E.;
                   76
                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
GGTGGAAAAAATCTA.....AAATCTCCCTCAAAAAGTAGAGGTCGACAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluMetLysMetValLysValLysArgGluGlySerIleAsnValAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spProTyrSerGlnIleArgAlaLeuGlnGlnProIleIleThrThrVal 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oArgSerAlaSerMetAsnIleTyrThrAspTyrTyrLeuAlaSerValA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leLysLeuThrSerAsnThrArgIleAspIleCysMetAlaAsnMetAsp 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...HisAspSerLeuValLeuPheTrpAsnGluGlySerThrAlaLeuSe 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spTyrTyrSerGlyMetThrAsnSerGluLysSerValGluValAsp...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....CGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnPheThrSerAspSerPheAsnTrpGluGluTrpThrHisAsnPhePr 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGG
                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                       77.50
1.123
55.200
                                                   from: 1 to: 1120
                                                                                                                                       Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1120
                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                       125
4
23.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270
                                                                                                                                                                                                                                                                                                                                                                                                                  ?
```

664 GlyAlaLysAsnMetPheGluLysLysAlaSerLysValThrValAspAl

CATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCG

```
alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                  SOR BERTITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: sp_invertebrate:Q20930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _documentation_block:
Q20930 PRELIMINARY;
                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
PARSON N., SMITH A., SOUNHAMMER E., STADEN R., WILLERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94150718.
WILSON R., AINSCOUGH R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F57B7.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            775 oGlnProLysAlaProArgAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 ATTTCGCAAAGCTCAGATTGGTCCT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             759 TyrLysGluIleIleGlyGlyGlySerLysSerAlaSerLysGlnThrPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   742 erArgArgGluArgArgArgGluGlnThrThrTyrSerValAspAspTyr 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 ..AGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 sSerPheGlnLysLysSerAsnAspLysValValGluTrpIleAsnProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 TTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709 GlnLysPheAsnGlyIleGluAsnGlnSerAlaTyrGluTrpAsnGlyLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 ATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     680 aAspIleAspAspIleLeuLysLysGlyGluGlnLysThrGlnGluLeu.
                                                                                                                                EMBL; 274037; CAA98493.1; -. PFAM; PF01421; Reprolysin; 1. SEQUENCE 508 AA; 57789 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                             elegans.";
Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AsnAlaLysTyrGlnSerLeuGlyLeuAspAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ACACC
75.50
1.079
47.297
Length: 148
Gaps: 5
Percent Identity: 22.297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                  B49E91AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
```

```
alignment_block:
US-09-240-675-1_COPY_27_427 x Q20930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: Q20930 from: 1 to: 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                           184 rAspSerAspAsnSerSerThrAspAlaLeuIleSerSerAspMetProL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 IleSerPheGlyAsnGluThrLeuHisMetValPheAlaGlyThrTrpIl
                                             350 TTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCA 393
                                                                                                                                           300 TAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGG 349
                                                                                                                                                                                                                                       250 AGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAAT 299
                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GTTGTCCGCAGCCGCAGGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 GTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCCGTGGGCCCATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgAspLeuAsnSerThrPheValAspAspThrPhePheMetAsnSerTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGACATC.....ATAGATGACAACTTTATCCTGAGGTGGAA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eAlaThrGlnGluArgAspCysProLeuTrpIleSerTrpAlaGluGluG
                                                                                                                                                                                                                                                                                       ys......PysLeuArgLysPheValAspIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luGluGluArgValLeuAsnGluGluIleArgArgLeuGluGluLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ......GGAAAAAATCTAAAATCTCCTCAAAAAGTAGAG
leAspLysPheThrIleTrpLeuLysGluGlnThrGlyLeuPro
                                                                                                                                                                                                                                                                                                                                        AAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACT
                                                                                              tThrLeuLysIleAspSerLysLys...........AlaI
                                                                                                                                                                                              .....LeuGluGluMetGlnGluAsnAsnSerThrGluMe
                                                                                                                                                                                                                                                                                                                                                                                                                                              199
                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                          249
                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                              222
```

```
A_Geneseq_36:W21804
A_Geneseq_36:W131867
A_Geneseq_36:W11867
A_Geneseq_36:W07702
A_Geneseq_36:W1866
A_Geneseq_36:W38558
A_Geneseq_36:W38558
A_Geneseq_36:W39562
A_Geneseq_36:W52962
A_Geneseq_36:W529640
A_Geneseq_36:W529640
A_Geneseq_36:W82400
A_Geneseq_36:W82400
A_Geneseq_36:W82499
A_Geneseq_36:W20115
A_Geneseq_36:W20554
A_Geneseq_36:R75075
A_Geneseq_36:W76186
A_Geneseq_36:W76186
A_Geneseq_36:W36875
A_Geneseq_36:X04994
A_Geneseq_36:R32882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: A_Geneseq_36.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database sequences: 18896
Database length: 23686106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score_list:
                                                                                                                                                                                                                                                                                                                           A_Geneseq_36:R97669
A_Geneseq_36:R87511
A_Geneseq_36:W31331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_36:W59912
A_Geneseq_36:R57474
A_Geneseq_36:W72048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_36:W21805
A_Geneseq_36:R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_36:W04827
A_Geneseq_36:W80491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_36:W44945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_36:W21806
A_Geneseq_36:R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MODEL-frame+_n2p.model -DEV-x1p
-O-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164311_24603/app_query.fasta.1
-OP-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164311_24603/app_query.fasta.1
-DB-A_Geneseq_36 -OFMT-fastan -SUFFIX-modif.rag -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPELY-0.000 -LOOPEXT-0.000
-OGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOENT-7.000 -START-1 -MOTRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \_Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \_Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \_Geneseq_36:R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _Geneseq_36:R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of: US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188963
3440.00

3440.00

3440.00

3440.00

3440.00

3440.00

67.00

68.00

68.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.00

69.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZSCORE
751.30
751.26
    751.26
750.05
751.26
751.26
751.26
752.05
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
748.97
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
O:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESCOTE Len
43.
5.2e-35 43.
5.2e-35 43.
5.2e-35 43.
5.5e-35 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_36:*
    111.39
115.97
119.15
24.08
22.05
22.12
22.12
22.12
22.12
22.12
22.11
22.11
22.11
22.11
23.11
24.01
31.06
31.06
31.06
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.36
31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            software,
        ! Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                S. pneumoniae ketoacyl reductas Sequence of Mycobacterium tuber Sequence of Mycobacterium tuber Human brx immunogenic peptide 1. CRFB4 protein. New recombinant Human SRE-ZBP analogue GRN 5060 RR. eutropha Mgt partial ORF3 en Human G3BP protein. New ubiquit Avian infectious bronchitis vir 1 Amino acid sequence of the mut 1 Amino acid sequence of the mut 5 P. falciparum transmission blc 1 HSV-2 strain SB5 Contig ID 104 Heart vascular endothelial grow Murine vascular endothelial grow Yeast presequence COX IV-wheat
                                  Chiken Yes proto-oncogene asso
Human c-mer protooncogene recept
Quaternary amine lipid compound
H. pylori secreted or periplasm
H. pylori secreted or periplasm
HCV core-envelope peptide N1N3N
Carbamoylphosphate-synthase hom
Actinoplanes sp. acarbose prote
Cancer suppressor transfer fact
Mycobacterium species protein s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human metastasis-associated an Mouse ETS2 repressor factor (EN) Mouse IRS-2. New insulin recept Mouse metastasis-associated an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of a soulble form of the Human interferon receptor. Mond Human IFN receptor. Compsn. of Transmembranal interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spliced-deleted interferon alph Human alpha-interferon receptor Complete interferon-alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spliced-deleted interferon alph
soluble interferon alpha/beta r
Sequence of a soulble form of t
IFN receptor extracellular doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brx protein. Breast canc
```

```
seq_documentation_block:
ID W21805 standard; Prot
AC W21805;
DT 23-SEP-1997 (first e
DE Spliced-deleted inter
KW Interferon alpha-rece
OS HOMO Sapiens.
FH Key
IT domain
FT domain
FT domain
FT domain
FT domain
FT domain
FT ALSAMOVICH C.
PI Abramovich C.
PI New mammalian soluble
PT inhibiting, modulatin
PS Example 2; F1g 7; 46p
CC (W21805) is character
CC seguence is predicted
CC splice-deleted forms
CC seguence of human
CC antagonists or by reg
CC subtypes. They can b
CC subtypes. They can b
CC tissues and organisms
SQ Seguence 434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_36:R78519
A_Geneseq_36:P81936
A_Geneseq_36:W54097
A_Geneseq_36:R41227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: A_Geneseq_36:W21805
                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_1_229 x W21805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PT New mammalian soluble interferon alpha-receptor forms - used for prinhibiting, modulating or modifying the activities of interferon(s) ps Example 2; F1g 7; 46pp; English.

CONOVEL splice-deleted interferon alpha-receptor (IFNAR) form 1 converged by a new domain (S) which follows an condition of the compared to transmembranal converged by a new domain (S) which follows an converged extracellular domain when compared to transmembranal converged by a new domain of the amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. Thom human myeloma U266 cells. Soluble, non-membrane bound IFNAR converged collected forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNs, either by acting as IFN antagonists or by regulating the activity of the multiple IFN converged in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, this uses and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: W21805 from: 1 to: 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spliced-deleted interferon alpha-receptor
Interferon alpha-receptor; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spliced-deleted interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W21805 standard; Protein; 434
                                                                                     3
                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                   ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                               AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                   CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCCTC
                   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                        lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                             yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratovitski E, Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11. 427
/label= Extracellular_domain
/label= "comprises amino acids
/note= "comprises amino acids
transmembranal IFNAR"
428. 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.81
117.18
108.55
107.61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
32
38
39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids 1-427 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1184
147
370
409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac adenylyl cyclase. Human basic fibroblast gro Homo sapiens B223 sequence 910 SLG protein. Isolated
                                                                                          50
                                                                                                                                                                                  ω
4
```

seq\_name: A\_Geneseq\_36:R14487

67

s >

67

documentation\_block:

```
seq_documentation_block:
ID R28495 standard; Prot
AC R28495;
DT 31-MAR-1993 (first of
DE Sequence of a soulblo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e de la company 
                                                                                                                                                                                 seq_name: A_Geneseq_36:R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1_COPY_1_229 x R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.

Fr2657881-A.

09-AUG-1991.

05-FEB-1990; 001298.

05-FEB-1990; FR-001298.

(EUBI-) LAB EURO BIOTECHNO.

Eid P. Gresser I. Lutfaila G. Meyer F.

Tovey MG, UZe G;

WPI: 91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mater-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 2; Page 45; 52pp; French.

The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R14487 standard; Protein;
R14487;
16-JAN-1992 (first entry)
                                                                                          R28495 standard; Protein; 436
                                                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble interferon-alpha/beta receptor. IFN; autoimmune disease; graft rejection; histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble interferon-a.
                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _
                                                                                                                                                                                                                                                                                                  A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                                                                                                                                                                                                                                                                                                            AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 AA;
(first entry)
a soulble form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent
      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
. Identity:
   interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.000
   (IFN)
                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
```

```
PR PN KKE DAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_1_229 x R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                              seq_name: A_Geneseq_36:R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune diseases and transplant rejections? Claim 2; Fig 1; S8pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water soluble cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind CIFN in the same way as antibodies on are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279
                                             Homo sapiens.
WO9507716-A.
                                                                                                                                                                                                                                                                                                                                                 Tovey M, Uze G;
WPI; 92-382110/46.
N-PSDB; Q30532.
                                                                          IFN receptor extracellular domain.
IFN receptor; interferon receptor; interferon-beta; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EUNO BIOTECHNOLOGIE.
ELIC P. Gresser I, Lutfalla G, Me
                                                                                                                                                                                                                                                             227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                      l6-OCT-1995 (first entry)
                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGATGGTCGTCCTGGGCGGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                           A 227
                                                                                                                                                                                                                                                                                        CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                s 67
                                                                                                                                                                                                                                                                                                                      AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                               yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 340.00
: 5.075
: 100.000
                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                      436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G, Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 67
Gaps: 0
Identity: 100.000
                                                                                          interferon-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                             immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mogensen
                                                                                                                                                                                                                                                                                                                      226
                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
```

SA

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                           seq_name: A_Geneseq_36:W21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1_COPY_1_229 x R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                             AU9475977-A.
11-MAY-1995.
20-OCT-1994: 075977.
24-OCT-1993: IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benizri EJ, Tov
WPI; 95-131187/1
N-PSDB; Q86457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English. A recombinant soluble form of the human interferon class I receptor protein extracellular domain, given in R71723, was expressed in either E. coli or COS cell hosts. The protein was used to raise immunomodulatory monoclonal antibodies. Seguence 436 AA;
                                                                                                                                                                                                                                                                                                                                                     documentation_block:
                                                                                                                                                                                                                                                                                               W21806;
23-SEP-1997 (first entry)
         (ABRA)) ABKARVYLLA ...
Abramovich C, Ratovitski E, Revel M;
WPI; 95-200634/27.
New mammalian soluble interferon alpha-receptor forms
                                                                                                                                                                                                                                                                                                                                                                                                                                 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                 Spliced-deleted interferon
                                                                                                                                                                                                                                                                                                                                       W21806
                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
inhibiting, modulating or modifying the Example 3; Fig 7; 46pp; English.
                                                                                                                                                                                                                                                                                 Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                       standard; Protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340.00
5.075
                                                                                                                                                                                     /label- Extracellular_domain
/note- "comprises amino acid residues 1-413 and
422-427 of transmembranal IFNAR"
420. 496
                                                                                                                                              transmembranal IFNAR"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                            /label= Intracellular_domain
/note= "comprises amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity:
                                                                                                                                                                                                                                                                                   IFNAR.
                                                                                                                                                                                                                                                                                              alpha-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 436
                                                                                                                                                             acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.000
                                                                                                                                                               481-557
               interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                           used for
```

```
seq_documentation_block:
ID R11958 standard; Prot AC R11958;
DT 18-JUL-1991 (first e DE Human alpha IFN; IFN KW drug targetting.
OS Homo sapiens. Locat FH Key Locat FH W09105862-A.
PD 02-MAY-1991.
PF 19-OCT-1990; FR-01377 PA (CNRS ) CNRS CENT NAT PI M09ensen KE, Uze G, I DR WPI; 91-148740/20.
DR WPI; 91-148740/20.
DR N-PSDB; 011701.
PT New human alpha-inter PT Interferon agonists a PS Disclosure; fig 4; 30 CC This recombinant human CC useful for the testin CC consis of viral diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: A_Geneseq_36:R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel splice-deleted interferon alpha-receptor (IFNAR) form 2 (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also T73521) obtd. Grown human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, or for disgnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                             -/ ULT-1990; F00758.

20-OCT-1989; FR-013770.

A (CNRS ) CNRS CENT NAT RECH SCI.

I Mogensen KE, Uze G, Lutfalla G, Gresser I;

RPI; 91-148740/20.

N-PSDB; 011701.

New human 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
   New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis disclosure; fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and discussed of viral diseases and tumours. Antibodies raised against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                            Human alpha-interferon receptor protein. Human alpha IFN; IFN agonists; antiviral; drug targetting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                        R11958 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: W21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496 AA;
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    x W21806
                                                                                                                                                                                                                                                                     signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 496
                                                                                                                                                                                                                                                                                                                                                                   anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
: 100.000
                                                                                                                                                                                                                                                                                                                                                                   tumour
                                                                                                                                                                                                                                                                                                                                                                   agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    នួននួននួន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: A_Geneseq_36:R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also 014239.
                                                                                                                                                                                                                                         09-AUG-1991.
05-FEB-1990;
05-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA;
                                                                                                                                                                    (EUBI-) LAB EURO BIOTECHNO.
Eld P. Gresser I. Lutfalla
Tovey MG, Uze G;
WPI; 91-319778/44
N-PSDB; 014240
                                                                                                                                                                                                                                                                                                                                                                                Complete interferon-alpha/beta receptor. IFN; autoimmune disease; graft rejection; histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
                                                                                                                                                                                                                                                                                   FR2657881-A.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                          001298.
FR-001298.
                                                                                                                                                                                                                                                                                                458. .55
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.000
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340.00
5.075
                                                                                                                                                                                                                                                                                                              /label= transmembrane
458. .557
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 67
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                         557 AA
                                                                                                                                                                                                             G, Meyer F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
6
                                                                                                                                                                                                             Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>د</u>
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name:
water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune diseases and transplant rejection claim 3; Fig 2; S8pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for colligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q3053), was incubated with oligos C the IFN-alpha and -beta receptor (Q3053), was incubated with oligos C the IFN-alpha and represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the conceptor side-effects of known immunosuppressants such as steroids. Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-1_COPY_1_229 x R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-1992.
17-APR-1991;
17-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P., Gresser I, Lutfalla G, Meyer F, Mogensen
Tovey M, Uze G;
WPI: 92-382110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q30533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITITION TO THE TOTAL STREET THE TOTAL S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 ATGATGGTCGTCCTGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_36:R28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ţo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO-F00318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F00318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쫎
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
```

Quality: 340.00 Ratio: 5.075 Percent Similarity: 100.000

Percent Identity:

67 0 100.000

```
alignment_block:
US-09-240-675-1_COPY_1_229
                                                                                                   alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: A_Geneseq_36:R42635
                                                 alignment_block:
US-09-240-675-1_COPY_1_229
                                                                                       Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: R28496 from: 1 to: 557
                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                             Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis Disclosure; Fig 3; 21pp; English.

Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell prollferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                   06-OCT-1993.
31-MAR-1992; EP-400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SA.
Benoit P, Maguire D, Meyer F, Plavec
WPI; 93-312951/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R42635 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 A 227
                                                                                                                                                                                  prophylaxis of disorders infection.
                                                                                                                                                                                                                                                                                                        P-PSDB; R42635
                                                                                                                                                                                                                                                                                                                                                                                                  EP-563487-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R42635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                           8
                                                                                                                                                                        557
                           R42635
                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                        /label-_extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               /note= "soluble, immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x R28496
                           from: 1
                                                    x R42635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $
                           .
0
                           557
                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                 ,
                                                                                           100.
                                                                                                                                                                                                                                                                                                                                 Tovey
                                                                                                                                                                                                                                                                                                                                                                                                               form of IFN-R"
                                                                                                                                                                                                                                                                                                                                   ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                    127
                                                                              17
                                                                                                       77
                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·w
```

```
seq_documentation_block:
ID R75356 standard; Prot
AC R75356;
DT 16-OCT-1995 (first e
DE Human IFN receptor: Interfe
KW IFN receptor: Locat
FH Key Interferon-beta; mono
OS Homo sapiens. Locat
FT domain /labe
PN W09507716-A.
PD 23-MAR-1995.
PD 23-MAR-1995.
PP 16-SEP-1994; E03114.
PF 17-SEP-1994; E03114.
PF 17-SEP-1993; E0-40227.
PA (EUBI-) LAB EURO BIOT
PA (EUBI-) LAB EURO BIOT
PA (EUBI-) LAB EURO BIOT
PR WPI; 95-131187/17.
DR N-PSDB; O86458.
PT Compsn. of monoclonal
PT useful as immuno:modul
PS Disclosure; Fig.3A-2E
CC given in R75356. A ra
CC domain of this recept
CC immunomodulatory mono
SQ Sequence 557 AA;
                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: A_Geneseq_36:R75356
                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                             Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q86458.

Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.

The amino acid sequence of human interferon class I receptor is given in R73356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizzi EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFN receptor; interferon receptor; interferon-alpha; interferon-beta; monoclonal antibody; immunomodulato Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>بــ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTC 126
                                                                                                             ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                   to: R75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .436
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                       x R75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557
                                                                                                                                                                                                                                                                                                                                                                Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ⋛
                                                                                                                                                                                                                                                                   ç
0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SA
                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulator;
                                                                                                                                                                                                                                                                                                                                                             67
0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
   226
                                         50
                                                                             176
                                                                                                                 34
                                                                                                                                                                                            17
                                                                                                                                                      126
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: A_Geneseq_36:W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) bisclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-1995.
20-CCT-1994; 075977.
24-CCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abramovich C, Ratovitski E, Revel M; WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembranal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W21804 standard; Protein; 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 s
ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                               AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                   CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                     ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon alpha-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label-
437. .45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label-
458. .55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      el- Transmembrane_domain
.557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .457
                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                           ë
                                                                                                                           176
  67
                                                                                 50
                                                                                                                                                                   34
                                                                                                                                                                                                                                                         17
```

127 34

17

27

```
seq_documentation_block:

ID w93941 standard; Prot AC w93941;

AC w93941 standard; Prot AC w3941;

DT 30-JUN-1999 (first e DE Human brx protein; breast c anti-protein; breast c anti-cancer; anti-protein; breast c anti-cancer; anti-protein; breast c www. Immune tissue; prever os tomo sapiens.

PN dimmune tissue; prever os spiens.

PN dimmune tissue; prever os protein.

PN descriper 1993; U19782.

PN 23-SEP-1998; U19782.

PR 23-SEP-1998; U19782.

PR 23-SEP-1998; U19782.

PR (RUBI/) RUBINO D M.

(RUBI/) PSCERS J.

PN 199-254688/21.

DR WPI; 99-254688/21.

DR WPI; 99-254688/21.

DR WPI; 99-254688/21.

DR WPI; 99-254688/21.

CC nuclear receptor-bin of escor con be detected usin the kit) to determin cc ther proliferative diseas sequence 1429 AA;
seq_documentation_block:
ID W31867 standard; Protein; 1382
AC W31867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                       seq_name: A_Geneseq_36:W31867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: A_Geneseq_36:W93941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: W93941 from: 1 to: 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1_COPY_1_229 x W93941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                         1282 uHis...ValArgArgGluAlaGlu.....ArgLeuSerGln
                                                                                                                                                                                                                                                                                                                       1266 AspLeuGluArgLeuArgAlaAlaGlnLysGlnLeuGluArgGluGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                               1249 rpLysArgSerGlyArgSerSerSerArgArgArgAlaH1sSerGlnTyr 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1236 .ProSerAlaArgArgArgCysSerArgGly.....SerArgThrT 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1226 ArgGluLeuArg......AspGlyArgProSerTrp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1b; Page 58-62; 69pp; English.

This invention describes a novel human breast cancer gene encoding a nuclear receptor-binding auxiliary protein, brx. The brx encoded protein has anti-cancer, anti-proliferative and mitogenic activity and acts as a transcription factor and tumour suppressor. Levels of expression of Brx can be detected using the primers, probes and antibodies (contained in the kit) to determine a predisposition to breast and ovarian cancer and other proliferative disorders of immune tissues. Vectors containing the Brx gene can be used for prevention and treatment of cancers and proliferative diseases of mammalian reproductive and immune tissues.
                                                                                                                                                                                                                           181 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226 |::: ||| ||||||::: |||||||||||:::
                                                                                                                                                                                                                                                                                                                                                                                   155 CAACTT.....TATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 GGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RUBI/) RUBINO D M.
(SEGE/) SEGERS J.
Driggers PH, Rubino DM,
WPI; 99-254688/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-SEP-1998; U19782.
23-SEP-1997; US-059621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brx protein; breast cancer; nuclear receptor-binding auxiliary protein; anti-cancer; anti-proliferative; mitogen; transcription factor; human; tumour suppressor; ovarian cancer; proliferative disorder; treatment; immune tissue; prevention; reproductive tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast cancer gene encoding a nuclear receptor-binding auxiliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W93941 standard; Protein; 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 CCCTAGTGCTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.00
1.837
52.439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Segers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 82
Gaps: 6
Percent Identity: 41.463
                                    ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
```

```
seq_documentation_block:

DW07702 standard; Protein; 543

AC W07702;

DT 06-APR-1997 (first entry)

DE Mouse ETS2 repressor factor '5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-240-675-1_COPY_1_229 x W31867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                   seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: W31867 from: 1 to: 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse and human metastasis-associated p150-derived antigens - useful for raising antibodies for therapy and diagnosis of tumours (Claim 3; Page 86-91; 111pp; English.

CThis protein comprises a novel human 150 kDa cell surface metastasis-associated antigen, designated p150. It is the homologue of a novel murine p150 metastasis-associated antigen (see w181866). Its amino acid sequence was deduced from an isolated cDNA (Clone (see T93627). A claimed method for determining the metastatic potential of a tumour cell comprises assessing the level (of p150 expression in the cell, a higher level of p150 expression to being indicative of a lower state of differentiation and consequently a higher metastatic potential. Immunogenic determinants of p150 and antibodies raised against them are useful in the diagnosis and treatment of metastatic potential in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-1997.
18-APR-1997; E01963.
28-FEB-1997; GB-004161.
29-APR-1996; US-016487.
(NOVS) NOVARTIS AG.
                                                                                                                                                        1035 AspArgGly 1037
                                                                                                                                                                                                                                       1018 roArgArgGlyLeuAspGluAspArgGlySerTrpArgThrAlaAspGlu 103.
                                                                                                                                                                                                  189 TCTGTCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                  985 spArgProSerTrpArgAsnThrAspAspAspArgProProArgArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            968 oArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAspA 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T93627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bachmann F;
WPI; 97-549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9741221-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR-1998 (first entry)
Human metastasis-associated antigen p150.
Antigen; p150; metastasis; tumour; cancer; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 TCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 CCAGATGATGGTCGTCCTCCT.....GGGCGCGACGACCCTAGTGCTCG
                                                                                                                                                                                                                                                                            TGAGG......TGGAACAGGAGCGATGAG
                                                                                                                                                                                                                                                                                                                   AlaAspGluAspArgGlyAsnTrpArgHis.AlaAspAspAspArgProP
                                                                                                                                                                                                                                                                                                                                                        TCCTCAAAAAGTAGAGGT.....CGACATCATAGATGACAACTTTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                     ......TGGAAAAATCT......AAAATC
                                                                                                                   A_Geneseq_36:W07702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97-549725/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.00
1.634
47.126
    factor (ERF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 87
Gaps: 6
Percent Identity: 32.184
                                                                                                                                                                                                                                                                                                                     1018
                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                  1001
                                                                                                                                                                                                                                                                                                                                                            165
                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
```

```
seq_documentation_block:
ID R96994 standard; Prot
AC R96994;
DT 16-AUG-1996 (first e
DE Mouse IRS-2; Insulin recept
KW IRS-2; Insulin recept
KW diagnosis; vector; an
OS Mus sp. Locat
FT domain Jabe
FT modifled_site Jabe
FT modifled_site Jabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_1_229/rev x W07702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA encoding ETS2 repressor factor - useful for reducing tumourigenicity, esp. oncogene associated tumour cells Disclosure; Page 70-72; 101pp; English.

Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS family and acts as a transcriptional repressor in mammalian cells. Its amino acid sequence was deduced from the murine ERF gene (T47198). Human ERF (see also W07700) has also been identified. ERF has tumour suppressor activity. Chimeric molecules comprising the ERF repressor domain in combination with a heterologous transcription factor having a binding domain can be used to reduce tumourigenicity associated with inappropriate expression of transcription factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TTCCACCTGCGGCTGCGGACAACACCCCATGGGCCCACGGCGACGAGCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-1996; U10177.
05-JUN-1995; US-469412.
(USSH ) US DEPT HEALTH &
Athanasiou MA, Beal GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETS2 repressor factor; ERF; transcriptional repressor; tumour suppressor; tumour; cancer; oncoprotein; therapy.
                                                                                                                                                                                                                                                                                                                      R96994 standard; Protein; 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9639517-A1.
                                                                                                                                                                                                                                                 IRS-2; insulin receptor substrate-2; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sgouras D N;
WPI; 97-043139/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T47200
                                                                                                                                                                                                                                                                                                                                                                                                                                           58 AGGGTCGTCGCGCCCAGGAGGA.....CGACCATCATCTGGGAGC 19
                                                                                                                                                                                                                                                                                                                                                                                                            aGlyGluLysAlaProGlyGlyThrAspLysSerSerGlyGlySer
                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_36:R96994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: W07702 from: 1 to: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 AA;
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.00
2.826
71.875
                                                                                     190. .366
/label= IH2
/note= "IRS-homology domain II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- DNA_binding_domain
/note- "ets-like DNA binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                    /note= "IRS-homology domain III"
                                                                                                                                            /label= IH1
/note= "IRS-homology domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Active_repressor_domain
       /note=
                                                        /label- IH3
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                               antibody; transgenic animal
                       . 80
                                                                         .527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  & HUMAN SERVICES.
J, Blair DG, Fisher RJ,
   "common phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 32
Gaps: 1
Percent Identity: 43.750
                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mavrothalassitis GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
```

```
alignment_scores:
Quality:
Ratio:
                                                                          New insulin receptor substrate polypeptide and corresp. nucleic acid receptor, antibodies etc., useful for diagnosis, treatment and receptor, antibodies etc., also for diagnosis, treatment and receptor substrate. Also for drug screening bisclosure; Page 47-33; 105pp; English.

Mouse insulin receptor substrate-2, or IRS-2 (R96994), is a substrate for the insulin receptor, interleukin-4 receptor and contain the insulin receptor, interleukin-6 tree by these receptors. It contains a number of phosphorylated by these common with IRS-1, showing the 2 proteins to be related. IRS-2 can be obtd. e.g. by affinity purification from insulin-stimulated FDC-P2 cells using immobilized SH2 domains of p85, or can be expressed in transformed host cells carrying an encoding cDNA sequence (T28933). Cells or animals having the IRS-2 transgene can be used to study insulin-related disorders, e.g. type II carrier.
                                                                                                                                                                                                                                                                                                                  03-OCT-1995; U13041.
03-OCT-1994; US-317310.
03-OCT-1994; US-317310.
(JOSL-) JOSLIN DIABETES CENT INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(USSH ) US DEPT MEALTH & HUMAN SERVICES.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9610629-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_site
                                                                   1321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "common reconstruction of the" 1031. 1036
/note= "unique phosphorylation site" 1060. 1065
/note= "unique phosphorylation site" 1241. 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= */
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-
499. .!
   63.50
1.984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627. .632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
135. .]
                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      570. .675
/note=_"common phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499. .504
/note= "common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .628
"common r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .125
"unique f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 542
                                                                                                                                                                                                                                                                                                                                                                                                                                     .1307
- "common phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "unique phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "unique phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "unique phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "unique phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "unique phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "common phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "unique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "common phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphorylation site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorylation
Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site"
 72
2
                                                                                                                                                                                                                                                                                                     acid
```

```
alignment_block:
US-09-240-675-1_COPY_1_229/rev x R96994
                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: R96994
                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                1078 aProProLysProGluGlyAlaArgValAlaSerProThrSerGlyLeuL 1095
                                                                                                                                                                                            1095 ysArgLeuSerLeu 1099
                                                                                                                                                                                                                                                            1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr
                                                                                                                              1062 ThrGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl 1078
                                                                                                                                                                                                                                                                                    124 GGAGATTTTAGATTTTTTCCACCTGCGGCTGCGGACAACACCCATGGGCC
                                                                                                                                                                40
                                17 GCCGCAGATCCCTG
                                                                                                  39
                                                                                                                                                                                                                           74 CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA.....
                                                                                                                                                                                                                                                                                                                                                                                                                    44.444
                                4
                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 29.167
                                                                                                                                                                                                                                                                                                                                 to: 1321
                                                                                               GGACGACCATCATCTGGGAGCC
                                                                                                                                                                40
                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                 1045
                                                                                               18
                                                                                                                                                                                                                                                                                                75
```

. 67

```
/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-06-09-4438-7 + 58-069-2-6/ptodata/1/1aa/5B_COMB.pep:US-08-09-09-4438-7 + 58-069-2-6/ptodata/1/1aa/5B_COMB.pep:US-08-59-0637-7 + 58-069-2-6/ptodata/1/1aa/5B_COMB.pep:US-08-505-218-4 + 58-069-2-6/ptodata/1/1aa/6_COMB.pep:US-08-46-509B-2 - 58-069-2-6/ptodata/1/1aa/5A_COMB.pep:US-08-48-518C-2 - 58-069-2-6/ptodata/1/1aa/5A_COMB.pep:US-08-348-518C-2 - 58-069-2-6/ptodata/1/1aa/5A_COMB.pep:US-08-348-518C-3 - 59-069-2-6/ptodata/1/1aa/5A_COMB.pep:US-08-348-518C-3 - 59-069-2-6/ptodata/1/1aa/5A_COMB.pep:US-08-348-518C-3 - 59-069-2-6/ptodata/1/1aa/5A_COMB.pep:US-08-095-734-2 - 59-069-2-6/ptodata/1/1aa/5A_COMB.pep:US-08-095-734-2 - 59-069-2-6/ptodata/1/1aa/5B_COMB.pep:US-08-095-734-2 - 59-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database sequences: 145308
Database length: 14437401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM of: US-09-240-675-1_COPY_1_229 to: Issued_Patents_AA:*
                                                 // Cgn2_6/ptodata/1/iaa/6_COMB.pep:US-08-471-869-2 - 57.00 100.00 20.53 / Cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:PCT-US94-08267-2 - 57.00 100.00 20.53 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-573-619B-7 - 56.00 113.07 18.50 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-675-629-58 + 56.00 113.07 18.50 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-673-269-2 - 55.50 115.76 19.43 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-6873-269-2 - 55.50 110.57 22.28 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-893-853-3 + 55.50 110.57 22.28 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-8440-845D-24 + 55.00 107.08 27.55 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-644-523B-30 + 55.00 107.08 27.55 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-840-845D-2 + 55.00 107.08 27.55 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-671-978A-10 + 55.00 107.08 27.55 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-804-227C-3 - 55.00 99.14 33.97 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-804-227C-3 - 55.00 91.52 41.53 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-805-528-2+ 55.00 91.52 41.53 / Cgn2_6/ptodata/1/iaa/5B_COMB.pep:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MODEL-frame+_n2p.model -DEV=x1p
-O-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164312_24612/app_query.fasta.
-DB-Issued_Patents_AA -OFMT-fastan -SUFFIX-modif.rai
-GAPOP-12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -OGAPOP-4.500 -GGAPEXT=-0.050 -XGAPOP-10.000
-XGAPEXT=0.000 -FGAPOP-6.000 -FGAPOXT-10.000
-YGAPEXT=0.500 -FGAPOP-6.000 -DELEXT=7.000 -YGAPOP-10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOXT-1
-MATRIX-blosum62 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-pct -ALIGN=15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext
-MINLEN=0 -MAXLEN=1000000 -USER-US09240675 -NCPU=6 -ICPU=3
-NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ptodata/1/18a/5B_COMB.pep:US-08-317-310A-64
/ptodata/1/18a/5B_COMB.pep:US-08-683-743-4 +
/ptodata/1/18a/5A_COMB.pep:US-08-323-170B-2 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ptodata/1/1aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1/1aa/5B_COMB.pep:US-08-469-412A-7
1/1aa/5B_COMB.pep:US-08-317-310A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMB.pep:PCT-US94-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pep:US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.00
58.00
58.00
58.00
57.50
57.50
57.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.00 127.23
63.50 114.96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Documentation 340.00 778.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.00
58.00
58.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               out_format :
                                                                                                                                                                                                                                                  00 109.49 25.85
00 107.08 27.55
0 107.08 27.55
0 102.02 31.49
99.14 33.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110.91
110.91
100.00
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.74
11.58
11.83
14.25
13.65
20.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00 20.53
18.50
22.64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/laa/5B_COMB.pep:US-08-835-231-18
/cgn2_6/ptodata/1/laa/5A_COMB.pep:US-08-188-582-22
                                                                                                                                                                                                           77
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                     US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-646-715-22 -
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US92-00331-3
                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                    Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: REVEL, Michel APPLICANT: ABRAMOVICH, Caroli APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                           TELEPHONE: 202-0-1
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: REV
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1, Application US/08328256 5643749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                           : 434 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.C.
                                                                                                                                                           to: US-08-328-256-11 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVEL, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVEL-13
                                                                                                                                                                                                                                        Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                                                                                                             434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.00
54.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.00
                                                                                              17
    176
                                 34
                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112.33
111.28
111.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.5
31.
31.
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-307-588-2
                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-307-588-2
                                                                                                                                                      Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                             Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SAXE, Bernhard D. REGISTRATION NUMBER: 28,665 REGISTRATION NUMBER: 177 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard REGISTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 A 227
27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
ZIP: 20007
                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Application US/08307588 5919453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BENOIT, Patrick MEYER, Francois MAGUIRE, Deborah PLAVEC, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLAVEC, Ivan
TOVEY, Michael G
                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/EP93/00770
                                                                                                                                                          Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17283/117/GUPL
                                                                                                                                                                                                 Length:
                                                                                                                                                        : 67
: 0
: 100.000
                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-328-256-12
                                                                                                                     alignment_scores:
                                                                                                                                                                            ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                             Percent Similarity:
                                                                                                                                                                                                                                                                TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-0CT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 yProTrpValLeuSerAlaAlaAlaGlyGlyLySASnLeuLySSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: REV
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12,
                                                                                                   Quality:
                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                             340.00
5.075
100.000
                                                                                                                                                                                                protein
                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                        REVEL-13
                                                             Gaps:
Percent Identity:
                                                           100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
```

```
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-328-256-10
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     guence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 41. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US//08/328,256 FILING DATE: 24-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERPERON ALPHA-RECEPTOR, ITS
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                 TELEFAX: 248633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                            NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REV
REFERENCE/DOCKET NUMBER:
                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGATGGTCGTCCTGGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ), Application US/08328256 5643749
                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVEL, Michel
                                                                                                                                                                                                                                                     202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BROWDY AND NEIMARK
                                                                                            protein
  340.00
                                                                                                                                                                                                                                                                                                                                  REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496
  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2,
                    TELEPHONE: (703) 816-400
TELEPAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                            REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,64
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GRESSER TITLE OF INVENTION:
                                                                                                                                 FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 NO CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUTFALLA,
                                                                                                                                                                                                                                                                                                          NUMBER: US/08/471,454
06-JUN-1995
                                                                                                                                                                                                                                                       US 07/900,642
                                                                                                                                     32,205
```

960-7

```
alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-328-256-10
                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                      77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08471454
1100 NORTH GLEBE ROAD
                                                                                                                                                                                  MOGENSEN, Knud E
                    NIXON & VANDERHYE P.C.
                                                                          PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                             CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR
                                                                                                                                                Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                             THE
```

LENGTH:

amino acid

557 amino acids

```
alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-471-454-2
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MOJERT GILLES APPLICANT: UZE, Gilles LUTEALLA, G
                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, ION
TITLE OF INVENTION: CDA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 s 67
                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Application US/08466974
5861258
                                                                                                                                                                                                                                                                                           22201-4714
                                                                                                                                                                                                                                                                                                                               VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                     E: NIXON & VANDERHYE P.C
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 557
                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: 15; MOLECULE TYPE: US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEEX: (703) OF TELEX: 200797 NIXN UR TELEX: 200797 NIXN UR INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: 57 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-466-974-2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08471453 Patent No. 5886153
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR THE TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOGENSEN, Knud E. APPLICANT: UZE, Gilles APPLICANT: LUTEALLA, Georges APPLICANT: GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 ATGATGGTCGTCCTGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
                                                                                                             STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                           CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BYRNE, THOMAS E. REGISTRATION NUMBER: 3
                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                          22201-4714
                                                                                                                                                                                   E: NIXON & VANDERHYE P.C
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                           GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                 LUTFALLA, Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340.00
5.075
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
```

OPERATING SYSTEM:

CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version #1.25

US/08/471,453

APPLICATION NUMBER:

```
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-471-453-2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 Amir-
                                                                                                                                                                Patent No.
                                                                                                                                                                              Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                         227 A 227
                                                                                                                                                                                                                                                                                                                                                                              177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                      APPLICANT:
                                                                        APPLICANT:
                                                                                           APPLICANT:
                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                       67 s 67
                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 ATGATGGTCGTCCTGCGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UFILING DATE: 15-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                  lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                              Application US/08307588
                                                BENOIT, Patrick
MEYER, Francois
MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340.00
5.075
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                    MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
 INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 557
                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-307-588-4
                  seq_documentation_block:
                                                        seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)672-5399 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 31-WAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhoud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: E
FILING DATE: 30-MAR-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                    227 A 227
                                                                                                                                                                                                                                                                        127 AAAAAGTAGAGGTCGACATCATAGATGACCAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            17 yProTrpValLeuSerAlaAlaAlaGlyGlyLySAsnLeuLysSerProG
                                                                                                67 s 67
                                                                                                                                                                          51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                  34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                              27 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                    77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 05-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Foley & Lardner
3000 K Street, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/08/307,588
05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17283/117/GUPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        557
                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                            17
```

GENERAL INFORMATION:

APPLICANT:

Aguet, Michel Bohni, Ruth

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

ADDRESSEE:

SSEE: Genentech, Inc.
T: 460 Point San Bruno Blvd
South San Francisco

ITLE OF INVENTION:

Hemmi, Silvio

Receptor Subunit Polypeptides

```
alignment_scores:
Quality:
                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-469-412A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-1_COPY_1_229 x PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: PCT-US94-14277-3
                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 8669
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 5.25 inch, 360 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC DOS/MS-SOFTWARE: PATIN (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/16 FILING DATE: 09-DEC-1993 ATTORNEY/AGENT INFORMATION: NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 5.25 in
                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                 208 TTTCATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                                                        158 CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 207
                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                   17 nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
                                                                                                                                                                                                                                                                                                                                                                                                         1 GluAsnLeuLysProProGluAsnIleAsp***TyrIleIleAspAspAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                              |||||| :::|||:::
heSerAlaGluTyrArg 39
                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94080
                                                                                                                                                   , Application US/08469412A 5856125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acids
       INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                    Fisher, Robert J.
Beal Jr., Gregory J.
Athanasiou, Meropi A.
                                                                                             Blair, Donald G.
                                                                                                          Mavrothalassitis, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112.00
3.613
79.487
Dionyssios N.
The ERF Genetic Locus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 39
Gaps: 0
Percent Identity: 48.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
   Its Products
```

```
seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-317-310A-64
                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-469-412A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1_COPY_1_229/rev x US-08-469-412A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                          Sequence 64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    APPLICANT: WHITE, MOTTIS F. APPLICANT: SUN, Xiao Jian APPLICANT: PIERCE, Jacalyn
                                                                                                                                                                                                                                                                                                                             383 aGlyGluLysAlaProGlyGlyThrAspLysSerSerGlyGlySer 398
                                                                                                                                                                                                                                                                                                                                                                                                           367 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 TTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCACT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                        NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..543
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                    58 AGGGTCGTCGCGCCCAGGAGGA.....CGACCATCATCTGGGAGC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER OF SEQUENCES:
                                                                                                   PPLICANT: PIERCE, Jacalyn H. ITLE OF INVENTION: THE IRS FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Garrett-Wackowski, EugreGISTRATION NUMBER: 37,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 05-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPOLOGY:
                                    DDRESSEE
                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                        1, Application US/08317310A
5858701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                     28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                         LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1fornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.00
2.826
71.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "murine ERF amino acid sequence
(first 8 amino acids from first exon no
included)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/469,412A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 32
Gaps: 1
Percent Identity: 43.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              015280-229000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eugenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acids from first exon not
                                                                                                     GENES
```

ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,065
REFERENCE/DOCKET NUMBER: JDPTELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

JDP-022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MSSOFTWARE: ASCII text

PC-DOS/MS-DOS

COUNTRY:

Massachusetts

02109

SOFTWARE: ASCII text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/317,310A FILING DATE: 03-OCT-1994 CLASSIFICATION: 435

TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:

(617)227-7400 (617)227-5941 OR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS: LENGTH: 1321 amino acids TYPE: amino acid

TOPOLOGY:

linear

protein

```
alignment_block:
US-09-240-675-1_COPY_1_229/rev x US-08-317-310A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: US-08-317-310A-64
                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-317-310A-64 from: 1 to: 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                      Sequence 4,
                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1045 oThrAlaGlySerSerMet.SerSerGluProGlyAspAsnGlyAspTyr 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                    1078 aProProLysProGluGlyAlaArgValAlaSerProThrSerGlyLeuL 1095
                                                                                                                                                                                                                  tent No.
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
ATREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1062 ThrGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl 1078
                                                                                                 APPLICANT: Pestka, Sidney
APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 GGAGATTTTAGATTTTTTCCACCTGCGGCTGCGGACAACACCCATGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA.....40
                                                                                                                                                                                                                                                                                                                                              ysArgLeuSerLeu 1099
                                                                                                                                                                                                                                                                                                                                                                                         GCCGCAGATCCCTG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                    , Application US/08683743 5843697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.50
1.984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
Gaps: 2
Percent Identity: 29.167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
```

```
alignment_scores:
                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-323-170B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-683-743-4 from: 1 to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-675-1_COPY_1_229 x US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                         Sequence 2, Application US/08323170B Patent No. 5733772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL: I
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TECHNOL ESC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                           APPLICANT: Williamson, Kim C.
APPLICANT: Kaslow, David C.
TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Tau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                                                                                                                                                                                            210 TCATTCGATTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 209
                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                               53 ThrAlaGlnTyr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.50
1.922
59.259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/683,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601-1-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _ 5
                                                                                                                Target Antigen, Pfs230
```

94111-3834

California

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-469-427A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-240-675-1_COPY_1_229 x US-08-323-170B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-03: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADDITION NUMBER: US/08/323,170B
                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Quine, Jonathan A.
REGISTRATION NUMBER: p-41,261
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          803 rCysPheGlu...GluMetIleProTyrAsnLysGluIleLysTrpAsnL 819
                                                           TITLE OF INVENTION: VASCULAR ENDOTHELIA TITLE OF INVENTION: DNA CODING THEREFOR NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             819 ysGluAsnLysSerLeuGlyAsnLeuValAsnAsnSerValValTyrAsn 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GGAGCGATGAGTCTGTCGGGAAT...GTGACTTTTTCATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 AAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 787 SerGlyAspIleGlyGlyIleLeuPheProLysAsnIleLysSerThrTh 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/010,409
FILING DATE: 29-JAN-1993 TATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    225 AAA 227
                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 TCCGCAGCCGCAGGTGGA.....AAAAATCTAAAATCTCCTCA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/OFILING DATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                      Lys 836
                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
                                                                                                                                                                                                                                                           Application US/08469427A
                                                                                                                           Eriksson, Ulf
Olofsson, Birgitta
Alitalo, Kari
Pajusola, Katri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3135 amino acids
1200 G Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.00
1.844
62.745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576-0300
576-0300
2:
                                                                                                         VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 37.255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     015280-113100US
Edwards & Lenahan
Suite 700
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-469-427A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                     seq_documentation_block:
                                                                            seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-609-443B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-469-427A-7 from: 1 to: 195
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 628-884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 01-MAR-1
                                                                                                                      149 sProProCys 152
                                                                                                                                                              193 TCGGGAATGT 202
                                                                                                                                                                                                     133 ProLysLysGluSerAlaValLysProAspSerProArgIleLeuCy 149
                                                                                                                                                                                                                                                                                       116 erGlnLeuGlyGluMetSerLeuGluGluHisSerGlnCysGluCysArg 132
                                                                                                                                                                                                                                                                                                                                 114 CTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE: adult mouse heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                             MOLECULE TYPE: PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          99 tGlnValProGlyProMetGlyGlnIleLeuMetIleGlnTyrProSerS 116
                                                                                                                                                                                                                                                                                                                                                                                                                64 TCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAAT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 ProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMe 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CCAGATGATGGTCGT......CCTCCTGGGCGCGACGACCCTAGTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/O FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
               lication US/08609443B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER: US 08/397,651
01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.00
1.611
51.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/469,427A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 24.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41979cp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 70
```

INFORMATION:

ERIKSSON, Ulf OLOFSSON, Birgitta

```
alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_1_229 x US-08-609-443B-7
                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-609-443B-7
                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D
REGISTRATION NUMBER: 26,269
REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US FILING DATE: 01-MAR-19 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: VASCULAR ENDOTHELIAL TITLE OF INVENTION: DNA CODING THEREFOR NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & STREET: 1200 G Street, N.W., Suite 700
                                    116 erGlnLeuGlyGluMetSerLeuGluGluHisSerGlnCysGluCysArg 132
                                                                            114 CTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTAT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MOLECULE TYPE: PI
                                                                                                                99 tGlnValProGlyPrometGlyGlnIleLeumetIleGlnTyrProSerS 116
                                                                                                                                                           64 TCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAAT 113
                                                                                                                                                                                                   83 ProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMe 99
                                                                                                                                                                                                                                          23 CCAGATGATGGTCGT......CCTCCTGGGCGCGACGACCCTAGTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1200 G ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAJUSOLA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adult mouse heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                    58.00
1.611
51.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/609,443B
                                                                                                                                                                                                                                                                                                                                                                            Length: 70
Gaps: 2
Percent Identity: 24.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1064/41979CP4
                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                  to: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lenahan, P.L.L.C.
```

149 sproproCys 152

```
Search information block:
Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: PIR_63:*
Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000
                                                                                                                                                                                                                                                                                                              pir2:A45283
pir2:S13141
pir2:S13141
pir2:S13181
pir2:UC5807
pir2:UC9803
pir2:T08930
pir2:T08930
pir2:T13088
pir2:T13088
pir2:T130841
pir2:H02841
pir2:T02841
pir2:T02841
pir2:T30255
pir2:A70034
pir2:A70035
pir2:A70035
pir2:A70035
pir2:A70035
pir2:T34674
pir2:T34674
pir2:T35558
pir2:T35558
pir2:T35558
pir2:T35558
pir2:T35558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                               pir2:D64969
pir2:JX0140
pir2:JX0563
pir2:I46480
pir2:I46480
pir2:I46479
pir2:I46479
pir2:B24853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MODEL-frame+_n2p.model -DEV=xlp
-0-/cgn2_1/USPT0_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-0-/cgn2_1/USPT0_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-0-B-FIR_63 -QFMT-fastan -SUFFIX-modif.rpr -GAPOP=12.000
-GAPEXT-4.000 -MINARCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-GAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALIGN-200 -THR_SCORE-pct
-TALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
                                                                                                                                                                                                                                                      pir2
pir2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of: US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000 12:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   orig
340.(
209.(
      ZSCOTE
728.23
440.02
      154.79
123.91
123.93
123.03
123.03
123.03
123.03
125.58
125.58
125.58
122.45
123.38
124.43
124.43
124.43
125.58
127.45
127.45
128.33
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
129.36
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR_63:*
      ESCO-78
2.0e-37
2.2e-17
2.2e-17
0.3143
0.3153
0.3153
0.3153
1.85
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36
1.7.36

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E Len : 557 | 560 | 590 | 590 | 304 | 304 | 304 | 1106 | 11106 | 571 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1257 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -NO_XLPXY -WAIT
| O-antigen transporter - Escheri | Cytochrome-c oxidase (EC 1.9.3. | phosphate acetyltransferase - I | c-mer tyrosine kinase receptor | calcium channel BI-2 - rabbit | calcium channel BI-2 - rabbit | tolacium channel BI-2 - rabbit | hypothetical protein (transducin hypothetical protein APE0658 - hypothetical protein R0785.3 - | hypothetical protein R0785.3 - | l class I histocompatibility anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I nuclear pore complex protein n
hypothetical protein Y105C5B.o.
I hypothetical 19.5K protein (W
hypothetical protein T15N24.90
major polyhedral calyx protein
DNA-packaging protein - phage N
comc-alpha protein - phage T4
PRJ64 protein - chicken
probable membrane protein MTCC
MHC class I histocompatibility
phospholipase C (EC 3.1.4.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon alpha/beta receptor interferon alpha receptor type interferon alpha/beta receptor hypothetical protein (ribosomal hypothetical protein F23K16.40 trp3 protein - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Documentation
                                                                                                                                                                                                                                                                                                                        phosphoenolpyruvate carboxylase hypothetical protein SC1A9.25c DNA-directed RNA polymerase all hypothetical protein F08D12.9 rtractin - medicinal leech probable cytochrome P450 monoox hypothetical protein T25F10.2 hypothetical protein T25F10.2 hypothetical protein T25F10.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inversin - mouse

pR564/SC35 protein - human

splicing factor SC35 - human

cytokine receptor family II, me

cytokine receptor family class

cytokine receptor family class

CLM3 protein - yeast (Saccharom

hypothetical protein RV0312 - M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pir2:T31639
pir2:A38845
pir2:S14016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                   seq_documentation_block:
interferon alpha recepto
                                                                                                         seq_name: pir2:S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                         227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                  A 227
                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                       receptor type 1
```

```
interferon alpha/Deta receptor precursor - hu
C;Species: Homo sapiens (man)
C;Species: 22-Jun-1990 #sequence_revision 22-Jun-
C;Accession: A32694; SI7112
R;Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-334, 1990
A;Title: Genetic transfer of a functional huma
A;Reference number: A32694; MUID:90124632
A;Accession: A32694
A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Gene: GDB:120078; OMIM:107450
A;Cross-references: GDB:120078; OMIM:107450
A;Cross-references: GDB:12021,
A;Map position: 21q22.1-12q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; glycoprotein; transmembrane #status predicted <TRN1>
F;4-121/Domain: transmembrane #status predicted <TRN2>
F;437-455/Domain: transmembrane #status predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate
                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A; Cross references: EMBL:X60459; NID:g32671
C; Genetics: TANNAL TRUE
                                                                                                                                                                                                                                                                                    R;Lutfalla, G. submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human interferon alpha/beta receptor gene.
A;Reference number: $17112
A;Accession: $17112
                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-557 <UZED
A; Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
121
120
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.32
1.72
1.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-Jun-1990 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
48
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .18
.57
.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon alpha receptor into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433
140
164
164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Y57A10. flagellar protein required X16 protein - mouse pre-mRNA splicing factor -
                                                                                                                                                                                                                                                                                                                                                                                                             PID: g306914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse
```

```
: 340.00
: 5.075
: 100.000
                                                              x A32694
                                                        from: 1 to:
                                                                         Length:
Gaps:
Percent Identity:
                                                                          : 67
: 0
: 100.000
                      176
                                    126
                                           17
                             34
                50
```

precursor

```
interferon alpha/Deta receptor - mouse (Species: Mus musculus (house mouse) C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A:Title: Behavior of a cloned murine interferon alpha/Deta receptor expressed in A;Reference number: A45283; MUID:92262522
A;Note: sequence extracted R;Lutfalla, G.; Uze, G. Gene 148, 343-346, 1994
                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <UZE>
                                                A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112
A;Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIP:102357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:.06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
A;Experimental source: lung
C;Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S33770
R:Mouchel-Vielh, E.: Lutfalla, G.: Mogensen, K.E.: Uze, G.
FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_1_229 x S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-421,'V',423-560 <LIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Lim, J.K.; Langer, J.A.

Biochim. Biophys. Acta 1173, 314-319, 1993

A:Title: Cloning and characterization of a bovine alpha
A;Reference number: S33770; MUID:93305725

A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-560 < MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Specific antiviral activities of the human alpha interferons are determined at A;Reference number: S27387; MUID:93076908 A;Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X68443; NID: g431; PIDN: CAA48484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 179 ::!|||||:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetLeuAlaLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209.00
3.800
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID: 9432
                                                                                                                                                                                                                                                             homospe
```

```
seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_1_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 177/3; 331/1 C;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DN/
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 426-445 <RE6>
A; Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: 148423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-sa; Reference number: I48423; MUID:95047447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DN/
A; Residues: 397-424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 243-264 < RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type:
A; Residues: 127-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262
A;Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 265-375 <RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: I48426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DN
A;Residues: 118-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated
                                                                              180
                                                                                                                                     34 snileAspValTyrileIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                    17
                                                                                                                                                                                                                   80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 129
                                        51
                                                                                                                                                                                                                                                                                                                     30 ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                 1 MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                oTrpValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA
                                      H1sGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg
                                                                            AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA
pir2:S13141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                   A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: U06244; NID: g497114; PIDN: AAA65008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL:U06241; NID:g497110; PIDN:AAA65006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198.00
3.536
86.154
                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                 ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
Identity:
                                                                                                                                                                                                                                                                                                                                                                 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.385
                                      65
                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID: 9510265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g755813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID: 9755812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:9755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: 9755810
```

seq\_documentation\_block:
hypothetical protein (ribosomal

RNA repeat region) -

Giardia lamblia

```
A;Note: the source is designated as Giardia intestinalis A;Note: readthrough of the terminator TAG is supposed to occur between residues 241-Ala R;Healey, A; Mitchell, R; Upcroft, J.A.; Boreham, P.F.L.; Upcroft, P. Nucleic Acids Res. 18, 4006, 1990
A;Title: Complete nucleotide sequence of the ribosomal RNA tandem repeat unit from Giard A;Reference number: S10886; MUID:90326542
A;Accession: S10886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T09357
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
hypothetical protein F23K16.40 - Arabidopsis thallana
C:Species: Arabidopsis thallana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X52949
A;Note: the source is designated as Giardia
A;Note: the assignment of the coding region
C;Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Upcroft, J.A.; Healey, A.; Mitchell, R.; Boreham, P.F.L.; Upcroft, P. Nucleic Acids Res. 18, 7077-7081, 1990
A;Title: Antigen expression from the ribosomal DNA repeat unit of Giardia intestinalis. A;Reference number: S13141; MUID:91088287
A;Accession: S13141
alignment_block:.
US-09-240-675-1_COPY_1_229 x T09357
                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.40
A;Experimental source: cultivar Columbia; BAC clone F23K16
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-304 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-240-675-1_COPY_1_229/rev x S13141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-294 <UPC>
                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                              A; Map position: 4
A; Introns: 129/2; 243/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z16652
A; Accession: T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: p1r2:T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-241 <HEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X52949
                                                                                                                                                                                                                                                                                                   A; Gene: ATSP: F23K16.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: S13141 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Giardia lamblia
;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 24-Nov-1999
;Accession: S13141; S10886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 AGGAGGACGACCATCATCTGGGAGCCGCCGCAGATCC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgArgSerAlaGlnGlyProArgAlaArgArgArgGlyAlaAlaArgPr 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oGlyAsnArgGlyAlaGlyGlyProArgArgArgSer 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGACAACACCCATGGGCCCACGGCGACGAGCACTAGGGTCGTCGCGCCC 44
                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.00
3.500
75.862
                                                                                     77.00
1.878
57.746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent
                                                                                           Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identity:
                                                                                        Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intestinalis
has been rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
0
51.724
                                                                                     71
4
33.803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             revised in reference S13141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mewes, H.W.; Mayer, K.F
```

```
R;Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I. Biochem. Biophys. Res. Commun. 240, 167-172, 1997
A;Title: Expression and characterization of a trpl homolog from rat. A;Reference number: JC5807; MUID:98042538
A;Accession: JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_1_229 x JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: TRPC3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-828 cPRE>
A;Experimental source: brain
C;Comment: This protein participates in store-operated Ca2+ entry into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trp3 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                           217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                            388
                                                                                                                                      174
                                                                                                                                                                                 371 etLysPheValAlaAlaSerPheIleIlePheLeuGlyLeuLeuValPhe
                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                                                                                     338 LeuValValLeuValValAlaLeuAlaLeuProPheLeuAlaIleGlyTy 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ATGAGTCTGTC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 sAsnThrAlaSerLeuGlyValValSerSerLeuLysMetLysLys.Leu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 AspAsnGlyArgHisHisHisHisAspThrProSerArgHisAspLysHi 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                     80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCT.... 125
                                                                                                                                                                                                                                                                                                                                                                                                               30 ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 GATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGT..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rGluValAspValLeuAspAspGlyTyr.....ArgTrpArgLysTyrG 232
l...IleAspTyrProLys 409
                                            TTCATTCGATTATCAAAAA 227
                                                                                                                                    AACAGGAGCGATGAGTCTGTCGGG......AATGTGACTTT 208
                                                                                                                                                                                                                              ..CAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyGlnLysVal 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysThrArgArgLysValArgGluProArgPheCysPheLysThrLeuSe 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTA 116
                                                                                         AsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIleThrVa 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .GAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.00
1.614
60.274
                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
3
34.247
                                                                                                                                                                                   387
                                                                                                                                                                                                                                                                           371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
```

```
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20208
A;Reference number: Z20208
A;Recession: T26391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-194 <WIL>
A;Residues: 1-194 <WIL>
A;Cross·references: EMBL:AL110479; NID:e1542153; PIDN:CAB54363.1; CESP:Y105C5B.o
A;Experimental source: clone Y105C5B
C;GenetLcs:
A;Gene: CESP:Y105C5B.o
A;Introns: 13/1; 56/3; 155/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nuclear pore complex protein nup153 - human C;Species: Homo sapiens (man) C;Pate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C;Pate: 13-Jan-1995 #sext_change 05-Nov-1999 C;Pate: 13-Jan-1995 #sext_change 05-Nov-1999 C;Pate: 13-Jan-1995 #text_change 05-Nov-1999 C;Pate: 13-Jan-1995 #sext_change 05-Nov-1999 C;Pate: 13-Jan-1995 P;Pate: 13-Jan-1995 P;Pate: 13-Jan-1995 P;Pate: 13-Jan-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Y105C5B.o - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T26391
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-240-675-1_COPY_1_229/rev x S42718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-1475 <MCM>
A;Cross-references: EMBL:225535; NED:g406224; PIDN:CAA80982.1; PID:g406225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: p1r2:T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:S42718
   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: S42718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1314 erAlaSerProAlaPheGlyAlaAsnGln 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1264 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1298 SerSerAlaGlySerSerPheValPheGlyThr.GlyProSerAlaProS 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 ACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTGTCATCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGACAACACC......CATGGGCCCACGGCGACGAGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTCCACCTGCGGCTG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGACGACCATCATCTGGGAGCCGCCGC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erAsnAsnThrThrThrSerGlyPheGlyPheGlyAlaThrThrSer 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.00
1.683
53.247
   68.50
1.756
69.643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....ACTAGGGTCGTCGCGCCCAG 42
                                        Gaps:
56
2
32.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
3
33.766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical 119.5k protein (uvrA region) - Micrococcus luteus N;Alternate names: ORF 1 protein C;Species: Micrococcus luteus, Micrococcus lysodeikticus C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993 C;Accession: JQ0405
C;Accession: JQ0405
C;Shiota, S; Nakayama, H.
R;Shiota, S; Nakayama, H.
A;Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: idental Reference number: S04781; MUID:89364717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1106 <SHI>
A;Cross-references: EMBL:X15867
A;Note: all the codons between
A;Note: the gene encoding this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_1_229/rev x JQ0405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_1_229 x T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: pir2:JQ0405
   seq_name: pir2:T08930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: JQ0405 from: 1 to: 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 TCATCTATGATGTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTCC 105
                                                                                                                                                                                                                                                                                                                                                                                                                    104 ACCTGCGGCTG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 TCACATTCCCGACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 GAGTCTGTCGGGAATGTG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 AGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGAT 185
                                                                        93
                                                                                                                                          34
                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 SerProThrGlyGluThrProValSerCysPro....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 GluGlnValAlaAsnMet 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 isIleAsnLeuLeu.....AsnGlyIleArgGlnLysAsnAlaIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 lLeuSerValThrValLysArgAsnMetThrGluTyrGluGlnLysIleH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 GTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 GTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetLeuLeuArgAlaIleLeuLeuIlePheIleSer...AlaProTrpVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .........CysProProLeuCysTrpProArgAlaGlnGluLeuLeuH
                                                                     gProArgAlaGlnProGluGlyArgGlyCysGln 104
                                                                                                                                      ACCATCATCTGGGAGCCGCCGCAGATCCCTGCAG 1
                                                                                                                                                                                                        ProArgArgAlaLeuGlyArgAlaGlyProHisArgArgProGlyAr
                                                                                                                                                                                                                                                                                                                                                  isHisArgLeuLeuArgArgArgGlyProArgArgArgProArgLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JQ0405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.50
1.875
46.154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             two in-frame stop codons are translated; protein overlaps uvrA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
                                                                                                                                                                                                                                                                                                                                                                                                                       .....CGGACAACACCCATGGGC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
3
30.769
                                                                                                                                                                                                                                                                                                                                                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene: identification
```

the

translat:

```
A;Molecule type: DNA
A;Residues: 1-252 <AXR>
A;Residues: 1-252 <AXR>
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66761.1; PID:g559200
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66761.1; PID:g559200
R:Oellig, C.; Happ, B.; Mueller, T.; Doerfler; W.
J. Virol. 61, 3048-3057, 1987
A;Title: Overlapping sets of viral RNAs reflect the array of polypeptides in the A;Reference number: A43679; MUID:87311863
A;Accession: C43679
                                                                                                                                                                                                                                                        R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus A;Reference number: A72850; MUID:94303173
A;Accession: D72866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z16518
A; Accession: T08930
                                                                                                                                                                                                                                                                                                                                                                               C; Accession: D72866; C43679
                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                    major polyhedral calyx protein - Autographa californica nuclear polyhedrosis virus C:Species: Autographa californica nuclear polyhedrosis virus, ACMNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: A; Introns: 76/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AL078465; GSPDB:GN00062; ATSP:T15N24.90
A;Experimental source: cultivar Columbia; BAC clone T15N24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-571 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Bevan, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:D72866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: ATSP:T15N24.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: T08930 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1_COPY_1_229 x T08930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: T08930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 pGlyTyr.....ArgTrpArgLysTyrGlyGlnLysValValArgGlyA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 luProArgValValValGlnThrLeuSer.GluValAspIleLeuAspAs 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 ProAspAsp.........AspAspProPheSerLysArgAr 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sn 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTC.....GGGA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gArgMetGluGlyAlaMetGluIleThrProLeuValLysProIleArgG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGCCCATGGGT......GTTGTCCGCAGCCGCAGGT
    preliminary
e type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76/3; 90/3; 142/3; 311/1; 363/2; 415/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.00
1.711
55.882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 68
Gaps: 5
Percent Identity: 33.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
C;Genetics:
A;Gene: Ac-PE/pp34
                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:T13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-252 <OEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: phage N15
                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      packaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
    ωS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene 2
                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
.CGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGC
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x T13088
                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: phage lambda DNA packaging protein
C;Keywords: DNA packaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, submitted to the EMBL Data Library, May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999 C;Accession: T13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_1_229/rev x D72866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: AF064539; NID: g3192683; PID: g3192685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z17603
A; Accession: T13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: terminase large chain gp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-640 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: D72866 from: 1 to:
                                      101 GluLeuLeuTrpLeuProThrAspGlyAspAlaAspAsnPheMetLysSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 CTGTTCCACCTCAGGATAAAGTTGTCATCTATGATGTCGACCTCTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 PheTyrArgArgArgSerArgSerArgSerArgSerArgSerArgSe 112
                                                                                   8 GATCTGCGGCGGCTCCCAGATGATGGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rSerProArgArgGlyArg 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTGGGAGCCGCCGCAGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgProArgSerArgSerArgSerArgSerArgSerArgSerArgSerSe 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCCACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGAGGACGACCATC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGAGGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTTGATAATCGAATGAAAAAGTCACATTCCCGACAGACTCATCGCTC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein - phage N15
                                                                                                                                to: T13088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:M17548; NID:g808747; PIDN:AAA66805.1; PID:g808750
                                                                                                                                                                                                                                            63.00
1.340
47.475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.50
1.924
45.205
                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
Percent Identity:
                                                                                                                                                                                                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....ArgSerArgSerProHisCys 126
                                                                                                                                ţ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
                                                                                                                                640
                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                            99
4
26.263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
2
31.507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.E.; Ravin, N.V.; Smirnov, I.K.
77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN: AAC19038.1
```

trans-

```
comC-alpha protein - phage T4
N;Alternate names: gp comC alpha
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C;Accession: A45731
seq_documentation_block:
PR264 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 26-May-1994 #sequence_revision
C;Accession: B42701; S17327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Map position: 5.848-6.274
C:Superfamily: phage T4 comC-alpha protein
C:Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Title: Sequence and characterization of A.Reference number: A45731; MUID:93015705 A.Accession: A4573 A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
                                                                                                                        seq_name: pir2:B42701
                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
    US-09-240-675-1_COPY_1_229 x A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: comC alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-141 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                 69
                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGAT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProTrpTyrGlyLysLysHisArgAspAsnThrLeuSerMetLysArgPh 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rHisValGluProThrIleArgAspValProSer.LeuLeuSerLeuAla 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yrArgGluLysSerValAspValValGlyTyrAspGluLeuAlaAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 173
                                                                                                                                                               sArgCysAlaGlyGly
                                                                                                                                                                                                                                                                                       CGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCG 141
                                                                                                                                                                                                                                                                                                                                                                      CTGGGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspAlaAspIleGluLysGluGlySerProThrPheLeuGlyAsp 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eThrAsnGlyArgGlyPheTrpCysLeuGlyGlyLysAlaAlaLysAsnT 167
                                                                                                                                                                                                                                                                                                                              LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:M89919; NID:g215829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.50
2.155
58.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ........GCCGCAGGTGGAAAAATCTAAAATCTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .........GTGTTGTCCGCA.....
                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                               to: 141
                       26-May-1994 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the bacteriophage T4 comCalpha gene product,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:AAA32485.1; PID:g215832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
: 34.000
                                                                                                                                                                   83
                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Vellard, M.; Sureau, A.; Soret, J.; Martinerie, C.; Perbal, B. Proc. Natl. Acad. Sci. U.S.A. 89, 2511-2515, 1992
A;Title: A potential splicing factor is encoded by the opposite strand of the A;Reference number: A42701; MUID:92212859
A;Accession: B42701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T02841
R; Myler, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                          alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T02841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:T02841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                A;Gene: MTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                     Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x B42701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, May 1998 A; Description: The nucleotide sequence of Leishmania major Friedlin chromosome A; Reference number: 214740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X62446; NID:g63751; PIDN:CAA44306.1; C;Superfamily: unassigned ribonucleoprotein repeat-containing F;15-82/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                          alignment_block:
US-09-240-675-1_COPY_1_229 x T02841
                                                                                                                                                                                                                                                                                                                        C; Superfamily: Saccharomyces probable membrane protein YOR271c
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-326 <MYL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
probable membrane protein MTCC - Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-221 <VEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AE001274; NID:g3264850; PID:g1617564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: B42701
                                                                      Align seg 1/1 to: T02841 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 lyArgArgSerArgSerProArgArgArgArgArgSerArgSerArgSer 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 .... GGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 sHisSerArgArgGlyProProProArgArgTyrGlySerSerGlyTyrG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AGGGATCTGCGG....CGGCTCCCAGATGATGGTCGTCCTCCT.....
TGCGGCGGCTCCCAGATGATGGTCGTCCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgSerArgSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAGTAGAGGTCGA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCGC.....AGCCGCAGGTGGAAAAATCTAAAATCTCCTCA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.50
2.083
54.545
                                                                                                                                                                                   62.50
1.645
57.576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent
                                                                                                                                                                                        Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
                                                                      to: 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identity:
                                                                                                                                                                                        Identity:
                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.182
                                                                                                                                                                                        30.303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 10-Dec-1999
    _ ନ
                             46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:g63752
proteins; ribonucleopro
```

	206	138	189	94	172	47	9CT
ri .	206 SerSerGlyGlnGlyIleArgValValAspAspAspGlyValThrArg 221	GTCGACATCATAGATGACAACTTTATCCTGAGG 170	189 erCysAlaAlaThrValAsnLeuAlaSerMetArgLysAsnGluTrpLeu 205	94 CAGCCGCAGGTGGAAAAAATCTTCTCCTCAAAAAGTAGAG 137	172 yThrThrThrSerThrLeuIleArgAlaThrValProPheLeuAlaValS 189	47 CGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTGTCCG 93	156 CysGlyGlySerLeuLeuAlaThrMetTrpLeuLySArglieProThrGL 1/2

```
Score_list:
Sequence
Svissprot_38:INR1_HUMAN +
Svissprot_38:INR1_BOVIN +
Svissprot_38:INR1_BOVIN +
Svissprot_38:INR1_MUMAN -
Svissprot_38:INR1_MUMAN -
Svissprot_38:IR52_HUMAN -
Svissprot_38:IR52_HUMAN -
Svissprot_38:IR52_HUMAN -
Svissprot_38:IF3A_HUMAN -
Svissprot_38:IF3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database: SwissProt_38:*
Database sequences: 83857
Database length: 30454973
Search time (sec): 45.030000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MODEL-frame+_n2p.model -DEV-xlp
-Q-/cgn2_1/USPTQ.spoo1/US09240675_runat_30052000_164313_24686/app_query.fasta.1
-Q-/cgn2_1/USPTQ_spoo1/US09240675_runat_30052000_164313_24686/app_query.fasta.1
-DB-SW1sSPTC_38 -QFMT-fastan -CUFFIX-modif.rsp -GAPOP-=12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -STARF-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results were produced by the Gene Copyright (c) 1993-2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           line parameters:
               rd Orig ZScore EX NN + 340,00 695 87 181 198.00 397.55 19 4 68.00 1121.79 N + 68.00 1121.79 N + 68.00 1121.75 11 66.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 1121.50 11 62.50 11 62.50 11 62.50 121.50 11 62.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 121.50 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e GenCore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESCOTE Len
6.5e-32
6.1.3e-16
7.5.0e-16
7.2.5e-15
80 3.20
9.4.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.40
15.93
15.93
219.94
210.84
221.41
223.32
23.32
37.32
37.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.93
43.02
                     53.13
52.57
53.77
55.73
56.24
56.24
56.42
56.42
56.40
57.92
57.92
61.56
                                                                                                                                                                                                                                                                                                                                                                          43.40
48.88
49.87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.29
13.93
15.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      software,
in i Documentation ...

557 | P17181 homo sapiens (human) ...

560 | 004790 bos taurus (bovine) ...

560 | 028589 ovis aries (sheep) ...

590 | P3896 mus musculus (mouse) ...

1475 | 049790 homo sapiens (human) ...

854 | 079069 homo sapiens (human) ...

858 | 079069 homo sapiens (human) ...

551 | P970459 mus musculus (mouse) ...

1341 | P31122 mus musculus (mouse) ...

1342 | P23116 mus musculus (mouse) ...

1343 | P070459 mus musculus (mouse) ...

1344 | 0201438 bacteriophage t4 ...

1346 | P08020 pseudomonas aeruginos ...

221 | P080352 gallus gallus (chicke ...

730 | P08034 homo sapiens (human) ...

580 | P13365 saccharomyces coerevis ...

580 | P13365 saccharomyces coericul ...

140 | P23452 bacillus ps3 (thermory ...

141 | 080910 human papillomavirus ...

1496 | P3150 homo sapiens (human) ...

1406 | P31670 methanococcus Jannas ...

1407 | P31671 musculus ...

1508 | P31672 homo sapiens ...

1608 | P31673 methanococcus Jannas ...

1709 | P31673 methanococcus Jannas ...

1809 | P31674 lotus tetragonolobus ...

1809 | P31675 methanococcus Jannas ...

1809 | P31675 methanococus ...

1809 | P31675 methanococcus ...

1809 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       out_format :
                                                                      21 | P81122 mus musculus (mouse)
44 | P3316 mus musculus (mouse)
44 | P3316 mus musculus (chicke
64 | Q01438 bacteriophage t4. com
75 | P30352 gallus gallus (chicke
76 | P66200 pseudomonas aeruginos
76 | P66200 pseudomonas aeruginos
77 | Q01334 homo sapiens (human).
77 | Q01334 homo sapiens (human).
77 | P13365 saccharomyces corevis
77 | P72404 streptomyces coelicol
77 | P72404 anabaena sp. (strain
77 | P72404 anabaena sp. (strain
77 | P72404 streptomyces coelicol
77 | P72404 anabaena sp. (strain
77 | P72404 anabaena spiens (human)
77 | P72404 anabaena spiens (human)
77 | Q80910 human papillomavirus telphan
78 | Q014562 homo sapiens (human)
79 | Q14562 homo sapiens (human)
70 | Q14562 homo sapiens (human)
71 | Q39610 chlamydomonas reinha
72 | Q14562 homo sapiens (human)
73 | Q14562 homo sapiens (human)
74 | P72633 prassica oleracea var
75 | P72633 spiroplasma virus spvl
76 | P72633 spiroplasma virus spvl
77 | P72633 spiroplasma virus spvl
77 | P72633 spiroplasma virus (chicke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       þfs
                        seq_name: SwissProt_38:INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:YA02_SCHPO
SwissProt_38:SRFA_MOUSE
SwissProt_38:MMS3_MYCTU
SwissProt_38:TAP_DROME +
                                                                                                                                                                                                                                                                                                             EMBL; J03171; AAA52730.1; -
EMBL; X60459; CAA42992.1; -
PIR; A32694; A32694.
PIR; S17112; S17112.
MIM; 107450; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              documentation_block:
                     DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INR1_HUMAN
P17181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                           Phosphorylation SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60:225-234(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90124632.
                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . + +
                           436
457
557
87
220
                                                                                                                                                                                            27
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.50
57.50
57.50
57.50
                                                                                                                                                                                                                                                                                     Glycoprotein; Signal; Polymorphism.
                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                    CHAIN.
                                                                                                                                                                                                  POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR ALPHA
```

a collaboration

```
PHOSPHORYLATION BY TYK2.

RY MEDLINE; 95059042.

RA COlamonici O., Yan H., Domanski P., Handa R., Smalley D.,

RA Mullersman J., Witte M., Krishnan K., Krolewski J.;

RA Mullersman J., Witte M., Krishnan K., Krolewski J.;

"Direct binding to and tyrosine phosphorylation of the alpha subunit

RT of the type I interferon receptor by p135tyk2 tyrosine kinase.";

RC INCLUDING JAMES TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

C INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

C SUBGUNITS THEMSELVES.

C INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

C SUBGULITAR LOCATION: TYPE I MEMBRANE PROTEIN.

C INTESUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND

EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.

C INTENDICTION SUBGUNIANES OF THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

C INTENDICTION SUBGUNIANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE; 92129376.

Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;

The structure of the human interferon alpha/beta receptor gene.";

J., Biol. Chem. 267:2802-2809(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uze G., Lutfalla G., Gresser I.;
"Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110.4
109.7
108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 41
J. 03
B. 57
. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.51
62.28
62.54
63.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ያ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i Q09675 schizosaccharomy
i Q60701 mus musculus (mo-
i Q10390 mycobacterium tul
O16867 drosophila melano-
```

```
REPRESENTATION OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: SwissProt_38:INR1_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_1_229 x INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
SEQUENCE FROM N.A.
TISSUE-LUNG;
MEDLINE; 93076908.
MOUCHE1-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
MOUCHE1-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
Specific antiviral activities of the human alpha interferons
determined at the level of receptor (IFNAR) structure.";
FEBS Lett. 313:255-259(1992).
                                                                                                                                                                                                                                                                                                                                                                 documentation_block:
                                                                                                                                                                                                                                                     004790;
01-0CT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last seq
01.NOV-1997 (Rel. 35, Last ann
INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Ru
                                                                                                                                                                 Bovinae; Bos.
                                                                                                                                                                                                                                         IFNAR1 OR IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                      INR1_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
50
58
81
110
1172
2254
4313
314
314
316
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INR1_HUMAN from: 1
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340.00
5.075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
50
58
81
110
117
225
44
113
311
43
168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63525
                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent
                                                                                                                                                                                  :a; Craniata; Vertebrata; Mammalia;
Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION PHOSPHORYLATION POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId-VAR_002717.
G -> A (IN REF. 2).
; 0F6744C8A1ADBE73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Gaps:
t Identity: 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
6
                                                                                                                                                                                                                                                                                                                                                  560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557
                                                                                                                                                                                                                                                                                                                                                  ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY TYK2) (PROBABLE). (BY TYK2) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
                                                                                                                                                                                    Bovidae;
                                      180
                                                                                                            130
                                                                        32
                                                                                                                                                16
                                                                                                                                                                                80
                                                                                                                                                                                                                                                        30
                                                                                                                                                                                                                    \vdash
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x INR1_BOVIN
                                                                                                                                                                                                                                                                                   alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S33770; S33770.
PIR; S27387; S27387.
PFAM; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lim J.-K., Langer J.A.;

"Cloning and characterization of a bovine alpha interferon receptor.";

"Cloning and characterization of a bovine alpha interferon receptor.";

Blochim. Blophys. Acta 1173:314-319(1993).

"IFUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

I IFUNCTION: TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 93305725. Lim J.-K., Langer
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
49
          AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA
                                                                                                                                                                                                                                                           Ratio:
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBURITS THEMSELVES.
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELULARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                             snValGluIleH1sIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                             AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                            gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                          ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCCTCAAA
                                                                                                                                               ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X68443; CAA48484.1;
L06320; AAA02571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                      560
                                                                                                                                                                                                                                                                                                                                                                         438
438
769
199
199
109
172
172
172
173
1313
                                                                                                                                                                                               INR1_BOVIN
                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                           209.00
3.800
84.615
                                                                                                                                                                                                                                                                                                                                                24
560
                                                                                                                                                                                                                                                                                                                                      63818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . . .
                                                                                                                                                                                                                                                           Length:
Gaps:
Percent Identity:
                                                                                                                                                                                               from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                POTENTIAL.

POTENTIAL.

F -> V (IN REF. 2).

66D76B72B61E1D11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                 560
                                                                                                                                                                                                                                                           65
2
69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                               .GlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ьy
                                                                                                32
                                                                                                                                               16
                                                48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
```

```
seq_name: SwissProt_38:INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  028589; Q95206;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                           DISULFID
DISULFID
CARBOHYD
            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            pregnancy.";
Endocrinology 138:4757-4767(1997).
-:- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO
-:- IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINCLUDING JAKS, TYXZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                    Receptor;
SIGNAL
                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            SUBURITS THEMSELVES.

SUBURITS THEMSELVES.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CONCEPTS AT DAY 15 OF PRESURANCY.

-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Cetartiodactyla; Caprinae; Ovis.
                                                                                                                                                                                                           EMBL; X95939; CAA65183.1; -. EMBL; U65978; AAB84231.1; -. PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
*Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of an ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 97135690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INTERFERON ALPHA/BETA RECEPTOR-1).
IFNAR1 OR IFNAR.
                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98006426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _SHEEP
                                                                                                                                                                                                Transmembrane;
  438
438
459
199
199
108
108
109
172
222
222
2313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
 437
458
560
220
220
47
55
108
108
109
172
222
232
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17:207-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaluzova M., Sheldrick E. interferon receptor and i
                                                                                                                                                                                    Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                      EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                            POTENTIAL.
                                                                                                                                                                         INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Flint A.P expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae;
                                                                                                                                                                                                                                                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS
  seq_name:
 EMBL; M89641; AAA37890.1;
PIR; A45283; A45283.
MGD; MGI:107658; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30
```

```
alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INR1_MOUSE P33896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   documentation_block:
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
IFNAR1 OR IFNAR OR IFAR.
                                                                                                                                                                                                                           UZe G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
"Behavior of a cloned murine interferon alpha/beta receptor exp
in homospecific or heterospecific background.";

Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778 (1992).

-: FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING
-: IFNS TRIGERES TYROSINE PHOSPHORYLATION OF A NUMBER OF PRO
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BET
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; C
Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 92262522.
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLySSer...GluA
                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr
                                                                                                                                                                                                             SUBUNITS THEMSELVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_38:INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ç:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359
377
352
522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204.00
3.778
83.077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
377
352
522
                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

POTENTIAL.

POTENTIAL.

S -> G (IN I

A -> D (IN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> G (IN REF. 2).
-> D (IN REF. 2).
E7198A1905D4805C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
2
69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                 PROTEINS
                                                                                                                                                                                                                                                                                                                          expressed
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: SwissProt_38:N153_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                              documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
DISULFID
DISULFID
                  MEDITINE; 94154002.

MEDITINE; 94154002.

*Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnup153 ";

Biochim. Biophys. Acta 1217:219-223(1994).

- i FUNCTION: POSSIBLE DNA-BIODING DOMAIN MAY BE INVOLVED IN ANCHORING COMPONENTS OF THE PORE COMPLEX TO THE PORE MEMBRANE.

- i SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. LOCATED TO THE PORE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
SIGNAL
                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD
                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
 -
                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 94154002.
                                                                                                                                                                                                                                                         P49790:
                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                               130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                        snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                                                                                                                                               AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                      oTrpValLeuProSerAlaAlaGlyGlyGluAsnLeuLysProProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGTCGTCCTCGGGGGGGGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                            H1sGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg
                                                                                                                                                                                                                                                                                                                                                   AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA
          TERMINAL RING STRUCTURE OF THE NUCLEOPLASMIC CAGE.
                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
1181
181
214
314
370
409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
430
450
78
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĄ,
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198.00
3.536
86.154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
109
181
214
314
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                    PRT;
REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7EC6DFF370185D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                    1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 55.385
                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                              Mammalia
                                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
```

```
alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRRR OCC OCT DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                         seq_name: SwissProt_38:KDPD_RATRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1_COPY_1_229/rev x N153_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                       1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles.com/services/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.isb-sentitles/www.i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 603948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                    Rathayibacter rathayi
Bacteria; Firmicutes;
                                                                                                                                                                                    KDPD
                                                                                                                                                                                                                                                                                                  034971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
Submitted (OCT-1997)
                     Labadie
                                                                                                                                                                                                                                                                                                                        KDPD_RATRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM;
                                                                SEQUENCE FROM
                                                                                                              Actinomycetales;
                                                                                                                                                                                                  i5-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
SENSOR PROTEIN KDPD (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST NUP1, NSP1, POM 121 AND MAMMALIAN P62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGACGACCATCATCTGGGAGCCGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erAsnAsnThrThrSerGlyPheGlyPheGlyAlaThrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGACAACACC......CATGGGCCCACGGCGACGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTCCACCTGCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTGTCATCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                       erAlaSerProAlaPheGlyAlaAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerSerAlaGlySerSerPheValPheGlyThr.GlyProSerAlaProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603948; -.
PF00641; zf-RanBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z25535; CAA80982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                        ဂ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N153_HUMAN
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.00
1.683
53.247
                                                                                                            thayi (Corynebacterium rathayi).
utes; Actinobacteria; Actinobacteridae;
Micrococcineae; Microbacteriaceae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
447
681
745
816
874
ូ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153889
the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....ACTAGGGTCGTCGCGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; 21
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLY.
C4-TYPE.
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4-TYPE
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3CB415A6909DF80E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>1</u>3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
6
                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger;
                                                                                                                                                                                                                                                                                                                        854
                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1475
                                                                                                                                                                                                                                                                                                                        ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
3
33.766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding
                                                                                                                Rathayibacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ín
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         way
```

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_1_229 x KDPD_RATRA
                                                                                                                                                                                                                                                                         seq_name: SwissProt_38:IF3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: KDPD_RATRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                              OCUMERICAL
IF3A_HUMAN STANDARICA,

O14152; O00653;
15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT
EUKARYOTIC TRANSLATION (EIF3 P185) (KIAA0139).
SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
MEDLINE; 96127530.
Nagase T., Seki N., 7
"Prediction of the co
                                                                                                                                                                                                                                            documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ002069; CAA05169.1; -. EMBL; AF030293; AAB84261.1; -.
                                                                                      Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                             645 aLeuHisArgAspAspProValCysArgArg.....ProGlyGlyAlaA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sensory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00512; signal;
                                                                                                                                                                                                                                                                                                                                                                                           47
                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                TCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                    AspLeuArgArgProPheAspGlyGlyAsnGlnLysGlyGlyTrpLeuAl 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCTGCGGCGCTCCCAGATGATGGTCGTCCTCCTGGG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM KDPD/KDPE INVOLVED IN THE REGULATION OF THE KDP OPERON, KDPD MAY FUNCTION AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT PHOSPHORYLATES KDPE IN RESPONSE TO ENVIRONMENTAL SIGNALS (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                                                                                                                                                    laargaspargargargLysProalaHisLeuSer
                                                                                                                                                                                                                                                                                                                                                                                         .....CGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
158
374
409
605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.00
2.519
60.000
, Tanaka
coding s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178
394
429
470
628
                                                                                   Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90670 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
  sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
              .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMITTER DOMAIN (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIN
 Ishikawa
ences of u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201867CADFDBB865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
 n K.-I., Nomura N.;
unidentified human
                                                                                                                                                                                                                                                                                                     671
                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
2
44.444
                                                                                                                                                          10 (EIF-3
                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
 genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration -
                                                                                                                                                          THETA)
  ۲
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                   US-09-240-675-1_COPY_1_229 x IF3A_HUMAN
                                                                      1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The codin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scholler J.K., Kanner S.B.;
Scholler J.K., Kanner S.B.;
"The human p167 gene encodes a unique structural protein that contains centrosomin A homology and associates with a multicomponent complex.";
DNA Cell Biol. 16:515-531(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum, Caenorhabditis elegans, and cerevisiae.";
J. Biol. Chem. 272:7106-7113(1997).
                                                                                                         122
                                                                                                                                         985
                                                                                                                                                                            104
                                                                                                                                                                                                          968
                                                                                                                                                                                                                                                                               952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D50929; BAA09488.1; -. EMBL; U58046; AAB41584.1; -. EMBL; U78311; AAB80695.1; -. MIM; 602039; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Johnson K.R., Merrick W.C., Zoll W.L., Zhu Y.; "Identification of cDNA clones for the large subunit of eukaryotic translation initiation factor 3. Comparison of homologues from huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 97207269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initiation factor; Protein biosynthesis; Repeat; Phosphorylation.

DOMAIN 925 1172 25 X 10 AA TANDEM REPEAT OF D-[DE]-D

[GP]-[PS]-[RW]-R-[GN]-[AM].

SEQUENCE 1382 AA; 166568 MW; 485CO1B28D67EBBA CRC64;
                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING METHIONYL-TRNAI AND MRNA.
SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by lysis of cDNA clones from human cell line KG-1."; Res. 2:167-174(1995).
                            TGAGG.....
                                                                    AlaAspGluAspArgGlyAsnTrpArgHis.AlaAspAspAspArgProP
                                                                                                                                                                                                          oArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAspA 985
                                                                                                                                                                                                                                           TCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGG.......
                                                                                                                                                                                                                                                                             ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr
                                                                                                                                                                                                                                                                                                              CCAGATGATGGTCGTCCT.....GGGCGCGACGACCCTAGTGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: PHOSPHORYLATED.
SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
TCCTCAAAAGTAGAGGT.....
                                                                                                                                     spArgProSerTrpArgAsnThrAspAspAspArgProProArgArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                        .....TGGAAAAATCT......AAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97294683
                                                                                                                                                                                                                                                                                                                                                  .
6
                                                                                                                                                                                                                                                                                                                                                IF3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                     67.00
1.634
47.126
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                       . CGACATCATAGATGACAACTTTATCC
                                  TGGAACAGGAGCGATGAG
                                                                                                                                                                                                                                                                                                                                                to: 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                       32.184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homologues fr
Saccharomyces
                                                                                                                                                                          121
                                                                      1018
                                                                                                                                         1001
                                      188
                                                                                                         165
                                                                                                                                                                                                                                             103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D- [DE] -D-R-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from human,
```

seq\_name: SwissProt\_38:Y481\_HUMAN

STANDARD;

PRT;

483 AA

AspargGly 1037 TCTGTCGGG 197

189

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Y481_HUMAN
                                                                                                                                                                                                                                                                                                                                                                             US-09-240-675-1_COPY_1_229/rev x Y481_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O75069;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL PROTEIN KIAAO481 (HH1480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 4:345-349(1997).
-I- SIMILARITY: SOME, TO HUMAN TEX28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima
Nakajima D., Nomura N., Ohara O.;
                                                                                                                                                                                                                                  172 CACCTCAGGATAAAGTTGTCAT...CTATGATGTCGACCTCTACTTTTTG
                                                                                                                                                                                                                                                                                                          222 GATAATCGAATGAAAAAGTCACATTCCCGACAGACTCATCGCTCCTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein DOMAIN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB007950; BAA32326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakajima D., Nomura N., Ohara O.;
"Characterization of cDNA clones in size-fractionated cDNA libraries
                                                                84
                                                                                                                                   71
                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                           6
                                25
                                                                                                    75
rSerSerArgArg 104
                                  TGGGAGCCGCCGC 13
                                                                LysArgGlyAlaSerLeuHisSerSerSerGlyGlyGlySerSerGlySe
                                                                                                  CCACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGAGGACGACCATCATC
                                                                                                                                 snArgValLeuGln.......GlnIleArgSerArgProSerIle
                                                                                                                                                                                                       rAlaMet.....SerLeuHisAspLeuProAlaArgProThrAlaPheA
                                                                                                                                                                                                                                                                        AspSerProAspGluLysGluArgSerProGluMetHisArgValSerTy
                                                                                                                                                                     AGGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 34 F
483 AA; 52462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               65.50
1.598
57.746
                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 71
Gaps: 3
Percent Identity: 33.803
                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLN.
, A9EBB8EFD793D866 CRC64;
                                                                                                                                                                                                                                                                                                                                            to: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     z
                                                                                                                                                                                                       71
                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                           56
                                                                  100
                                                                                                    26
                                                                                                                                     83
                                                                                                                                                                     76
```

alignment\_block: US-09-240-675-1\_COPY\_1\_229/rev x ERF\_MOUSE

Align seg 1/1

to: ERF\_MOUSE

from: 1 to: 551

375 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 108 TTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCACT

391 59

58 AGGGTCGTCGCCCCAGGAGGA.....CGACCATCATCTGGGAGC 19

alignment\_scores:

Percent Similarity:

Quality: Ratio:

65.00 2.826 71.875

Percent Identity:

Length: Gaps:

32 1 43.750

```
Seq_documentation_block:
ID ERF_MOUSE STANDARD;
AC P70459;
DT 15-JUL-1998 (Rel. 36, Creation of P70459;
DT 15-JUL-1998 (Rel. 38, Last DT 15-JUL-1999 (Rel. 38, Last DE ERF.

OC Eukaryota; Metazoa; Chorda OC Eutheria; Metazoa; Chorda OC Eutheria; Metazoa; Chorda OC Eutheria; Metazoa; Chorda OC Eutheria; Metazoa; Companization RT analysis of the human and Oncogene 14:1445-1451(1997)
CC I-FUNCTION: POTENT TRANSCC I-FUNCTION: POTENT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: SwissProt_38:ERF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U58533; AAC09474.1; --
EMBL; U58534; AAC09474.1; JOINED.
HSSP, Q01543; IFLI.
MGD; MGI:109637; ERF.
PRINTS; PRO0454; ETS_DOMAIN.
PROSITE; PS00345; ETS_DOMAIN.1; 1.
PROSITE; PS00346; ETS_DOMAIN.2; 1.
PROSITE; PS00346; ETS_DOMAIN.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu D., Pavlopoulos E., Modí W., Moschonas N., Mavrothalassitis G.J.;
"ERF: genomic organization, Chromosomal localization and promoter
analysis of the human and mouse genes.";
Oncogene 14:1445-1451(1997).
-i- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1
ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
IN CELLULAR PROLIFERATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the companies of the ENTRY of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- PIM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
-!- PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Nurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                      PPAM; PF00178; Ets; 1.
Transcription regulation; Repressor; DNA-binding; Nuclear protein;
           59050
           ¥.
                                                                                                               POLY-SER.
POLY-GLY.
POLY-SER.
POLY-PRO.
           SIMILARITY).
: 5AC1B72FB2743FE5 CRC64;
                                                                          PHOSPHORYLATION (BY ERK2) (BY
                                                                                                                                                                                                                                                             ETS-DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
```

its

```
alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_38:VPHE_NPVAC
                                                                                                                                                                                                                       Align seg 1/1 to: VPHE_NPVAC
                                                                                                                                                                                                                                                         US-09-240-675-1_COPY_1_229/rev x VPHE_NPVAC
                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
VPHE_NPVAC STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
POLYHEDRAL ENVELOPE PROTEIN (PE) (POLYHEDRAL CALYX PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M17548; AAA66805.1; -. EMBL; L22858; AAA66761.1; -. PIR; C43679; C43679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.; "The complete DNA sequence of Autographa californica nuclear polyhedrosis virus."; Virology 202:586-605(1994).
-I- FUNCTION: MAJOR COMPONENT OF THE POLYHEDRA ENVELOPE.
-I- SIMILARITY: TO PE FROM OTHER BACULOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deallig C., Happ B., Mueller T., Doerfler W.;
"Overlapping sets of viral RNAs reflect the array of polypeptides
the EcoRI J and N fragments (map positions 81.2 to 85.0) of the
Autographa californics nuclear polyhedrosis virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autographa californica nuclear polyhedrosis virus (ACMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P24728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
                                                                                                                                                                                    228
                                                                                                                                                                                                                                                                                                                                                                                                                       Envelope protein; Viral occlusion body.

DOMAIN 98 140 ARG/SER-RI
SEQUENCE 252 AA; 29079 MW; 3252B0C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virol. 61:3048-3057(1987).
                                                                       rArgSerProHis
                                                                                            CTGTTCCACCTCAGGATAAAGTTGTCATCTATGATGTCGACCTCTACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aGlyGluLysAlaProGlyGlyThrAspLysSerSerGlyGlySer 406
                                    TTGAGGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATG
                                                                                                                                              PheTyrArgArgArgSerArgSerArgSerArgSerArgSerArgSe
                                                                                                                                                                                  TTTTTTGATAATCGAATGAAAAAGTCACATTCCCGACAGACTCATCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87311863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94303173
                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                               63.50
1.924
45.205
                                                                                                                                                                                                                                                                                                             Length:
Gaps:
Percent Identity: 31.
                                                                                                                                                                                                                       from: 1 to: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           RG/SER-RICH.
3252B0C8E195A15D
.ArgSerArgSerProHisCys 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252
                                                                         CysArgPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ያ
                                                                                                             129
                                      79
                                                                                                                                                112
                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
```

```
alignment_block:
US-09-240-675-1_COPY_1_229/rev x IRS2_MOUSE
                                                                      seq_name: SwissProt_38:IRS2_MOUSE
                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _documentation_block:
                                                                                                                DOMAIN
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun X.J., Wang L.-M., Zhang Y., Yenush L., Myers M.G. Jr., Glasheen E., Lane W.S., Pierce J.H., White M.F.; "Role of IRS-2 in insulin and cytokine signalling."; Nature 377:173-177(1995).

-i- FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:109334; IRS2.
PRINTS; PR00628; INSULINRSI.
PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                           DOMAIN
                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                               Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P35568; 1IRS
                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95405472.
Sun X.J., Wang L.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00169; PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgProArgSerArgSerArgSerArgSerArgSerArgSerArgSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTGGGAGCCGCCGCAGA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCCACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGAGGACGACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: SKELETAL MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rSerProArgArgGlyArg 149
                                                                                                                                                                                                                                                                                                                                                                                                                             HEART AND SPLEEN
                                                             Ratio:
                                                                                                                                                                                                    1242
                                                                                                                                                                                                                         970
                                                                                                                                                                                                                                              911
                                                                                                                                                                                                                                                                  671
                                                                                                                                                                                                                                                                                      649
                                                                                                                                                                                                                                                                                                           187
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                 ξ
                                                  63.50
1.984
44.444
                                                                                                                                                                                                   1242
                                                                                                                                                                               1303
                                                                                                                           28
449
641
939
                                                                                                                                                                                                                         970
                                                                                                                                                                                                                                             911
                                                                                                                                                                                                                                                                  671
                                                                                                                                                                                                                                                                                     649
                                                                                                                 136526
                                                  Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                       PH DOMAIN.
PTB DOMAIN
                                                                                                                  ₹.
                                                                                                                           POLY-SER.
POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                               <u>, .</u>
                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
                                                                                                                                                                                                   PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                        PHOSPHORYLATION
                                                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                             PHOSPHORYLATION
                                                                                                                                                                                          (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                 5069CE9D614960C7 CRC64;
to: 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                       LUNG,
                                                   72
2
29.167
                                                                                                                                                                               (BY
                                                                                                                                                                                                                        (BY
                                                                                                                                                                                                                                             (BY INSR)
                                                                                                                                                                                                                                                                  (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                       BRAIN, LIVER,
                                                                                                                                                                                                                         INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
```

Align seg 1/1

to: IRS2\_MOUSE

from: 1

```
seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P23116; 060697; 062162;

15-P2316; 060697; 062162;

15-P25-2000 (Rel. 20, Created)

15-P25-2000 (Rel. 39, Last sequence update)

15-P25-2000 (Rel. 39, Last sequence update)

15-P25-2000 (Rel. 39, Last sequence update)

10 EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10

11 EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10

12 EUKARYOTIC TRANSLATION (EIF3 P185) (P162 PROTEIN) (CEIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN) (CEIF3 P187) (EIF3 OR CSMA.

12 EUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mais musculus (Mouse).

13 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mais musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1045
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                           Joswig G., Petzelt C., Werner D.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING METHIONYL-TRNAI AND MRNA.
-i- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fisher R., Fillmore H., Reynolds A.B.;
"Molecular cloning and characterization of the 162 kDa component of a multi-protein complex phosphorylated by Src.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petzelt C., Joswig G., Mincheva A., Lichter P., Stammer H., "The centrosomal protein centrosomin A and the nuclear protecentrosomin B derive from one gene by post-transcriptional protections."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IF3A_MOUSE
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 514-790 FROM N.A. (CENTROSOMIN A) MEDLINE; 91277032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                      REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                Murine
                                                                                                                                                                                                                                                                                                                                                                                                 Joswig G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involving RNA editing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 514-961 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSUE-LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                       swig G., Petzelt C., Werner D.; urine cDNAs coding for the centrosomal antigen Cell Sci. 98:37-43(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aProProLysProGluGlyAlaArgValAlaSerProThrSerGlyLeuL 1095
                                                                                                                                                          SIMILARITY: BELONGS TO THE EIF3S10 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ysArgLeuSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCGCAGATCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oThrAlaGlySerSerMet.SerSerGluProGlyAspAsnGlyAspTyr 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCC
                                                                                                                                                                               PTM: PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_38:IF3A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Šc1. 110:2573-2578(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98039715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CENTROSOMIN B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . GGACGACCATCATCTGGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿
                                                                                              and the
                                                                                                                                                                                                                                                                                                                                                                            centrosomin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 (EIF-3 THETA) (CENTROSOMIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Werner D.;
                                                                                                                                                                                                                                                           읶
```

```
seq_documentation_block:
ID COMA_BPT4 STANDA
AC 001438;
DT 01-OCT-1993 (Rel. 27,
DT 01-FEB-1995 (Rel. 27,
DT 01-FEB-1995 (Rel. 31,
DE COMC-ALPHA PROTEIN.
GN COMCA OR GOF.
OS Bacter1ophage T4.
OC Viruses; dsDNA viruse;
OC T4-like phages.
RN [1]
RP SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_1_229 x IF3A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: SwissProt_38:COMA_BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: IF3A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                              1035
                                                                                                                                                                                                                                                                 1019
                                                                                                                                                                                                                                                                                                                    1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                                                                          168
                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                      986
                                                                                                                                                                                                                                                                                                                                                                                                                          969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U14172; AAA90910.1;
EMBL; X84651; CAA59144.1;
EMBL; X17373; CAA35246.1;
                                         Bacteriophage T4.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          952 oAspAspAspArgIleProArgArgGlyLeuAspAspAspArgGlyProA 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                936 LeuArgArgLeuGlyGlyAspAspGluGluArgGluSerSerLeuArgPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S13800; S13800.
MGD; MGI:95301; EIF3.
Initiation factor; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 CTGCGGCGGCTC......CC
                                                                                                                                                                                                                                        TGTCGGG 197
                                                                                                                                                                                                                                                                ArgargGlyLeuAspAspGluArgGlySerTrpArgThrAlaAspGluAs
                                                                                                                                                                                                                                                                                    yAspAspAspArgGlySerTrpArgHis.ThrAspAspAspArgProPro
                                                                                                                                                                                                              pargGly 1037
                                                                                                                                                                                                                                                                                                                                            CTCAAAAAGTAGAGGT.....CGACATCATAGATGACAACTTTATCCTG
                                                                                                                                                                                                                                                                                                                                                                      ArgProSerTrpArgAsnAlaAspAspAspArgProProArgArgIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                         rgArgGlyProAspGluAspArgPheSerArgArgGlyThrAspAspAsp 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATGATGGTCGTCCT.....GGGCGCGACGACCCTAGTGCTCGTC 68
                                                                                                                                                                                                                                                                                                                                                                                             .....TGGAAAAATCT..........AAAATCTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      683
717
766
787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.00
1.432
42.718
                                                                                          27,
27,
31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          684
717
766
790
793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161949 MW;
                                                                                           Last
Last
                                                                                                                       Created)
                                          0
                                                                                                                                                                                                                                                                                        .....TGGAACAGGAGCGATGAGTC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                          RNA
                                                                                             annotation
                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis; Repeat; Phosphorylation.
21 x 10 AA TANDEM REPEAT OF D-[DE]-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REF. 2 AND 3).

EL -> DY (IN REF. 2 AND 3).

Q -> H (IN REF. 2 AND 3).

A -> V (IN REF. 2 AND 3).

RHSR -> SIVA (IN REF. 3).

E -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 x 10 AA TANDEM REPEAT OF D-[DE]-D-R-
[GP]-[PS]-[RW]-R-[GN]-[AM]-
ROEAKEREKEBELIDEHSOLIKKKTVERLEOIKKTE ->
PRGKGAREGTNPSRTRANQEENCSGAVRADQEDR (IN
                                                                                                                                               PRT;
                                         stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F4CAE2169F577712 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Gaps:
                                                                                                                                               141
                                          Tailed
                                                                                           update)
                                                                                                                                               ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.068
                                         phages;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                952
                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
                                                                                                                                                                                                                                                                  1035
                                                                                                                                                                                                                                                                                                                                                                        1002
                                                                                                                                                                                                                                                                                                                     1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-[DE]-D-R-
```

```
S K D D C C C C C C C C C C C T T D X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_1_229 x COMA_BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: SwissProt_38:SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                   documentation_block:
SFR2_CHICK STANDARD;
                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Sequence and characterization of the bacteriophage T4 gene product, a possible transcription antitermination J. Bacteriol. 174:6539-6547(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M89919; AAA32485.1; -. PIR; A45731; A45731.
                                         P30352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation. SEQUENCE 141 AA; 16682 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanson B., Uzan M.;
 <del>+</del> ÷
                                                                                                                                            vellard M., Sureau A., Soret J., Martinerie C., Perbal B.;
*A potential splicing factor is encoded by the opposite st
                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                        TISSUE-THYMUS;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93015705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sArgCysAlaGlyGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTC
SUBCELLULAR LOCATION: ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           spIleLeuAspGluAsnPheIle.....TrpLeuSerThrAsnGluAla
                                                                                                                                                                           92212859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMA_BPT4 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.50
2.155
58.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 50
Gaps: 3
Percent Identity: 34.000
 DIFFERENT FORMS
             NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96C9EFA8C673C479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 141
                                                                                                                                                                                                                                                                                                                                                                                    221
                                                                                                                                                                                                                                                                                                                                                                                    B
 OF THE
                                                                                                                                               opposite strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
   PROTEIN MAY
                                                                                                                                                                                                                                      Gallus
                                                                                                                                                                                                                                                  Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comC alpha
factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                              SC35) (SC-35)
                                                                                                                                               of.
                                                           FOR
                                                                                                                                               the
```

```
Sed Cocos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_1_229 x
                                                                                                                                                                                                                                                                    seq_name: SwissProt_38:PHLC_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                        _documentation_block:
                                                                                                                         PHIC_PSEAE STANDARD; PRT; 730 AA.

P06200;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 16, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
HEMOLYTIC PHOSPHOLIPASE C. PRECURSOR (EC 3.1.4.3) (HEAT LABORDLYSIN) (PHOSPHATIDYLCHOLINE CHOLINEPHOSPHOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRODUCED BY ALTERNATIVE SPLICING.
-!- PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES DOMAIN (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP)
-!- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING F
                                                                                                                                                                                                                                                                                                       133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00030; RNP_1; 1.

PFAM; PF00076; rrm; 1.

Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing; Nuclear protein.

Phosphorylation.

Phosphorylation.

21 RNA-BINDING (RNP2) (BY SIMILARITY).

DOMAIN

55 62 RNA-BINDING (RNP1) (BY SIMILARITY).

DOMAIN

111 116 GLY-RICH (HINGE REGION).

DOMAIN

117 221 ARG/SER-RICH (RS DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
                                                                            Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                   116 lyArgArgSerArgSerProArgArgArgArgArgSerArgSerArgSer 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X62446; CAA44306.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                             SEQUENCE FROM N
Pritchard A.E., Vasil M.L.;
              MEDLINE; 86250607
                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGATCTGCGG...CGGCTCCCAGATGATGGTCGTCCTCCT......
                                                                                                                                                                                                                                                                                                    ArgSerArgSerArg 137
                                                                                                                                                                                                                                                                                                                                     AAAAGTAGAGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                  TCCGC.....AGCCGCAGGTGGAAAAAATCTAAAATCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                  sHisSerArgArgGlyProProProArgArgTyrGlySerSerGlyTyrG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                .... GGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgGluLeuArgValGlnMetAlaArgTyrGlyArgProProAspSerHi 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S17327; S17327.
B42701; B42701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1SXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
62
116
221
25524 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.50
2.083
54.545
                                                                                                                                                                                                                                                                                                                                     142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XW.
                                                                            gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75A4D8FF9170F1BF CRC64;
                                                                             subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Gaps:
: Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ç
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.182
                                                                             Pseudomonas group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESIDUES
                                                                                                                                             (HEAT LABILE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
                                                                                                                                                                                                                                                                                                                                                                                                    127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RS
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_1_229 x PHLC_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: PHLC_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS.

Pritchard A.E.;

Pritchard A.E.;

Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence and expression of a phosphate-regulated gene encoding a secreted hemolysin of Pseudomonas aeruginosa.";
J. Bacteriol. 167:291-298(1986).
[2]
                                                                                                     443
                                                                                                                                                          171
                                                                                                                                                                                                                                                                                                                    415
                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN 39 730 HEMOLYTIC PHOSPHOLIPASE C. SEQUENCE 730 AA; 82655 MW; F1D3695824445FBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHATIDYLCHOLINE.
-!- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)0 = 1,2-DIACYLGLYCEROL + CHOLINE PHOSPHATE.
-!- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.
                                                    218
                                                                                                                                                                                                         426 alLeuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemolysis; Toxin; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M13047; AAA25966.1; -. PIR; A26391; A26391.
457 pPheGln 459
                                                                                                                                                                                                                                                                                                                                                                   113 TCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTA 162
                                                                                                ...TGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGA 217
|||:::|||:::|
|||::::|||
ProTrpArgArgAla.....ValCysGlyAspLeuThrSerLeuPheAs 457
                                                 TTATCAA 224
                                                                                                                                                                                                                                                  TCCTGAGG.....
                                                                                                                                                                                                                                                                                                              ......LysValSerAlaGluValPheAspHisThrSerV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.00
1.824
49.275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 69
Gaps: 4
Percent Identity: 26.087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 730
```

```
Query: US-09-240-675-1_COPY_1_229
Query length: 229
Database: SPTREMBL 12.*
Database: SPTREMBL 12.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_invertebrate:Q9XZV7
sp_human:Q15778 +
sp_human:Q14152 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database sequences: 225878
Database length: 69334122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Command line parameters:
                                                                                                                                                                                                                 sp_invertebrate:002424 +
sp_invertebrate:023047 +
sp_rodent:060805 +
sp_human:09Y5L9 -
                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_bacteria:086774
sp_bacteria:09X4V6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_invertebrate:Q94603
sp_plant:023212 +
sp_mammal:077699 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_human:Q13507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:088970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mhc:Q30849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_invertebrate:076514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_vertebrate:Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time (sec): 89.940000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_bacter1a:Q9ZBS7
sp_human:Q9Y4L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_bacteria:007239
sp_bacteria:054272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_phage:064317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL-frame+_n2p.model -DEV-x1p
-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24664/app_query.fasta.
-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24664/app_query.fasta.
-DB-SPTREMBL_12 -QFMT-fastan -SUFFIX-modif.rspt -GAPOP-12.000
-GAPOP-4.000 -MIMANCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -BELEXT-7.000 -START-1 -MATRIX-blosun62
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosun62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NORM-ext -MINLEN-0
                                                                                                                                       sp_archea:Q9YEB6
                                                                                                                                                                 sp_human:Q14396
                                                                                                                                                                                                                                                                                                                                  sp_plant:064410
                                                                                                                                                                                                                                                                                                                                                         sp_invertebrate:018465
                                                                                                                                                                                                                                                                                                                                                                                           sp_rodent:Q9Z0H1
                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:P91232 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_human:095927
                                                                                                                                                                                             sp_virus:069088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rodent:Q9WVR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_vertebrate:Q9W721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rodent:089019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by Copyright (c) 1993-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1_COPY_1_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10rig
113.50
79.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orig ZSCORE ESCORE LE

113.50 225.40 2.3e-05

79.00 144.87 0.2831

- 77.00 152.39 0.5389

67.00 127.43 8.13

67.00 119.45 7.62

+ 66.00 127.08 10.85

63.50 116.61 20.67

63.00 116.55 23.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.50
63.00
63.00
                                                                                   60.00 10
60.00 9
60.00 9
59.50 12
59.50 12
59.50 11
                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                               62.000
62.000
62.000
61.500
61.000
61.000
60.500
60.500
                                                                                                                                                                                                                                                                                                                                                                                           60
     59.50
59.00
59.00
                                                                                                                                 60.50 111.41 47.60.50 116.46 57.60.00 116.46 57.60.00 114.25 57.60.00 106.90 53.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.87 49.60.00 98.60.00 98.87 49.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.00 98.60.0
                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.50
                                                                                                                                                                                                                                                                                                                                                                                                                     . 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                            116.29
126.88
120.69
110.69
1113.57
1112.41
112.23
1112.95
1118.65
118.21

50 113.9

112.72

120.46

112.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the GenCore
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç
O:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120.43
                                                                                   . 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPTREMBL_12:*
                                                                                                                                                                                                                                                                              84 49.25
47.52
30 44.51
57.26
25 56.25
38 56.12
  53.01
49.69
49.51
70.84
69.33
67.18
67.18
64.27
79.14
74.51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.50
22.87
3 28.52
                                                                                                                                                                                                                                                                                                                                                                                                                                            32.94
30.51
30.51
42.13
41.44
41.34
41.24
41.24
49.25
49.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Te Len | Documentation | 15 | 569 | Q9yhw0 gallus | 1429 | Q9y5t6 homo | 189 | 286 | Q9yzv7 giar | 466 | Q15778 homo | 1382 | Q14152 homo | 1382 | Q14152 homo |
                                                                                                                                                                                     622 | Q9z0hl mus muscullus (mouse). bi

1880 | O94465 hirudo medicinalis (m

270 | O64410 zea mays (maize). cytoch

365 | O02424 caenorhabditis elegans

379 | Q23047 caenorhabditis elegans

379 | Q23048 mus muscullus (mouse). c-

2971 | Q9y519 homo saplens (human). t

3164 | Q69088 human herpesvirus 1. vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
358 !
734 !
640 !
                                                                                                                                                                                                                                                                                                                                                                                                                                               620
616
644
673
129
232
340
                                                                                                          2971 | O9y519 homo sapiens (human). v 3164 | O59088 human herpesvirus 1. v 75 | O14396 homo sapiens (human). li 108 | O9yeb6 aeropyrum pernix. 108aa 184 | O62143 mus musculus (mouse). q
                                                                                                                                                                                                                                                                                                                                                                                                               3 1 023212 arabidopsis thaliana (mc
7 1 077699 bos taurus (bovine). trp
0 1095927 homo sapiens (human). dj
62 1 089019 mus musculus (mouse). i
0 1 007239 mycobacterium tuberculos
7 1054272 streptomyces hygroscopic
6 1 09w721 brachydanio rerio (zebra
4 1 09w725 brachydanio rerio (zebra
5 1 09w74 mus musculus (mouse). fx
9 1 09w74 mus musculus (mouse). fx
1 09w74 musculus (mouse). fx
1 09w74 mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Q15778 homo sapieus (human). k
! Q14152 homo sapieus (human). k
55 | Q76514 caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              088970 mus musculus (mouse). ir
064317 bacteriophage n15. termi
  Q21784 caenorhabditis el
Q9y775 candida tropicalis
P79321 sus scrofa (pig). k
088073 streptomyces coelic
                                                                                                                                       Q9yeb6 aeropyrum pernix. 108aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              013507 homo sapiens (human). ta
060697 mus musculus (mouse). p
094603 leishmania major. mtco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9xzv7 giardia lamblia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gallus (chicken)
                                                                                      elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_bacteria:007452
sp_fung1:012405
sp_plant:008700
        sp_plant:Q9XFW6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
     Eukaryota;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                              rAlaGlnTyrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ţ
O:
           Primates;
```

```
seq_documentation_block:
ID Q9YHW0
AC Q9YHW0
AC Q9YHW0
AC Q9YHW0
AC Q9HW0;
DT Q1-MAY-1999 (TIEMBLIED Q1 Q1-MAY-1999 (TIEMBLIED Q1-MAY-1999 (TIEMBLIED Q1-MAY-1999 (TIEMBLIED Q1-MAY-1999 (TIEMBLIED Q1-MAY-1999 (TIEMBLIED Q1-MAY-1999 (TIEMBLIED Q1-MAY-1999)
BE EMBL; AF082664; AAD13 MW RECUENCE 569 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-240-675-1_COPY_1_229 x Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: sp_vertebrate:Q9YHW0
                                                                                                                                                                                                      seq_name: sp_human:Q9Y5T6
                                                                                                                                  Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL; AF082664; AAD13669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TIEMBLIEL 10, Created)
01-MAY-1999 (TIEMBLIEL 10, Last sequence up
01-MAY-1999 (TIEMBLIEL 10, Last annotation
INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                 01-NOV-1999 (TremBLrel.
01-NOV-1999 (TremBLrel.
01-NOV-1999 (TremBLrel.
BREAST CANCER NUCLEAR RE
                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 CysAlaSerGlyArgLeuAlaAlaValLeuLeu...
                                                                                                                                                                                                                                                                             ATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                              ATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                    ATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       lLeuValValValSer....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGGACGACCCTAGT
                                                                                                                                                                                                                                                                                                              ThrLeuMetTrpAsnTyrThrGlyAspGlyThr...AsnValThrPheSe
                                                                                                                                                                                                                                                                                                                                                                                  snLeuLysSerProGlnAspIleGlnValTyrAlaValAsnThrAsnPhe
                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113.50
2.365
67.606
                                                                                                                                                                                                                                            67
Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8888
                                                                    RECEPTOR-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ArgCysCysAlaGlyGlnThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112.
110.
110.
                                                               Last sequence update)
Last annotation update)
TOR-BINDING AUXILIARY PROTEIN
 Craniata; Vertebrata; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F99BC099 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
O:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.33
73.74
73.14
73.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Gaps:
                                                                                                                                                         1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O07452 alcaligenes eutrophogl2405 saccharomyces cerevol08700 brassica napus (rapogexiw6 brassica oleracea (
                     Mammalia
                                                                                                                                                                                                                                                                                                                                                    211
                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                                                                                                         31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aves;
```

```
seq_documentation_block:
ID Q9XZV7
AC Q9XZV7
DT 01-NOV-1999 (TIEMBLIG OPEN OF THE CONTROL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_1_229 x Q9Y5T6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: sp_invertebrate:Q9XZV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q9Y5T6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 91088287.
UPCROFT J.A., HEALEY A.,
"Antigen expression from
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DNA FOR RRNA TANDEM REPEAT UNIT (FRACKENT).
Giardia lamblia (Giardia intestinalis).
                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 90326542.

HEALEY A., MITCHELL R., UPCROFT J.A., BOREHAM P.F.L., UPCROFT P.;

"Complete nucleotide sequence of the ribosomal RNA tandem repeat
from Giardia intestinalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RUBINO D.M., DRIGGERS P.H., Submitted (FEB-1999) to the EMBL; AF126008; AAD21311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RUBINO D., DRIGGERS P., ARBIT D., KEMP L., MILLER B., COSO O., PAGLIAI K., GRAY K., GUTKIND S., SEGARS J.; "Characterization of Brx, a novel Db1 family member that modulates estrogen receptor action."; oncogene 16:2513-2526(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 98288806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACTT.....TATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATGATAGATGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTAGTGCTCGTCGCCGTGGGCCCATGGGTTGTCCGCAGCCGCAGGT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspLeuGluArgLeuArgAlaAlaGlnLysGlnLeuGluArgGluGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpLysArgSerGlyArgSerSerSerArgArgArgAlaHisSerGlnTyr 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uHis...ValArgArgGluAlaGlu......ArgLeuSerGln 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .ProSerAlaArgArgArgCysSerArgGly.....SerArgThrT 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                       Res. 18:4006-4006(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.00
1.837
52.439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                          MITCHELL R., BOREHAM P.F.L., I the ribosomal DNA repeat unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILLER B., SEGARS J.H.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542BBC25 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
6
41.463
                       UPCROFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                          Giardia
                                                                                                                                                                                                                            repeat unit
```

```
seq_documentation_block:
ID 015778;
AC 015778;
AC 015778;
AC 01-NOV-1996 (TrEMBLrel. 01
DT 01-NOV-1998 (TrEMBLrel. 01
DT 01-NOV-1998 (TrEMBLrel. 02
DE 0167 (FRAGMENT).
OS HOMO sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90239007.
RA MEDLINE; 90239007.
RA MEDLINE; 90239007.
RA MEDLINE; S.B., REYNOLDS A.B.
RT "MONOCIONAI antibodies to
RT substrates of oncogene-ency
RL Proc. Natl. Acad. Sci. U.S
RN [2]
RP SEQUENCE FROM N.A.
RA SCHOLLER J.K., KANNER S.B.
RA SCHOLLER J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_1_229 x Q15778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_human:Q15778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: Q15778 from: 1 to: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: Q9xZV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-240-675-1_COPY_1_229/rev x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 90239007.
KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
SANDACTOR OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLE4C ACIDS Res. 18:7077-7081(1990)
EMBL; X52949; CAB44501.1; -.
NON_TER 286 286
SEQUENCE 286 AA; 28277 MW; 53B8409
                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SCHOLLER J.K., KANNER S.B.;
SCHOLLER J.K., KANNER S.B.;
SNON CE11 Biol. 0:0-0(0).
EMBL; U58047; AAB41586.1; -.
NON TEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
             69
                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                                                                            23 CCAGATGATGGTCGTCCTCCT.....GGGCGCGACGACCCTAGTGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGG...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgArgSerAlaGlnGlyProArgAlaArgArgArgGlyAlaAlaArgPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGACAACACCCATGGGCCCACGGCGACGACCACTAGGGTCGTCGCGCCC 44
spArgProSerTrpArgAsnThrAspAspAspArgProProArgArgIle
                                                                                                                                                                                OArgArgGlyProGluGluAspArgPheSerArgArgGiyAlaAspAspA 69
                                                                                                                                                                                                                                                                                                                                                            ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr 52
                                                                                   ......TGGAAAAATCT.................AAAATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.00
1.634
47.126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.00
3.500
75.862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XZV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08C47A4E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53B84096 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
0
51.724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
6
32.184
         85
                                                                                                                                                                                                                                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
```

Align seg 1/1

ç Ö

Q14152

from:

μ

. 6

```
seq_documentation_block:
ID Q14152 OPELIMINA
AC Q14152; OPO653;
DT Q1-NOV-1996 (TIEMBLIED TO 01-NOV-1996 (TIEMBLIED TO 01-NOV-1996)
OS HOMO SAPIENS (HUMAN).
OC EUKARIYOTA; Metazoa; COC EUKARIYOTA; Metazoa; COC EUKARIYOTA; Metazoa; COC EUKARIYOTA; Metazoa; COC EUKARIYOTA; SEKI N., TARI NAGASE T., SEKI N., TARI NAGASE T., SEKI N., TARI PREDLINE; 9023907.
RA NAGASE T., SEKI N., TARI PREDLINE; 9023907.
RA NAGASE T., SEKI N., TARI PREDLINE; 9023907.
RA NAGASE T., SEKI N., TARI DNA RES. 2:167-174(15 R.)
RA SEQUENCE FROM N.A.
RA SEQUENCE FROM N.A.
RA SCHOLLER J.K., KANNER S.B., REYNOLLER J.K., KANNER R. SCHOLLER J.K., KANNER R. SCHOLLER J.K., KANNER R. SCHOLLER J.K., KANNER R. SEQUENCE FROM N.A.
RA SCHOLLER J.K., KANNER R. SEQUENCE FROM N.A.
RA SCHOLLER J.K., KANNER R. SEQUENCE FROM N.A.
RA MEDLINE; 97207269.
RA JOHNSON K.R., MERRICH RT Identification of cit ranslation initiatical receives tabe "."
RP SEQUENCE FROM N.A.
RA JOHNSON K.R., MERRICH RT Identification of cit ranslation initiatical receives tabe. "."
J. Biol. Chem. 272:71 RN [5]
RA SEQUENCE FROM N.A.
RA JOHNSON K.R., MERRICH RT Identification of cit ranslation initiatical (NOV-1996) BABO946
DR EMBL; USB046; AAB4156
                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: sp_human:Q14152
                                                                                                                                                    alignment_scores:
US-09-240-675-1_COPY_1_229 x Q14152
                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE: 96127530.

NAGASE T., SEKI N., TANAKA A., ISHIKAWA K., NOMURA N.;

NAGASE T., SEKI N., TANAKA A., ISHIKAWA K., NOMURA N.;

"Prediction of the coding sequences of unidentified human

The coding sequences of 40 new genes (KIAA0121-KIAA0160) d

analysis of cDNA clones from human cell line KG-1.";

DNA Res. 2:167-174(1995).
                                                                                                                                                                                                                                                                   ZHŪ Y., JOHNSON K.R.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
EMBL; D50929; BAA09488.1; -.
EMBL; U58046; AAB41584.1; -.
EMBL; U78311; AAB80695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KANNER S.B., REYNOLDS A.B., VINES R.R., PARSONS J.T.;
"Monoclonal antibodies to individual tyrosine-phosphorylated protein substrates of oncogene-encoded tyrosine kinases.";
Proc. Natl. Acad. Sci. U.S.A. 87:3328-3332(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. SCHOLLER J.K., KANNER S. Submitted (FEB-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHNSON K.R., MERRICK W.C., ZOLL W.L., ZHU Y.; "Identification of cDNA clones for the large subunit of eukaryotic translation initiation factor 3. Comparison of homologues from hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum, Caenorhabditis elegans, and cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 272:7106-7113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGTCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGG.....TGGAACAGGAGCGATGAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspArgGly 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roArgArgGlyLeuAspGluAspArgGlySerTrpArgThrAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaAspGluAspArgGlyAsnTrpArgHis.AlaAspAspAspArgProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCAAAAAGTAGAGGT.....CGACATCATAGATGACAACTTTATCC
                                                                                                                            Quality:
                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                          67.00
1.634
47.126
                                                                                                                                                                                                                                 166568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .B.;
                                                                            Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                 AEF0846C
                                                                            Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1382
                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ž
                                                                          87
6
32.184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologues from human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n genes.
deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IV.
```

```
SQ RALL
                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_1_229 x 076514
                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: sp_invertebrate:076514
                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1035 AspargGly 1037
                                                                                                                                                                                                                                                                                                                 HSSP; P18075; 1BMP.
PFAM; PF00019; TGF-beta;
PRINTS; PR00438; GFCYSKN
                                                                                                                                                                                                                                                                                                                                                          MORITA K., CHOW K.L., UENO N.;
"Body Length and Male Tail Ray Pattern Formation of C. (
Regulated by a Member of TGFb Family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF074395; AAC26791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CET-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                968 oArgArgGlyProGluGluAspArgPheSerArgArgGlyAlaAspAspA 985
                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                  GACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTGTCCGCAGCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGATGATGGTCGTCCTCCT.....GGGCGCGACGACCCTAGTGCTCG
GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGT
                       nThrGlyAsnSerGluArgLysAsnArgLysLysGlyArgLysHisHis.
                                                       GTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT
                                                                                  GluProSerSerValArgArg.....LysArgSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roArgArgGlyLeuAspGluAspArgGlySerTrpArgThrAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCAAAAAGTAGAGGT......CGACATCATAGATGACAACTTTATCC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spargProSerTrpargAsnThraspaspaspargProProargargIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGTCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGG......TGGAACAGGAGCGATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......TGGAAAAATCT......AAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProAspAspAspArgValProArgArgGlyMetAspAspAspArgGlyPr
                                                                                                                                                                                                                                          Quality:
                                                                                                                                          to: 076514
                                                                                                                                                                                                                                                                                                      365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                66.00
1.941
62.963
                                                                                                                                                                                                                                                                                                    GFCYSKNOT.
A; 41781 MW;
                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08,
12,
                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                          .
6
                                                                                                                                                                                                                                                                                                    54051BEE CRC32;
                                                                                                                                                                                                                  Identity:
                                                                                                                                                                                                                              Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ζ
                                                                                                                                                                                                                54
2
31.481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                        152
                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                       elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
                             255
```

```
SECTION OF THE PROPERTY OF THE
seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_1_229 x Q30849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: Q30849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q30849 PRELIMINARY; PRT; 358 AA.
Q30849;
Q1-NOV-1996 (TREMBLrel. 01, Created)
Q1-NOV-1996 (TREMBLrel. 02, Last sequence update)
Q1-NOV-1999 (TREMBLREL. 12, Last annotation update)
MHC CLASS I ANTIGEN PRECURSOR;
ORYSTOLAGUS CUNICULUS (RABDIT).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYROCINSKI M.L., MARCHE P.N., MAX E.E., KINDT T.J.;
"Rabbit class I MHC genes: cDNA clones define full-length
of an expressed gene and a putative pseudogene.";
J. Immunol. 133:2261-2269(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; K02442; AAA98731.1; -. HSSP; P30460; IAGE. PFAM; PF00047; 1g; 1. PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-B/J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 84290724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT 152
                                                                                                                                                                                                                                                                                                                                                                                                        GACAACTTTATCCTGAGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rGluThrArgThrGlySerHisSerLeuArgTyrPheThrThrAlaValS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysGlyAla.....LeuLeuLeuLeuLeuAlaGlyAlaLeuThrLeuTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGT 61
                                                                                                                             GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erArgProGlyLeuProGluProArgPheMetSerValGlyTyrValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCGTCGCCGTGGGCCCATGGGTGTTG.....TCCGCAGCCGCAG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspPheTyrVal 271
                                                                                                                                                                                                uProArgAlaProTrpMetArgGlnValAspProGlyTyrTrpAspArgG
                                                                                                                                                                                                                                                                                                                                        AspThrGlnPheValArgPheAspSerAspAlaAlaSerProArgAlaGl
                                                                                                                                                                                                                                                          .....TGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....AsnThrGluAlaGluSerAsnLeuCysArgArgThr
                                                                lnThrGluArgAlaLysAsnThrAlaLeuSerPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_mhc:Q30849
sp_rodent:088970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.50
1.296
51.579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 P
358 MW;
39828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
MHC CLASS I ANTIGEN.
86894130 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
3
23.158
                                                                                                                                                                                                                                                                                                                                                                                                        . . . . . . . . . . . .
                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                        170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcripts
```

```
seq_documentation_block:
ID 064317
AC 064317;
DT 01-AUG-1998 (TrEMBLrel. 07
DT 01-AUG-1998 (TREMBLREL. 07
DT 01-AUG-1998 (TREMBLREL. 07
DT 01-AUG-1998 (TREMBLREL. 07
DE TERMINASE LARGE SUBUNIT.
GN GENE 2.
OS Bacteriophage N15.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RA HENDRIX R.W., RAVIN V.K.,
RA SMIRNOV I.K.;
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-240-675-1_COPY_1_229/rev x 088970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQUENT RACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: sp_phage:064317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8661-AON-10
8661-AON-10
8661-AON-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XU G., ULMER W.T., WOLF B.A.;
"Partial genomic DNA sequence of mouse beta-cell IRS-2.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF090738; AAC61743.1;
NON TER
1
SEQUENCE 734 AA; 75251 MW; B3410CAF CEC22.
                                                                                                              HENDRIX R.W., RAVIN V.K., CASJENS S.R., FORD M.E., RAVII SMIRNOV I.K.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL: AF064539; AAC19038.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 oThrAlaGlySerSerMet.SerSerGluProGlyAspAsnGlyAspTyr 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCATGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INSULIN RECEPTOR SUBSTRATE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 CACGGGGACGAGCACTAGGGTCGTCGCGCCCAGGA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 GCCGCAGATCCCTG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysArgLeuSerLeu 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aProProLysProGluGlyAlaArgValAlaSerProThrSerGlyLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrGluMetAlaPheGlyValAlaAlaThrProProGlnProIleValAl 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence up)
(TrEMBLrel. 08, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     088970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.50
1.984
44.444
    63
                                                                                          73094 MW;
    .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to:
                                                                                                                                                                                                                                                                                                                                              07,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                        E1B34267 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .GGACGACCATCATCTGGGAGCC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     734
                                                                                                                                                                                                                                                                                                                                                                                                                                         640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     734
                                                                                                                                                                                   FORD M.E., RAVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
2
29.167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
```

```
alignment_block:
US-09-240-675-1_COPY_1_229 x 064317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: sp_human:Q13507
alignment_block:
                                                                                  alignment_scores:
                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: 064317 from: 1 to: 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||
| 134 ProTrpTyrGlyLysLysHisArgAspAsnThrLeuSerMetLysArgPh 150
                                                                                                                                                                                                      MEDLINE; 97358541.
XU X.C.S., LI H.S., GUGGINO W.B., MONTELL C.;
"Coassembly of TRP and TRPL produces a distinct store-operated conductance.";
Cell 89:1155-1164(1997).
Cell 89:1155-1164(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 11, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN
TRPC3 OR HTRP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 AACAGGAGCGATGAGTCTGTCGGGGAATGTGACTTTTTCATTCGAT 218
::: ::: ||||::: ||||::: |||||||
                                                                                                                                   EMBL; U47050; AAC51653.1; -.
EMBL; Y13758; CAA74083.1; -.
PFAM; PF00023; ank; 2.
PRINTS; PR01097; TRNSRECEPTRP.
SEQUENCE 848 AA; 97354 MW;
                                                                                                                                                                                                                                                                                                                                               "trp, a novel mammalian gene family essential for agonist-activated capacitative Ca2+ entry.";
Cell 85:661-671(1996).
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 96234226.
ZHU X., JIANG M., PEYTON M.,
BIRNBAUMER L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q13507; 000593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 yrArgGluLysSerValAspValValGlyTyrAspGluLeuAlaAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 eThrAsnGlyArgGlyPheTrpCysLeuGlyGlyLysAlaAlaLysAsnT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 rHisValGluProThrIleArgAspValProSer.LeuLeuSerLeuAla 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GluLeuLeuTrpLeuProThrAspGlyAspAlaAspAsnPheMetLysSe 117
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 97358541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aspalaaspileGluLysGluGlySerProThrPheLeuGlyAsp 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATCTGCGGCGGCTCCCAGATGATGGT..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCATGG......GTGTTGTCCGCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....CGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......GCCGCAGGTGGAAAAATCTAAAATCTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.340
47.475
                              63.00
1.537
54.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 4
Percent Identity: 26.263
                           Length: 75
Gaps: 3
Percent Identity: 33.333
                                                                                                                                                                                                                                                                                                                                                                                                                   BOULAY G., HURST R., STEFANI E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                         78AC2E9D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                      986
                                                                                      104
                                                                                                                        969
                                                                                                                                                                                             952
                                                                                                                                                         69
                                                                                                                                                                                                                           25
```

```
seq_documentation_block:
ID 060697
AC 060697;
AC 060697;
AC 01-NOV-1996 (TIEMBLIEL 01.
DT 01-NOV-1996 (TIEMBLIEL 01.
DT 01-NOV-1996 (TIEMBLIEL 01.
DT 01-NOV-1996 (TIEMBLIEL 07.
DE p162 PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chorda:
OC Eutheria; Rodentia; Sciuroo
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOID TUMOR;
RA FISHER R., FILLMORE H., RE:
RA SUBMILTER R., FILLMORE H., TENBL; U141172; AAA90910.1;
SQ SEQUENCE 1344 AA; 16194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_1_229 x Q60697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_rodent:Q60697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1_COPY_1_229 x Q13507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: Q60697 from: 1 to: 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-LYMPHOID TUMOR;
FISHER R., FILLMORE H., REYNOLDS A.B.;
FISHER R., SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14172; AAA90910.1; -.
SEQUENCE 1344 AA; 161949 MW; 88593FEF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-AUG-1998 (TIEMBLIEL. 07, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 eThrValThr...AspTyrProLys
936 LeuArgArgLeuGlyGlyAspAspGluGluArgGluSerSerLeuArgPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 GACTTTTTCATTCGATTATCAAAAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIl 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 etLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeuLeu 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 rTrpIleAlaProCysSerArgLeuGlyLysIleLeuArgSerProPheM 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 LeuValValleuValValAlaLeuGlyLeuProPheLeuAlaIleGlyTy 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                            AAGTAGAGGTC......GACATCATAGATGACAACTTTATCCTG 167
                                                                            ArgProSerTrpArgAsnAlaAspAspAspArgProProArgArgIleGl 1002
                                                                                                                                                                                                                                  oAspAspAspArgIleProArgArgGlyLeuAspAspAspArgGlyProA
                                                                                                                                                                                                                                                                                                                          AGATGATGGTCGTCCTCCT......GGGCGCGACGACCCTAGTGCTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTGGAACAGGAGCGATGAGTCTGTCGGG......AATGT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                 rgArgGlyProAspGluAspArgPheSerArgArgGlyThrAspAspAsp 985
                                                                                                                                .....TGGAAAAATCT......AAAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: Q13507 from: 1 to: 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.00
1.432
42.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 31.068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                     123
                                                                                                                                                                                                                                                                                                 969
                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                      952
```

```
seq_documentation_block:
ID. 023212 PRELIMI
AC 023212;
DT 01-JAN-1998 (TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_1_229 x Q94603
                                                                                                                                                                      seq_name: sp_plant:023212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: Q94603 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
Q94603 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SISK E., SUNKIN S., SWARTZELL S., WESTLAKE T., MAGNESS C., BASTIEN FU G., IVENS A., STUART K.; "Leishmania major Friedlin chromosome 1 has only two polycistronic units of protein coding genes.";
                                                                                                                                                                                                                                                                                                                         138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1002 yAspAspAspArgGlySerTrpArgHis.ThrAspAspAspArgProPro
                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                               189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The nucleotide sequence of Leishmania major Friedlin chromosome Submitted (MAY 1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB001274; AAC24664.1; .
SEQUENCE 326 AA; 36141 MW; A629D498 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 CysGlyGlySerLeuLeuAlaThrMetTrpLeuLysArgIleProThrGl 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major.
Eukaryota: Euglenozoa: Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 TGTCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYLER P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCGACGACCCTAGTGCTCGTC...GCCGTGGGCCCATGGGTGTTGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erCysAlaAlaThrValAsnLeuAlaSerMetArgLysAsnGluTrpLeu 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pArgGly 1037
                                                                                                                                                                                                                                            SerSerGlyGlnGlyIleArgValValAspAspAspGlyValThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgArgGlyLeuAspAspGluArgGlySerTrpArgThrAlaAspGluAs 1035
                                                                                                                                                                                                                                                                                                                  .....GTCGACATCATAGATGACAACTTTATCCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_invertebrate:Q94603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAY-1998)
   (TrEMBLrel.
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.50
1.645
57.576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02,
09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes.";
the EMBL/GenBank/DDBJ databases
   ,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
   Created)
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAACAGGAGCGATGAGTC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosomatidae;
                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
3
30.303
                                                                                                                                                                                                                                                                                                                  170
                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٦.
SO STARTED BY A RESTRICT OF THE RESTREE OF THE REST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SO DE REPRESENTATION DE LA COMPTANTA DE LA COM
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_mammal:077699
                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID 077699 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: 023212 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1_COPY_1_229 x 023212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent
   NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                         WISSENBACH U., PHILIPP S., FLOCKERZI V.;
"Cloning and analysis of TRP channels.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AJ006781; CAA07246.1; -.
                                                                                                                                                                                                                                                                     01-NOV-1998 (TrembLrel. 08, 01-NOV-1998 (TrembLrel. 08, 01-NOV-1998 (TrembLrel. 08, TRP3 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1998) to the EMBL; 299708; CAB16828.1; -. HSSP; P19339; ZSXL. PFAM; PF00076; rrm; 2. SEQUENCE 573 AA; 63551 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TIEMBLIEL 10, I
01-NOV-1999 (TIEMBLIEL 12, I
SPLICING FACTOR-LIKE PROTEIN.
C7A10.670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEVAN M., TERF
                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                          Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           rArgGluArgGlyGluArgArgGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...argaspargaspGlyGluLysSerLysGluArgSerArgAspLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGGAGCGATGAGTCTGTCGGGAA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgAspH1sArgGluArgH1sH1sArgSerSerArgH1sArgAspH1sSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sAspArgGluArgAspSerGluValSerArgArgSer......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgGluThrSerArgSerLysAspArgGluArgGluLysGlyArgAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGATCTGCGGCGCCTCCCAGATGATGGTCGTCCTCCTGGGCGCGAC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....AGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                                                            Bos.
117
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TERRYN N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....GACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTG 89
     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.50
1.645
50.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2.
63551 MW;
       13295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VOS P.,
     WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEIJNEN L.,
     B9F9B808 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07954A00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEWES
                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                           Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHUELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ر</u>
```

```
alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-240-675-1_COPY_1_229 x 077699
                                                                                                                                                                                                                        alignment_block:
US-09-240-675-1_COPY_1_229 x 095927
                                                                                                                                                                                                                                                                                                                                                                                                     SORRAR RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID 095927 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: sp_human:095927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 62.00
Ratio: 1.512
Percent Similarity: 54.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: 077699 from: 1 to: 117 *
                                                                                                                                                                                          Align seg 1/1 to: 095927 from: 1 to: 290
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL031432; CAB37992.1; -. SEQUENCE 290 AA; 33613 MW; B59EOC18 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 AGGTGGAACAGGAGGGATGAGTCTGTCGGG......AATGT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 AAGTAGAGGTC......GACATCATAGATGACAACTTTATCCTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-MAY-1999 (TrEMBLrel. 10, Created)
Ol-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Ol-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DJ465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DJ465N24.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GACTTTTTCATTCGATTATCAAAAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 .....AGGTGGAAAAAATCT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 eThrVal...IleAspTyrProLys 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIl 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 etLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeuLeu 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaIleGlyTy 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                             82 GGGTGTTGTCCGCAGCCGC......100
                                     27 rSerArgLeuSerSerArgSerArgSerArgSerPheSerArgSerSerA 44
                                                                                                                                                                                                                                                                                    62.00
2.296
43.548
                                                                                                                                                                                                                                                                    μength: 62
Gaps: 1
Percent Identity: 29.032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 33.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 AA.
```

```
44 rgSerH1sSerArgValSerSerArgPheSerSerArgSerArgArgSer 60
```

<sup>116</sup> AAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGA 151 ||| |||::::|||||| |||||:::||| 61 LysSerArgSerArgSerArgArgArgHisGlnArg 72

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                     166.5
144
142
131.5
131.5
111
1111
1111
1111
                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                  1072
                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                      100.0
100.0
100.0
100.0
100.0
100.0
99.5
99.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-2_COPY_27_229
1072
1 GKNLKSPQKVEVDIIDDNFI.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             June 1, 2000, 00:40:12; Search time 42.08 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188963 seqs, 23686106 residues
                                                                           881101112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKNLKSPQKVEVDIIDDNFI......WKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                            R75783
W97864
W97861
                                                                                                                                                                                                                                                                                                                         R14488
                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114.265 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188963
                                                                                                                               Human cytokine rec
Human cytokine rec
Gamma interferon r
Gamma interferon r
Gamma interferon r
Gamma interferon r
                                                                                                                                                                                                                                       spliced-deleted in
Transmembranal int
CRFB4 protein
                                                                                                                                                                                                                                                                                       Complete interfero
Sequence of a soul
Human interferon r
Human IFN receptor
                                Human
Human
                                                                                                                                                                                                                                                                                                                                 Sequence of a soul
IFN receptor extra
Human alpha-interf
                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                      Human
Human
                                                                                                                                                                                                                                                                                                                                                                  Soluble interferon
                                                                                      Soluble human inte Human truncated ti
                                                                                                            Plasmid pBABLUE hu
Gamma-IFN-R-GBP 13
                                                                                                                                                                                                              Human IFN-gamma ac
                                                                                                                                                                                                                      IFN-gamma receptor
Zcytor7 cytokine r
                                                                           Human
                                                                                                                                                                                                 IFN-gamma receptor
n tissue facto
IFNAB-BPI en
truncated ti
truncated ti
tssue facto
tissue facto
CD45 for use
truncated ti
 RESULT
R28495
ID R2
AC R2
DT 31
                                                                          5
```

g Q	g 8	g v	g Q	ጃ ዘነርን	00000000000000000000000000000000000000	אלם היק היק היק היק	אסקקקקק אסקקקקקקקקק	RESULT R14487 ID R AC R AC R DT 1 DE S KW I		
181 207	121 147	61 87	N	Query Ma Best Loc Matches	The transport transport to the transport trans	New Dett	FR20 09-2 05-1 05-1 70v	ULT 487 R144 R144 16-:		00000000000000000000000000000000000000
	ω <del></del> ω	$\alpha - \alpha$	1 GKNLKSI         7 GKNLKSI	atch cal 20	he transmembrane ave been deleted eceptor. Potenti erivatives obtaire also claimed eceptor (or deriee also 014240. equence 436 AA	SDB; Q142 water-sc water-sc h - used h - used h stic and	FR2657881-A. 09-AUG-1991. 09-AUG-1991. 05-FEB-1990; FR-001298 05-FEB-1990; FR-0011. (EUBI-) LAB EURO BIG Eld P, Gresser I, L. Tovey MG, UZe G;	1 187 stand 187; JAN-1992 ible inte		8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9
GVYSPVH	SVMWALD	CLNVYEE CLNVYEE	POKVEVD POKVEVD	Similarity 3; Conserv	nsmembrane en deleted r. Potentia ives obtain o claimed a: r (or derivo Q14240.	214239. 214239. r-soluble paed to tread to tread to tread to tread an anaemia, of page 45;	001298 FR-001 EURO B	ard; Protein; (first entry rferon-alpha,		00000000000000000000000000000000000000
LTSWKIGVYSPVHCIKTTVENEL	GLSFTYS        GLSFTYS	IKLRIRA          KLRIRA	IIDDNFI	100. 100. ative	and cytoplasmic to obtain a solly immunogenic ly immunogenic ed by substitut s are hybrid mo.) and an immun	polypep at e.g. diabete	98. 01298. BIOTECHNO. Lutfalla	otein; entry alpha, ase;		219 1 263 1 263 1 263 1 2213 1 239 1 239 1 239 1 219 1 219 1
	TTIWI      TTIWI	EKEN	LRWNI           RWNI	0	oplas in a unoge ubsti	tide( lupu s mel	ဂ္	, 436 F Deta r		
203 229	PGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENTYSRHKTYKLSPETTYCLKVKAAL 	NESSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPERKAQIGPPEVHLEAEDKAIVIHI 	KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITST 	Score 1072; DB 1; Length Pred. No. 1.1e-101; ; Mismatches 0; Indels	, circulating corrections of the many corrections to the compression of the comprision of the comprision bulin such as	inity fo osus, Be matoid a	Meyer F, Mogensen KE;	AA. receptor. rejection; histocompatibilit	ALIGNMENTS	W17732 W17744 W17724 W17724 W17724 W17726 R80067 R80065 W19065 W17752 W17752
	STINCT	EAEDK	\$25573        	Δ. W	. 8.3 p. E.	alph dis		bilit		Human Human Human Human Human Rabbi Human Human Human
	.KVKAAL 180        KVKAAL 206	AIVIHI 120        AIVIHI 146	NITSTK 60  - - - -   NITSTK 86	0; Gaps	If receptor of the en eliminated. s sequence soluble	and tc.		<b>4</b>		truncated ti truncated ti tissue facto tissue facto tissue facto tissue facto tipl recepto IFNAB-BPII. N truncated ti truncated ti
				0;						

R28495 standard; Protein; 436 AA. R28495; 31-MAR-1993 (first entry)

N

```
ş
                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases and transplant rejection

Claim 2; Fig 1; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN alpha and beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN alpha and beta receptor (030533), was incubated with oligos 030534 and 030535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the
N-PSDB; Q86457.

Compsn. of monoclonal antibodies against interferon useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.28-2B; 105pp; English.

A recombinant soluble form of the human interferon c protein extracellular domain, given in R71723, was e
                                                                             16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI: 95-131187/17.
                                                                                                                                                                                                                                           R71723
R71723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with a hi
                                                                                                                                                                                     16-OC7-1995 (first entry).
IFN receptor; interferon receptor; interferon receptor; interferon antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                  WO9507716-A.
23-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune
                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eid P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1991; F00318.
17-APR-1991; WO-F00318.
                                                                                                                                                                                                                             16-0CT-1995 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tovey M, Uze G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EUBI-) LAB EURO BIOTECHNOLOGIE.
                                                                                                                                                                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                          207
                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKNLKSPQKVEVDIIDDNEILRWNRSDESVGNVTESFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                         CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                       LTSWKIGVYSPVHCIKTTVENEL
LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                             CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92-382110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ce of a soulble form of the interferon (IFN) receptor
high affinity for IFN-alpha and -beta.
eron receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.
hilarity 100.
Conservative
                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1072;
Pred. No. 1.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 203
                                                                                                                                                                                                                                                        ₹
                                                                                                           SA
                                                                                                                                                                                    interferon-alpha;
dy; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .le-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΚE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
  class I receptor expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                             146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

```
Š
                                   δÃ
                                                           밁
                   ₽
                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  윉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868
                                                                                                  Query Match
Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 203
                                                                                                                                                          New human alpha-interferon receptor protein - useful for testin interferon agonists and in treatment or diagnosis
Disclosure; fig 4, 30pp; French.
This recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and discousis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when require eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.
                                                                                                                                                                                                                                                                                                                02-MAY-1991.
19-OCT-1990;
20-OCT-1989;
                                                                                                                                                                                                                                                                                            20-OCT-1989; FR-013770.
(CNRS ) CNRS CENT NAT RECH SCI.
Mogensen KE, Uze G, Lutfalla G,
                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                        Human alpha-interferon receptor protein.
Human alpha IFN; IFN agonists; antiviral;
                                                                                                                                                                                                                                                                          N-PSDB; Q11701
                                                                                                                                                                                                                                                                                                                                               WO9105862-A.
                                                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                R11958 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         either E. coli or COS cell hosts. The protein was immunomodulatory monoclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147
 121
                                                                                                                                                                                                                                                                                                                                                                                                                            8-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                     87
                                       61
                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 100.0%;
Local Similarity 100.0%;
les 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                 LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                     91-148740/20
                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n residues
se 557 Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
                                                                                                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                        signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                557
                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1072;
Pred. No. 1.1
); Mismatches
                                                                                                 Score 1072; DB Pred. No. 1.5e-1; Mismatches
                                                                                                                                                                                                                                                                                              Gresser
                                                                                                                                                                                                                                                                                                                                                                                                        anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
.1e-101;
                                                                                                           DB 1;
5e-101;
                                                                                                   0
                                                                                                                     Length
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used
                                                                                                                                                                                                    required,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ç
                                                                                                                                                                                                                                                                testing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raise
                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                       diag-
                                                                                                                                                                                                                                  is
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                       120
                                                           86
                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
```

```
RESULT
R28496
ID R2
AC R2
DT 31
DE Se
DE W1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                        õ
                                                                                                                                             ő
                                                                                                                                                                 В
                                                                                           밁
                                                                                                                              ₽
                                                                                                                                                                                 Ş
                                                                                                                                                                                                      문
                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 203; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             FR2657881-A.
09-AUG-1991.
05-FEB-1990; FR-001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
EIG P, Gresser I, Lutfalla G
TOVEY MG, UZE G;
WPI; 91-319778/44.
                                                                                                                                                                                                                                                                                       New water-soluble polypeptide(s) with affinity for IFN-alpha and beta used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv. s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
R28496;
31-MAR-1993 (first entry)
Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-1992 (first entry)
Complete interferon-alpha/beta
IFN; autoimmune disease; graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R14488
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q14240
                                             R28496 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                            207
                                                                                                             181
                                                                                                                                                  121
                                                                                                                                                                   87
                                                                                                                                                                                     61
                                                                                                                                                                                                        27
                                                                                                                                                                                                      s
                                                                                                     LISWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                               LTSWKIGVYSPVHCIKTTVENEL
                                                                                            LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                    CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                              CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
458. .55
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane
                                               557
                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                            Score 1072;
Pred. No. 1.5
0; Mismatches
                                                                                                             203
                                                                                                                                                                                                                                                                                                                                                                                                                                    Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ያ
                                              ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                    F, Mogensen
                                                                                                                                                                                                                                                      DB 1;
1.5e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                histocompatibility.
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                  180
                                                                                                                                                                     146
                                                                                                                                                                                                          86
                                                                                                                                                                                                                                               0
  Š
                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                 R42635;
R42635;
                                                                                                                         Key
         Monoclonal antibody
                    P-PSDB; R42635
                                                                                                               domain
                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                        بر
```

```
Mater soluble polypeptide(s) strongly bind interferon(s) alpha pr and beta - useful as immunosuppressants, for treating auto:immune pr and beta - useful as immunosuppressants, for treating auto:immune pr diseases and transplant rejection soluble polypeptide with a high affinity for Claim 3; Fig 2; 58pp; English.

CLAIM 3; Fig 2; 58pp; English.

CLAIM encoding the water-soluble polypeptide with a high affinity for CLAIM and obeta is isolated by PCR, using appropriate coligonucleotides as primers and cloned cDNA as template. For example, bacterlophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos CLAIM and Q30535. R28496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind CLAIM in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the CLAIM is side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                              EP-563487-A.
06-OCT-1993.
31-MAR-1992; 400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SI
BENO1L P. Maguire D. Meyer F. 1
WPI; 93-312951/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.

W09218626-A.

29-OCT-1992.

17-APR-1991;

17-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen
Tovey M, Uze G;
WPI; 92-382110/46.
N-PSDB; Q30533.
                                                                                                                                                                                                                                                 Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection;

cell proliferation; allograft rejection; systemic lupus erythematosus;

psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;

immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                20-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                       Location/Qualifiers
1. 436
/label= extracellular_domain
/note= "soluble, immunogenic"
                ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
o human i
against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
 interferon
t human type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1072; DB 1;
Pred. No. 1.5e-101;
                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                    SA.
Plavec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
 type-I receptor
                                                                    μ
                                                                    Tovey
                                                                                                                                                                          form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         줆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                            of IFN-R
   used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
```

```
RESULT RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   £ & S S S S S S S S
                                                                                                    B
                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B 5
                                                Š
     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Sin
Matches 203;
                                                                                                                                                                                                        Query Match
Best Local S
Matches 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy and diagnosis pisclosure; Fig 3; 21pp; English.

Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral infection.
                                                                                                                                                                                                                                                                                                                                                       Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.
The amino acid sequence of human interferon class I receptor is given in R75356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R75356 standard; Protein; 557
R75356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q86458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IFN receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                        Local Similarity 100
mes 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
        87
                                                   65
                                                                                                      27
                                                                                                                                                       \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    æ
                                                                                                    GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                           CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKNLKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LISWKIGVYSPVHCIKTIVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .436
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular_domain
                                                                                                                                                                                                                                   .00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                        Score 1072; DB 1;
Pred. No. 1.5e-101;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1072; DB 1;
Pred. No. 1.5e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

```
밁
                      Ş
                                              8
                                                                  Š
                                                                                               유
                                                                                                                     ğ
                                                                                                                                                밁
                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                              멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
                                                                                                                                                                                                                                                                     IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21805) probably regulate the response of human cells to IFNA, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 2; Fig 7; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Novel splice-deleted interferon alpha-receptor (IFNAR) form 1 (W21805) is characterised by a new domain (S) which follows an end-deleted extracellular domain when compared to transmembranal
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abramovich C, Ratovitski E, WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spliced-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W21805
                                                147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
207
                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                87
                                                                                                                       61
                                                                                                                                                27
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                        щ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
                                                                                               GKNLKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFDYOKTGMDNWIKLSGCQNITSTK
              LTSWKIGVYSPVHCIKTTVENEL
                                                             SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTSWKIGVYSPVHCIKTTVENEL
                                                SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENTYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembranal IFNAR" 428. 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=_Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                            99.5%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-receptor IFNAR.
                                                                                                                                                                                                0
229
                                                                                                                                                                                                            Score 1067;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ጅ
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                                                                                                                                                                                                            DB 1;
).5e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-427
                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of.
                                                                                                                                                                                                0
                                                                                                                                                                                               Gaps
                                                                                                146
                                                                                                                       120
```

W21806

```
RESULT
W21804
ID
AC
W211
AC
Tra
DT
Tra
KW
Int
OS
Hom
FH
Key
FT
dor
                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          멅
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel splice deleted interferon alpha-receptor (IFNAR) form 2 (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also T73521) obtd. If from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, or Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV C
(ABRA/) ABRAMOVICH C.
Abramovich C. Ratovitsk
                                                                                             W21804;
23-SEP-1997 (first entry)
Transmembranal interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 3; Fig 7; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W21806;
W21806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spliced-deleted interferon Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                 Homo sapiens.
                                                                                                                                                                  W21804 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1997 (first entry)
                                                                       Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                         207
                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match
Local Similarity
hes 202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                               GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTESFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                               LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                         LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratovitski E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Intracellular_domain /note= "comprises amino acids transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .419
1. .41
  Location/Qualifiers
1. .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ၀
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LID
                                                                                                alpha-receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496
                                                                                                                                                                     557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-receptor form IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1067; DB 1;
Pred. No. 4.3e-101;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                     ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Revel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481-557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဝ္ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 202
                                                                                   22-JAN-1998. U2-683743. U7-U1-1997; U1-683743. (UYNE-) UNIV NEW JERSEY. KOTENKO SV, PESTKA S; WPI; 98-110590/10. N-PSDB; V19874. NA COM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purposes.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s Disclosure; Fig 7: 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21805) have been detected that lack this transmembrane denain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
rejection

Claim 2; Page -; 79pp; English.

This sequence is the human CRFB4 sequence, DNA encoding it is used in the recombinant DNA (I) of the invention. (I) comprises a sequence (S1) encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)
                                                                New recombinant DNA and CRFB4 linked to
                                                                                                                                                                               Homo sapiens. W09802542-A1.
                                                                                                                                                                                                                   CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection; vaccine; photosensitivity; inflammation; autoimmune disease;
                                                                                                                                                                                                                                  CRFB4 protein CRFB4; interl
                                                                                                                                                                                                                                                                       W52296 standard; Protein; W52296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abramovich C, Ratovitski E, WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                         septic shock; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU9475977-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                            23-JUN-1998
                                                                                                                                                                                                                                                                                                                                                  207
                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                  LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                              LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                  SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENTYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                              SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 99.1
02; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557
                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       075977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label-
458. .55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
437. .45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label-
                                                                operator,
                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      el- Transmembrane_domain
.557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 el= Extracellular_domain .457
                                                              comprises sequences encoding interleukin-10 perator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIT
                                                                                                                                                                                                                                                                                   325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1067; DB 1
Pred. No. 5e-101;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 229
                                                                                                                                                                                                                                                                                                                                                                         203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Revel
                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                         organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used for interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

```
RESULT
R75782
ID
AC
R75782
AC
R7
AC
AC
AC
R7
AC

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC encoding CRFB4, both operably linked to expression control sequences.
CC cells containing (I) may be used to identify agonists/antagonist of CC II-10. Agonists are potentially useful, e.g. for preventing allograft CC rejection, as vaccine adjuvants, for treatment of photosensitivity.
CC inflammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, corruses, bacteria and parasites (especially intracellular pathogens) and CC for preventing organ rejection. A vector containing (I) is used to crestore, e.g. by gene therapy, II-10 sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind II-10 but not to transduce a csignal. Antisense CRFB4 sequences (especially ribozymes), can inhibit CL-10 activity in cells. Antibodies specific for CRFB4 are used to CC measure and localise CREP4, for diagnosts of defective II-10 activity. CC Fragments of (I) are used as primers or probes to assay CREP4-specific CC RNA. Agonists/antagonists may be administered parenterally, orally or crectally especially by intravenous injection or directly into a tumour or allocative interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                15-JUN-1995.
07-DEC-1994;
09-DEC-1993;
Novel interferon gamma receptor beta chain treatment of inflammatory bowel disease and Claim 3; Fig.2A; 86pp; English.
The IFN-gamma receptor beta-subunit encoded
                                                                                                                                                            (HEMM/) HEMMI S.
Aguet M. Boehni R.
WPI: 95-224321/29.
                                                                                                                                     N-PSDB; Q90808
                                                                                                                                                                                                                                                                   (AGUE/) AGUET M.
(BOEH/) BOEHNI R
                                                                                                                                                                                                                                                                                                                                                                                                                                W09516036-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pept1de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon-gamma-antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interferon-gamma receptor beta subunit; muIFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFN-gamma receptor beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R75782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R75782 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allograft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 30.9 nes 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRNKAGEWSEPVCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSWKIGVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENEYETWIMKNYYNSWIYNVQYWKNGIDEKFQIIPQYDFEVLRNLEPWIIYCVQVRGFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POKVEYDIIDDNFILRWNRSDESYGNYTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI
                                                                                                                                                                                                                                                                                                                                US-164596
                                                                                                                                                                                                                                                                                                                                                               U14277
                                                                                                                                                                                                                                                                   ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Transmembrane_anchoring_domain
267. .332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=_Extracelular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
30
                                                                                                                                                                                                  Hemmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 266
beta-subunit encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic_domain
                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 214; DB 1;
Pred. No. 4.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                ain polypeptide -
and liver damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
   D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 325
   cDNA clone derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                  ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
```

밁 Ş 밁 Š 밁 ð 밁 δÃ

```
RESULT
W79159
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               片
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ភន្តន្តន្តន្ត្
                                For treating renal, neural, pancreatic and prostatic diseases

Claim 1, Pages 55-59; 72pp; English.

Chaim 2, Pages 55-59; 72pp; Pages 1, Pages 2, Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be may be used to treat pathological conditions associated with endogenous IFN-gamma production.

Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2cytor7 cytokine receptor polypeptide.
Ccytor7; cytokine receptor; ligand-binding polypeptide; kidney; pa
type 2 cytokine receptor family; CRF2; prostate tissue; nervous ti
type 2 cytokine receptor family; CRF2; prostate tissue; nervous ti
agonist; cell proliferation; cell differentiation; renal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1998.
18-FEB-1998; U03029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
                       diseases
                                                                                                                                                                                                                                                                                                                                                       Novel
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; V57515
                                                                                                                                                                                                                                                                                                                                                                                                                   Adams RL, Fa
Whitmore TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9837193-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                 98-480798/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF----IDGSWHRLLEPNCT
                                                                                                                                                                                                                                                                                                                                                       human 2cytor7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZYMOGENETICS INC.
L, Farrah TM, Jelmberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-943087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "extracellular (ligand-binding) domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-
                                                                                                                                                                                                                                                                                                                                                       DNA encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%;
30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ۵
ک
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                       ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                     type
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kho CJ, Lok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199; DB 1;
No. 1.4e-12;
                                                                                                                                                                                                                                                                                                                            2 cytokine receptor -
and prostatic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                     useful
                                       prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
```

Sequence

Job time: 20019 sec

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  용
                                                                                                                Š
                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCCCC PATER PART OF THE PART O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.5%; Score 166.5; DB 1; Best Local Similarity 26.1%; Pred. No. 6.1e-09; Matches 49; Conservative 34; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.4%; Score 144; DB 1; Length 337; Best Local Similarity 24.7%; Pred. No. 6.2e-07; Matches 56; Conservative 39; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-1995.
22-AUG-1994; U09438.
20-AUG-1993; US-110119.
(UYNE-) UNIV NEW JERSEY.
Cook JR, Donnely RJ, Ema
Pestka S, Schwartz B, Schwartz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suppressing tumours in mammals with accessory factor 1 (AF-1) for interferon gamma, specifically induction of class I HLA antigens, including use of AF-1:DNA in gene therapy Disclosure; Fig 21A; 114pp; English.

The sequence is that of human interferon-gamma accessory factor-1. Incorporation of AF-1 into immune and tumour cells re-establishes normal function with elimination of malignant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R71035;
11-OCT 1995 (first entry)
Human IFN-gamma accessory factor-1.
Interferon-gamma; AF-1; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9505847-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R71035 standard; Protein; 337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 TYCLKVKA 178
||:|::
213 LYCVHVES 220
                                                                                                                                                                                                                                                                                                                                      103 GPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 PGTK-----DSVMWALDGL6FTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
194 SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMAD 240
                                                                                                                160 RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVE 200
                                                                                                                                                                                                                                 141 GPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 NCTQITATECDETAASPSAGEPMDENV----TIRLRAELGALHSAWVTMPWEQHYRNVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 FSSLKLNYYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 LPAPOHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFKYTDSK-----WFTADIMSIGV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKSPQKVEVDIIDDNFILRW------NRSDESVGNVTFSFDYQKTGMDNWIKLS----- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emanuel S, Soh J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kotenko S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mariano TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
```

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0% Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                              490.5
214
199
                                                                                                                                                                                                                                                                            Score
 seq length: 0 seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA: *
  11000
10000
10000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
                                                                                                                                                                                                                               0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-2_COPY_27_229
1072
1 GKNLKSPQKVEVDIIDDNFI.........WKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145308 segs, 14437401 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                        /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/5COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/backfiles1.pep:*
                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000, 04:17:53; Search time 23.82 Seconds (without alignments) 123.039 Million cell updates/sec
                                                                                                                                                                                                                                                                            BB
US-08-328-256-11
US-08-328-256-12
US-08-328-256-10
US-08-471-454-2
US-08-471-453-2
US-08-471-453-2
US-08-471-453-2
US-08-471-453-2
US-08-683-743-4
PCTT-US94-14277-2
PCTT-US94-14277-2
PCT-US94-14277-2
PCT-US94-14277-6
US-08-943-087-5
US-08-943-087-5
US-08-943-087-1
US-08-943-087-2
US-08-943-087-2
US-08-943-087-2
US-08-943-087-2
US-08-943-087-2
US-08-943-087-2
US-08-943-087-2
US-08-943-087-2
US-08-943-087-2
US-08-943-087-3
US-08-943-087-3
                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145308
                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                     Sequence 11, 1
Sequence 2, Applications 12, 1
                                    Sequence
Sequence
                                                              Sequence
Sequence
                                                                                        sequence
sequence
sequence
sequence
sequence
sequence
                                                                                                                                                       Sequence
Sequence
                                                                                                                                                                         Sequence
Sequence
                                                                                                                                                                                          Sequence
Sequence
                                                                                                                                                                                                                     Sequence
Sequence
                          Sequence
                                                                                 Sequence
                                                                                                                                                                                                             Sequence
                                                       Sequence
                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-328-256-11
                  Query Match
Best Local Sim
Matches 203;
                                                                                                                                                                                                                                                                                                               ZIP: 20004
                                                                                                                                                                                                                                                                                                                               STATE: D.C
1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
```

45	44	43	42	41	40	39	ა 8	37	36	35	34	33	32	31	30
89	89.5	92	111	111	131.5	142	145	160.5	163.5	165.5	166.5	166.5	166.5	166.5	166.5
8	8.3	8. 6	10.4	10.4	12.3	13.2	13.5	15.0	15.3	15.4	15.5	15.5	15.5	15.5	15.5
239	2213	265	489	489	574	337	200	221	221	221	553	553	553	553	553
N	ب	N	u	4	N	4	4	N	N	N	N	N	N	N	N
US-08-385-191A-6	US-08-727-034-3	US-08-385-191A-14	5221789-1	PCT-US93-11110-1	US-08-906-713-2	PCT-US94-14277-8	PCT-US94-14277-4	US-08-943-087-58	US-08-943-087-60	US-08-943-087-52	US-08-943-087-48	US-08-943-087-46	US-08-943-087-44	US-08-943-087-42	US-08-943-087-40
6	Sequence 3, Appli	Sequence 14, Appl	Patent No. 5221789	Sequence 1, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 58, Appl	Sequence 60, Appl	Sequence 52, Appl	Sequence 48, Appl	Sequence 46, Appl	Sequence 44, Appl	Sequence 42, Appl	Sequence 40, Appl

## ALIGNMENTS

```
TOPOLOGY: linear; MOLECULE TYPE: protein US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08328256 Patent No. 5643749 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-POS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

AFTORNEY/AGENT INFORMATION:

NAME: BROWDY, ROGET L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618
                                                                                                                                                                                            TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: AERVEL, Michel
APPLICANT: AERAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTER:
TITLE OF INVENTION: PREPARATION AINUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                             TELEPHONE: 202-628-5197
                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                    Similarity
                                                                                                                                                                                                434 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
Conservative
                  100.0%;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERFERON ALPHA-RECEPTOR, ITS
Score 1072; DB 1;
Pred. No. 4.9e-112;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite
                                     Length
Indels
0
Gaps
```

```
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
  밁
                      Ş
                                                                                                               ; MOLECULE TYPE: US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5919453
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 92400902.0 FILING DATE: 31-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3000 K S
CITY: Washington
                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 30-MA
  27
                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 17
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                         TOPOLOGY:
GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                              436 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLAVEC, Ivan
TOVEY, Michael G.
                                                                                                                                                                                                   (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGUIRE, Deborah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEYER, Francois
                                                                                                                                                                                                                                                                 Bernhard D.
                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                               30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                   05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patrick
                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                               . US/08/307,588
                                                                                                                                                                                                                                                                                                                                          PCT/EP93/00770
                                                                                                                                                                                         2:
                                                  0
                                               Score 1072; DB 2;
Pred. No. 5e-112;
                                                                                                                                                                                                                                         17283/117/GUPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suite 500
                                                  Indels
                                                                          Length
                                                                           436;
                                                  0
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                  0;
             밁
                                   Š
                                                              밁
                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                               27
```

```
; TOPOLOGY: 11; MOLECULE TYPE: US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-328-256-12
                                                                                                                                                Query Match
Best Local Sim
Matches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: U5/08/328,2
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, ECMARIC
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
             61 CNESSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BROWDY, Roger L. REGISTRATION NUMBER: REV REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-
TELEX: 248633
                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                             1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNESSLKLNVYEEIKLRIRAEKENTSSWYEVDSETPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                       GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20004
                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ص
.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVEL, Michel
                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/328,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVEL-13
                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
                                                                                                                                                Score 1072; DB 1;
Pred. No. 6e-112;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                    Indels
                                                                                                                                                                                  Length
                                                                                                                                                                                        496;
                                                                                                                                                  0,
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                         86
                                                                                                                                                    0
```

```
Š
                                                                                               밁
                                                                                                                             ş
                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: 11; MOLECULE TYPE: US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                             밁
                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-328-256-10
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
                                                                                                                                                                                                                            Matches 203;
                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/
FILING DATE: 24 -OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107
FILING DATE: 24 -OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                 FORMATION FOR SEQUENCE CHARACTERISTICS:
FENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: REVEL, Michel APPLICANT: ABRAMOVICH, C APPLICANT: RATOVITSKI, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, EGWAI'd
RITLE OF INVENTION: SOLUBLE INVERFERON ALPHA-RECEPTOR,
FITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 248633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 25
ELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                 147
 181 LTSWKIGVYSPVHCIKTTVENEL 203
                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 419 Seve
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 20004
                                                                                                87
                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BROWDY, ROGER L. REGISTRATION NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                             1-GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                            CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
                                                  SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                              GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JMBER: IL 107378
24-OCT-1993
                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/328,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                         10:
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25,618
                                                                                                                                                                                                                          Score 1072; DB 1;
Pred. No. 7.2e-112;
); Mismatches 0;
                                                                                                                                                                                                                                                        Length 557;
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITS
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                            Gaps
                               206
                                                                                                                                                             86
                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-471-454-2
                                                            Š
                                                                                                В
                                                                                                                             Ş
                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-410
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20-CCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYPNE """"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFILING DATE: 06-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207
 181 LTSWKIGVYSPVHCIKTTVENEL 203
                                                               121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION:
                                                                                                               61 CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 15-JUN-1992 APPLICATION NUMBER: FR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                             1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                              GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFS÷DYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                            203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Application US/08471454 5731169
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                       i: 557 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BYRNE, THOMAS E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRESSER, Ion
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOGENSEN, Knud E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JUTFALLA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 816-4000
                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/471,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32,205
                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                             Score 1072;
Pred. No. 7.
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                                                                                                                                                          7.2e-112;
es 0;
                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                            Length 557;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR THE
                                                                                                                                                                                                                            Gaps
                                    206
                                                                                                  146
                                                                                                                                                                86
```

```
멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                δÃ
                                                                                                                                     Ş
                                                                                                                                                                            밁
                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: 1; MOLECULE TYPE: US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-466-974-2
S
                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                Matches 203;
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION UNMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 07/900,642
APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
APPLICATION NUMBER: FR 89/13770
FILING DATE: THOMAS E.
REGISTRATION UNMBER: 32,205
REGISTRATION UNMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                    147
 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (/ט־/ NIXN UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A
                                                                                                        87
                                                                                                                                           61
                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                             1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                    CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSWKIGVYSPVHCIKTTVENEL 229
LTSWKIGVYSPVHCIKTTVENEL 203
                                                     SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                          GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
                                  SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08466974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703) 816-4000
(703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOGENSEN, Knud E.
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUTFALLA, Georges
                                                                                                                                                                                                                                                                                                                                                                       .inear
                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                              Score 1072; DB 2;
Pred. No. 7.2e-112;
; Mismatches 0;
                                                                                                                                                                                                                                                                             Length 557;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROCESS
                                                                                                                                                                                                                                              <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOR THE
                                                                                                                                                                                                                                              Gaps
                                    206
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                 밁
                                                              Š
                                                                                                    В
                                                                                                                                     δÃ
                                                                                                                                                                          В
                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-471-453-2
                                                                                                                                                                                                                                              Best Local Sir Matches 203;
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200797 NIXN UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION UMBER: US 07/9
ETLING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/
ETLING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-UUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: UZE, Gilles APPLICANT: LUTFALLA, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 LTSWKIGVYSPVHCIKTTVENEL 229
                                  147
                                                                  121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                      87 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                         61 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                           1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO.
LISWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                            GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Application US/08471453 5886153
                                                                                                                                                                                                                                              Similarity 100.
03; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRGINIA
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703)
                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCES PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               816-4000
                                                                                                                                                                                                                                                               100.0%; Score 1072; DB 2; 100.0%; Pred. No. 7.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR 89/13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/900,642
                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version
                                                                                                                                                                                                                                                                               Length 557;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROCESS FOR
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                              Gaps
                                                                                                                                         120
                                                                   180
                                                                                                        146
                                                                                                                                                                            86
```

```
Š
                                                                 밁
                                                                                             á
                                                                                                                                밁
                                                                                                                                                              οy
                                                                                                                                                                                                 밁
                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-307-588-4
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 203; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Applic
Patent No. 5919453
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, BETNHARD D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 17
FELECOMMUNICATION INFORMATION: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C. 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 LTSWKIGVYSPVHCIKTTVENEL
207
                                                                               121 SPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                    87
                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000 K St
CITY: Washington
                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                     1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                               LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
                                                                                                                                CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                               SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08307588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAGUIRE, Deborah
PLAVEC, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEYER, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOVEY, Michael G.
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BENOIT, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bernhard D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JO-MAR-1993
                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4..
                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17283/117/GUPL
                             203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                  Score 1072; DB 2;
Pred. No. 7.2e-112;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                  Length 557;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                    0
```

```
밁
                                                                         밁
                                                                                                            Š
                                                                                                                                                      밁
                                                                                                                                                                                       Š
                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 8666
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aguet, M:
APPLICANT: Bohni, R:
APPLICANT: Hemmi, S:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                           121
                                                                                                                  121
181
                                  181 LTSWKIGVYSPVHCIKTTVENE
                                                                                                                                                                             62 NFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                    61 EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415/225-55: TELEFAX: 415/952-9881
                                                                                                                                                                                                                                <u>بــ</u>
                                                                                                                                                                                                                                                          2 KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKC 61
                                                                                                                SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                ENLKPPENIDXYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDERKWLKXPECQHTTTTKC 60
PSLKKHSNYSTXQCISTTVANK
                                                                         SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
                                                                                                                                                                                                                                                                                                         ch 45.8%; Score 490.5; DB 4
l Similarity 48.5%; Pred. No. 2.4e-47;
98; Conservative 34; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                i: 202 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aguet, Michel
Bohni, Ruth
Hemmi, Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US94/14277
202
                                    202
                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                  202;
                                                                                                                                                                                                                                                                                                             ۲.
                                                                                                                                                                                                                                                                                                           Gaps
```

RESULT 10 US-08-683-743-4

Sequence 4, Application US/08683743 Patent No. 5843697 GENERAL INFORMATION:

APPLICANT:

```
PCT-US94-14277-2; Sequence 2, Application PC/TUS9414277; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                 TITLE OF INVENTION: RENUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 07601
                                                                                                                                                                                                                                                      197 DRNKAGEWSEPVCEQTT 213
                                                                                                                                                                                                                                                                                        182 TSWKIGVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                          137 ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 17-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                 67 KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 POKVEYDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66
                    DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                             KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
                                                                                                                                                                                                                                                                                                                                                                                                 -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                      Bohni, Ruth
Hemmi, Silvio
                                                                                                                          Aguet, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David A. Jackson,
 Genentech, Inc.
O Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serguei
CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.0%;
                                                                     Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/683,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 214; DB 2; I
Pred. No. 4.9e-16;
9; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US94-14277-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local :
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                       Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            -US94-14277-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                               APPLICANT: Aguet, Michel APPLICANT: Bohni, Ruth APPLICANT: Hemmi, Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
                                                                                                                                                                                                                                                                                                                                                                                                 198 KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                 167 SPETTYCLKVKAAL-LISWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                       STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                  TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: (CLASSIFICATION:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94080
94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         South San Francisco
: California
                                                                         94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                       Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Love, Richard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 amino acids
                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.6%;
                                                                                                                                                                                                                Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 199; Db ., pred. No. 2.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
```

12;

밁 Ş 밁 Š 밁 Ş В

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US94-14277-6
                                                                                                                                                                                                                                                                                                                                                                                                     US-08-943-087-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Lok, Si
APPLICANT: Kho, Choon J
                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                      STREET: 1201 E
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                               PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 KPYRVYCLQTERQLILKNKKIRPHGLLSNVSCHETT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
                                                       COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 NITSTKCNESS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LARPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
RRENT APPLICATION DATA:
                                                                                                                       COUNTRY: US
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-98
                                                                                                                                                                    NDDRESSEE: ZymoGeneric, ....
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHONE:
                                                                                                                                                                                                                                                                                                                                                        INFORMATION
                                                                                                                                                                                                                                                                                                                                                                        b, Application US/08943087
5945511
                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415/952-9881
                                                                                                                                                                                                                                                                                            Adams, Robyn L
                                                                                                                                                                                                                                                                                                         Jelmberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                       IBM Compatible
                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.98;
                                                                                                                                                                                                                                                                                                       Anna C.
               US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 192; DB 4; Pred. No. 8.1e-14; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-56
                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-943-087-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                 STREET: 1- CTTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 TYCLKVKA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 LYCVHVES 191
                                                                                                                                                                                          ADDRESSEE: 47
                                                                                                                                      COUNTRY: U
ZIP: 98102
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                               INVENTION:
                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
```

```
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 PGTK------DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LSAETSDYEHQYYAKVKAIWGSKCSKWAESGRFYPFLESQIGPPEVALTSDEKSISVVLS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                           ER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08943087
                                                                                                                                                                                                                                                                                                                                Jelmberg, Anu
Adams, Robyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206-442-6678
                                                                                                                                                                                                                                                                                                                                                                        Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                     Whitmore,
                                                                                                                                                                                              ZymoGenetics, Inc.
01 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                             CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                           Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%;
                                                                                                                                                                                                                                                                                                                                                        Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/803,305
                                                                                                                                                                                                                                                                                                                 Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 172.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..2e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 221;
```

Gaps

5.

PLICATION DATA:

AGENT INFORMATION:

20-FEB-1997

08/803,305

REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627

```
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.1
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-943-087-50
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ent No.
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      ERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 LYCVHVES 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 TYCLKVKA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 APEKWKRNPEDLPVSMQQLYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 PGTK------DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                                                                                                                                                                          STREET: 1201 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                APPLICATION NUMBER:
                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LPKPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFLYGQKKWLNKSECRNINRTYCD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELEFAX: 206-442-6678
                                                                                                                                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                 ESPONDENCE ADDRESS:
                                                                                                                                                                   98102
                                                                                                                                                                                                                                                                                                                                                                                                                                     u, Application US/08943087
5945511
                                                                                                                                                                                                                                                                                                 T: Farrah, Theresa M.
INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                 WA
                                                                                                                                                                                                                                  E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                 Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                  Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                    Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 167.5; DB 2; Length y 26.1%; Pred. No. 4.5e-11; rvative 34; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                     Theodore E.
                                                US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
```

```
밁
                               Š
                                                                       용
                                                                                                   δÃ
                                                                                                                                        밁
                                                                                                                                                                        δÃ
                                                                                                                                                                                                              ᅜ
                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-50
                                                                                                                                                                                                                                                                               Query Match 15.5%;
Best Local Similarity 26.1%;
Matches 49; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
184 LYCVHVES 191
                                                                       128
                                   171 TYCLKVKA 178
                                                                                                     122 PGTK-----DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                                                                                                                                          63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 20-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                            8 LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 67
                                                                                                                                                                                                                                               4 LKSPOKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYOKTGMDNWIKLSGCONITSTKCN 62
                                                                     APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT
                                                                                                                                          LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/803,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50:
                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                    Score 166.5; DB 2; Pred. No. 5.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96-24C1
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                                                                                                                                     Length 221;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                 Gaps
```

Ş

5.

Search completed: June 1, 2000, 04:17:54 Job time: 15448 sec

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 1, 2000, 04:35:09 ; Search time 64.83 Seconds (without alignments)
. 183.585 Million cell updates/sec

Title: Perfect score: Sequence: US-09-240-675-2\_COPY\_27\_229
1072
1 GKNLKSPQKVEVDIIDDNFI.....WKIGVYSPVHCIKTTVENEL 203

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : PIR\_63:\*
1: pir1:
2: pir2:
3: pir3:
4: pir4: pir1: \* pir2: \* pir3: \* pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ъ	4	ω	2	ш	No.	Result	
/ 7	86.5	87	87	-1	87.5	88	89	89	89	89	10	89.5	90	90.5	92	N)	(n	97.5	v	~1	111	144	199	214	216	219	525.5		1072	Score		
					8.2								٠		8.6		٠	٠	9.1	٠	10.4	•	•	•	20.1	•	•	66.0	100.0		Query	æ
295	429	26926	639	6805	575	515	1152	515	331	331	2215	2033	315	1304	477	292	925	7160	6839	6831	489	337	332	325	349	273	590	560	557	Length		
<u>, , , , , , , , , , , , , , , , , , , </u>	N	<b>J</b> +4	N	N	N	N	N	N	N	N	N	N	<b></b>	<b>د</b> سو	N	بر	N	N	N	N	N	N	N	N	N	N	N	N	N	BB		
KFHU3	S59773	I38344	JC1391	S20901	A49667	I39073	S20106	S59502	S59501	A54295	T00348	T09123	S14222	A46546	A34368	KFBO3	T29585	T27935	S57242	T27934	A31555	I38500	A49947	A47003	JC6311	G01418	A45283	S27387	A32694			
									=											٠												
.سو	265	t.	dn	tit	in	in	hy	in	in	inte	LR11	hyl	ch	le	in	11	hy	hy	tw	hy	in	in:	in	су	in	сy	in:	in	in	De		
sue factor pre	pro		dnaK-type molecula	in - rabbit	nterleukin-10 rec	굅		nterferon recepto	nterferon recepto	7	11 protein - mou	brid receptor So	chalcone reductase	common	gan	н	hypothetical prote	1ca	twitchin - Caenorh	hypothetical prote	nterferon gamma r	feron gamma	9	ecept	B	tokine receptor	nterferon alpha/b	nterferon alpha r	nterferon alpha/b	escription	•	

밁

207 LTSWKIGVYSPVHCIKTTVENEL 229

## ALIGNMENTS

RESULT 1 A3294 A3294 A3294 A3294 A3294 CDEETED AND SEQUENCE TEVEL TO BE ASSESSED AND ASSESSED AND ASSESSED ASSE		LTSWKIGVYSPVHCIKTTVENEL 203	181	Qy	
11 1 1 2 0 1 1 9 9 1 1 1 2 0 1 1 1 1 2 0 1 1 1 1 1 1 1 1 1			121 147	g 8	
860 C 48 OF 199			61 87	gg Qy	
ps	86	GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTESFDYQKTGMDNWIKLSGCQNITSTK	1 27	Дy	
Ca 48		100.0%; Score 1072; DB 2; Length 557; Similarity 100.0%; Pred. No. 3e-87; 3; Conservative 0; Mismatches 0; Indels 0;	ry Ma t Loc ches	Que Bes Mat	
human  Jun-1990 #text_change 22-Oct-199  human interferon alpha receptor  piDN:AAA52730.1; piD:g306914  interferon alpha/beta receptor  17>		### JENAR1; IFNAR; IFRC  ###################################	e: GI ss-re posi rons: words 1/Don -455,	A;Gen A;Gen A;Gen C;Key F;1-2	
human  Jun-1990 #text_change 22-Oct-199  human interferon alpha receptor  piDN:AAA52730.1; piD:g306914		terferon alpha/beta	tted cript erencesic ecule idues	submi A; Des A; Ref A; Acc A; Mol	
human Jun-1990 #text_change 22-Oct-199	}	694; MUID:90124632 J03171; NID:9184645; PIDN:AAAS2730.1; PID:	erencesices recule	A; Ref A; Ref A; Rol A; Res	
	199	human Jun-1990 #text_change 2	feror feror cies: essic	RESUL A3269 Inter C;Spe C;Dat C;Acc R;Uze Cell	

```
Interferon alpha receptor type 1 precursor - bovine C:Species: Bos primigenius taurus (cattle) (C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C:Accession: S27387; S3770 R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G. FEBS Lett. 313, 255-259, 1992 A:Title: Specific antiviral activities of the human alpha interferons are de A:Reference number: S27387; MUID:93076908
                                                                                                                                                                                                     interferon alpha/beta receptor - mouse

;Species: Mus musculus (house mouse)

C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429

R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.

Proc. Natl. Acad. Sci. U.S.A. 89, 474-4478, 192;

A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in A;Reference number: A45283; MUID:92262522

A;Reference number: A45283; MUID:92262522

A;Status: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha
A;Reference number: S33770; MUID:93305725
A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: lung
C;Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status predicted
Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta
A;Reference number: 148423; MUID:95047447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-421,'V',423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187;
                                                                               A; Note: sequence extracted R; Lutfalla, G.; Uze, G.
                                                                                                     A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; A;Note: sequence extracted from NCBI backbone (NCBIN:102354,
                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-590 <UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X68443; | A; Experimental source: MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 LLTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NLKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSSLKL-NVYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRLQSRVGCYSPVYCINTTERHKV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPPGTKDSIMWAMDRSSFRYSVVIWKNSSSLEERTETVYPEDKIYKLSPEITYCLKVKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-PGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSSVELENVFEKIELRIRAEEGNNTSTWYEVEPFVPFLEAQIGPPDVHLEAEDKAIILSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLK-PENVEIHIIDDNFFLKWNSSSESVKNVTFSADYQILGTDNWKKLSGCQHITSTKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 708; DB 2; 1
Pred. No. 5.1e-55;
8; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAA02571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                          receptor-encoding gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID: 9432
                                                                                                       PID: 9194112
NCBIP: 102357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۸
                             high-free
                                                                                                                                                                                                                                                                                  homospe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at
```

```
A; Accession: I48423
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 118-125 <
                                                                                                                                                                           RESULT
G01418
                                                                                            cytokine receptor family II, member 4 - human c;Specles: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision O6-Jun-C;Accession: G01418
submitted to the EMBL Data Library, R:Reference number: G06935 A:Accession: G01418 A:Status: preliminary; translated fi
                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                    δÔ
                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 426-445 <RE6>
A; Cross-references: EMBL:
A; Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: I48426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 265-375 <RE4>
                                                                                R; Lutfalla, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 177/3; 331/1
C; Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 473-590 <RE7>
A;Cross-references: EMBL:U06244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 397-424 < RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I48427
A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 127-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL:U06240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DN
A; Residues: 243-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated
                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKNIKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                            LLTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                             CEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAEDKAILVH
                                                                                                                                                                                                                                                                                                                                                                                                                                 CNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDEAKWLKVPECQHTTTTK 85
                                                                                                                                                                                                                                                      HPSLKKHSNYSTVQCISTTVANKM
                                                                                                                                                                                                                                                                                                                                  ISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEVKAI 205
                                                                                                                                                                                                                                                                                                                                                                  ISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 51.(
104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177/3; 331/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: U06242; NID: g497112; PIDN: AAA65007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: U06237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g497108; PIDN:AAA65005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID: g497114; PIDN: AAA65008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID: g497103;
    from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 525.5; DB 2
Pred. No. 7.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from
                                                                                                                                                                                                                                                      229
                                                          April 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
  GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB/EMBL/DDBJ
                                                                                                                  06-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN: AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                    #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g510265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g755812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g510262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:9755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:g755810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g755813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲.
```

```
interferon receptor-class II cytokine receptor - mouse C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 *sequence_revision 16-Jul-1999 *tey
C;Accession: JC6311
R;Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A;Title: CRF2-4:isolation of cDNA clones encoding the PA;Reference number: JC6311
A;Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:CRFB4; CRF2-4
A;Cross-references: GDB:138168; OMIM:123889
A;Map Position: 21922.-2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             吊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-273 <LUT>
                                  RESULT
A47003
                                                                                                                                               Ş
                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                      맗
                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U08988; NID:g571295;
cytokine receptor family class II C; Species: Homo sapiens (man)
                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:U53696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-349 <GIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
                                                                                                                  190
                                                                                                                                                                                       135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 TSWKIGVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                  55
                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH-ISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS- 79
                                                                                                              QVQGFLLDQNRTGEWSEPICERT
                                                                                                                                                                                                                                                                                      SLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRNKAGEWSEPVCEQTT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LSKYGDHTLRVRAEFADEHSDWVNI-TFCFYDDTIIGPPGMQVEVLDDSLHMRFLAPKI 136
                                                                                                                                                  KVKAALLTSWKIGVYSPVHCIKT 197
                                                                                                                                                                                     QIENEPET----WILKNIYDSWAYRVQYWKNGTNEKFQVVSPYDSEVLRNLEPWTTYCI
                                                                                                                                                                                                                        -----PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCL 174
                                                                                                                                                                                                                                                                 --HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPEMQIESLAESLELRFSAP
                                                                                                                                                                                                                                                                                                                                      PEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH-----CKRTASTQCDFS
                                                                                                                                                                                                                                                                                                                                                                           PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
                                                                                                                                                                                                                                                                                                                                                                                                              20.1%; Score 216; DB 2; ilarity 28.6%; Pred. No. 1e-11; Conservative 43; Mismatches 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA clones encoding the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 219; DB 2; 1
Pred. No. 3.9e-12;
1; Mismatches 84;
                                                                                                                212
                   protein CRF2-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g571296
                     precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                  76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
```

```
C;Date: 09-Sep-1994 #Sequence_rections
C;Accession: A47003
R;Lutfalla, G; Gardiner, K; Uze, G.
R;Lutfalla, G; Gardiner K; Uze, G.
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family
A;Reference number: A47003; MUID:93300510
A;Accession: A47003
                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-332 <HEM>
A;Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; PID:9545842
A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
C;Keywords: cytokine receptor
                                   Š
                                                                                 멁
                                                                                                                 δÃ
                                                                                                                                                             밁
                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A novel member of the interferon receptor family complements functionality A;Reference number: A49947; MUID:94170381 A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Hemmi, S.; BOILLI, S.;
Cell 76, 803-810, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon gamma receptor beta subunit - mouse
N;Alternate names: ITN-gamma R beta chain; IFN-gamma R species-s
C;Species: Mus musculius (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ႘
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 21q
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
A;Cross-references: GB:Z17227; NID:g393378; PID:g393379
    몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
  143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 DRNKAGEWSEPVCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 TSWKIGVYSPVHCIKTT 198
                                                                                                      29 LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 KLNYYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 PQKYEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66
                                                                                                                                                                                                     4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S.; Bohni, R.; Stark, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
                                       LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
    VTPGKGSLVIHFSPPFD--
                                                                                 DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 142
                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
                                                                                                                                                                                                                                                              h 18.6%;
Similarity 30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%;
Similarity 30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                               Conservative
-VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                           38; Mismatches
                                                                                                                                                                                                                                                                Score 199; DB 2
Pred. No. 3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 214; DB 2;
Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Di Marco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-Sep-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFN-gamma R species-specific cofactor; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>'</u>
                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aguet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 325;
                                                                                                                                                                                                                                                                                       Length 332,
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196
      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
```

```
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S. Cell 76, 793-802, 1994
A;Tittle: Identification and sequence of an accessory factor required for activation of t A;Reference number: A49946; MUID:94170380
A;Recession: I38500
A;Molecule type; mRNA
A;Residues: 1-337 <RES>
A;Cross-references: EMBL:U05875; NID:9463549; PIDN:AAA16955.1; PID:9463550
A;Experimental source: clone pSK1
A;Accession: I38501
A;Molecule type; mRNA
A;Residues: 1-63,'0','65-337 <RE2>
A;Cross-references: EMBL:U05877; NID:9463551; PIDN:AAA16956.1; PID:9463552
A;Cross-references: EMBL:U05877; NID:9463551; PIDN:AAA16956.1; PID:9463552
A;Experimental source: clone pJS3
C;Genetics: 21
C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interferon gamma receptor accessory factor-1 precursor - human C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
C:Accession: I38500; I38501
R:Soh_J.; Donnelly, R.J.; Kotenko, S.: Mariano Ture Control To
A;Gene: GDB:IFNGR1; IFNGR
A;Cross references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembran
                                                                                                                                                                                                                                            interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Fe
C;Accession: A31555
R;Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280; 1988
                                                                                                                                                                                    A;Title: Molecular cloning and expression A;Reference number: A31555; MUID:89003065 A;Accession: A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                  A;Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915
C;Genetics:
                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-489 <AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 GPPE-NIEVTPGEGSLIIRFSSPEDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                             194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 GPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 NCTQITATECDFTAASPSAGFPMDFNV----TLRLRAELGALHSAWVIMPWFQHYRNVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEKENT-SSWYEVDSFTPFRKAQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFKYTDSK-----WFTADIMSIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYQKTGMDNWIKLS-----
                                                                                                                                                                                                                                                                                                                                                                                                 φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
  cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.48; 24.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 144; DB 2;
Pred. No. 2.3e-05;
9; Mismatches 86;
                                                                                                                                                                                                                                                                                                               28-Feb-1990
                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198
                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                             #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 46;
                                                                                                                                                                                                                             interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                             receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Emanuel, S
                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                             밁
                                                                                                                                                               밁
                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                   멍
                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status:
                                                                                 1963
                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
```

```
hypothetical protein ZK617.la - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T27934; T28030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-6831 <WT2>
A;Cross-references: EMBL:273899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
A;Experimental source: clone ZK829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-6831 <WIL>
A;Cross-references: EMBL:273897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
A;Experimental source: clone ZK617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1996
A;Reference number: Z20442
A;Accession: T27934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
A; Introns: 10/3; 61/3;
144/3; 6683/3; 6768/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A; Reference number: 220458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: ZK617.la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T28030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.1%;
Best Local Similarity 22.8%;
                                                                                                                                                                                                                                                                                                                    1856 LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDDGGEPIEYYEVEKLDTATGRWVP---CAKV 1912
                                                                                                                                                                                                           1913 KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT------ 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 QCQLAIPVSSLNSQYCVSAEGVL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 YSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 DIFHPSVFVNGDEQEVDYDPETTCY;RVYNVYVRMNGSEIQYKILTQK-----EDDCDEI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 HI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 NISDHVGDPSNSLWVRVKARVGQKE--SAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 NFSSLKLNVYEEIKLRIRA---EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI 118
                                                                                                                                                                                                                                                                                                                                                                     4 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NLKSPOKVEVDIIDDNFILRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKC 61
VIEKKGKHGRDWQ
                                                 CLKVKAALLTSWK 185
                                                                                                                                                                                                                                                          TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVPTPTNVTIESYNMNPIVYWEY--QIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYC 85
                                                                                                                                                    IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY 172
                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                     -GTPDVVDWDADRVS--
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3 6800/3
  2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.4%; Score 111; DB 2; Length 489 22.2%; Pred. No. 0.031; tive 41; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SPGTK-----DSVMWALDGLSFTYSLLIWKNSSGVEERIENI 157
                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97.5; Di
Pred. No. 15;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                     -LEWEPPKSDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             мау 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                          74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6831;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                     APITOY 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
```

```
A:Map position: IV
A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60
152/3; 6691/3; 6776/1; 6808/3
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
C:Superfamily: twitchin; fibronectin duplication; muscle; phosphotransferase; serine/th;
P:806-980,899-990,991-1083,1084-1175,1178-1273,1474-1567,1770-1864,2065-2158,2358-2450,2
96-5790,6263-6356,6386-6478,6541-6635,6649-6742,6745-6838/Region: mottif
P:1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2451-3
23,4215-4313,4314-4415,4416-4516,4612-4710,4711-4811,4908-5009,5010-5109,5110-5210,5399-F;5940-6197/Domain: protein kinase homology <KIN>
P:5940-6197/Domain: protein kinase ATP-binding mottif
F:5971/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 C;Accession: S57242; S07571; S06797; S57218 R;Benian, G.M.: L'Hernault, S.W.: Morris, M.E. submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Benian, G. submitted to the EMBL Data Library, November a;Reference number: S07571
                                                      ş
                                                                                                                밁
                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Experimental source: var. Bristol
C;Comment: Lack of unc-22 leads to a constant twitching of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,'I'
A; Cross-references: EMBL:X15423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Sequence of an unusually large protein A; Reference number: S06797; MUID: 90044042 A; Accession: S06797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: var. Bristol R; Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Nature 342, 45-50, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-6839 <BEN1>
A;Cross-references: EMBL:L10351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: myosin-regulating N;Contains: protein kinase (EC 2.7.1. C;Species: Caenorhabditis elegans
      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Additional sequence complexity in the muscle gene, unc-22, A;Reference number: S57218; MUID:93387664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics 134, 1097-1104, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: var. Bristol R; Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: unc-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     twitchin - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Experimental source: var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
Residues: 792-6839 <BEN2>
Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reference number: Accession: S07571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type:
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: S57242
      1921
                                                                                                                   1864
                                                         57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        片
                                                                                                                                                                      LKSPOK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYOK--TGMDNWIKLSGCQNI 56
                                                         TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                                   LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV: 1920
KDTKAHIDGLKKG---QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT---
                                                                                                                                                                                                                                   44:
                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Additional sequence complexity within mber: S57242
                                                                                                                                                                                                                                                           9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bristol
                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                             Score 97.5; Di
Pred. No. 15;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moerman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      twitching of the
                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               implicated in regulation of myosin
                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               twitching of
                                                                                                                                                                                                                                                                                      Length 6839;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         body muscles
                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded
                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prot
```

C;Accession: T29585
R;Gattung, S.; Scheet, P.; Kemp, K.
submitted to the EMBL Data Library, November
A;Description: The sequence of C. elegans cos
A;Reference number: Z20647
A;Accession: T29585
A;Status: preliminary; translated from GB/EMB

cosmid F55F8

GB/EMBL/DDBJ

hypothetical protein F55F8.3 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #t

15-Oct-1999 #text\_change 15-Oct-1999

```
hypothetical protein ZK617.1b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T27935; T28031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                  Š
                                                                                                             Ş
                                                                                                                                                      밁
                                                                                                                                                                                        Ş
                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-7160 <WI2>
A;Cross-references: EMBL:Z73899; P.
A;Experimental source: clone ZK829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: T28031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A; Reference number: Z20442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
밁
                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 4
A; Introns: 10/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 10/3; 61/3; 1
3067/1; 3141/3; 3269/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-7160 <WIL>
A;Cross-references: EMBL:Z73897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: ZK617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T27935
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1971
2323
                                                                             2292
                                                                                                                                                                                                                                   2185 LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP---CAKV 2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002 VIEKKGKHGRDWQ 2014
                                                                                                                                                        2242 KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT------
                                                                                                               116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CLKVKAALLTSWK 185
                                    173 CLKVKAALLTSWK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                            57 TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                   4 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 56
VIEKKGKHGRDWO
                                                                           -----GTPDVVDWDADRVS-----LEWEPPKSDGG
                                                                                                               IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GTPDVVDWDADRVS----LEWEPPKSDGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 6473/3; 7012/3; 7097/1; 7129/3
2335
                                                                                                                                                                                                                                                                                                                              9.1%;
                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                          Score 97.5; D
Pred. No. 15;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Мау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996
                                                                                                                                                                                                                                                                                                                                                   BG
                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                 Length 7160
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -APITQY 2001
                                                                                                                                                                                                                                                                                                                                                                                                                              508/3;
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                        2292
                                                                                                                                                                                                                                                                                                                                                                                                                              542/3; 574,
                                                                                                                                                                                                                                                                                                              10;
```

밁

187

WKASSTGKKKATTN--TNGFLIDYDKGENYCFHVQAVIL-SRRVNQKSPESPIKCT

```
A; Molecule type: DNA
A; Residues: 1-925 <GAT>
A; Cross-references: EMBL: U80447; PIDN: AAB37807.1; GSPDB: GN00019; CESP: F55F8.3
A; Experimental source: Strain Bristol N2; clone F55F8
C; Genetics:
A; Gene: CESP: F55F8.3
A; Map position: 1
A; Introns: 6/3: 44/2; 76/1: 109/2; 159/2; 204/3; 327/1; 469/3; 617/1; 775/1; {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S74147; NID:g241438; PIDN:AAB20755.1; PID:g241439
A;Experimental source: adrenal gland
A;Note: part of this sequence, including the amino end of the mature proto:C;Comment: Tissue factor is an integral membrane glycoprotein that serves C;Comment: Expression of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be induced in a variation of tissue factor can be in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: coagulation factor III
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 22-Jun-1999
C;Accession: JQ1319
R;Takayenoki, Y:; Muta, T.; Miyata, T.; Iwanaga, S.
Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
A;Title: cDNA and amino acid sequences of bovine tissue factor.
A;Reference number: JQ1319; MUID:92109720
A;Accession: JQ1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;249-271/Domain: transmembrane #status predicted <TMM>
F;272-292/Domain: intracellular #status predicted <INT>
F;272-292/Domain: intracellular #status predicted <INT>
F;472-292/Domain: intracellular #status predicted f;81-89,215-238/Disulfide bonds: #status predicted
F;118.124/Binding site: carbohydrate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane F;1-35/Domain: signal sequence #status predicted <SIG>F;36-292/Product: tissue factor #status experimental <MAT>F;36-248/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                         Ş
                                                                                                                       밁
                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-292 <TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: part of this sequence, including the amino end of the mature protein, was confined to comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor Comment: Expression of tissue factor can be induced in a variety of tissues by certain Superfamily: tissue factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
132 YLETNLGQPTIQSFEQVGTKLNVTVQDARTLVR----ANSAFLSLRDVFGKDLNYTLYY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                 44 MDNWIKLSGCONITSTKCNFS-SLKLNYYEEIKLRIRAEKENTSS------WYEVDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 MDNWIKLSGCQNIT -- STKCNFS9LKLNVYEEI -- KLRIRAEKENTSSWYEVDSFTPFRK 99
                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQIGPPEVHLEAEDKAIVIHI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHEFGKSIENKVYNPFSLSRTYKLSSDS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IWKNSSGVEERIENIYSRHKIYKLSPET 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSISPSGYHLLASDERGVVHFVHLLSEFKIYTFRSNKPIGSLQWSPDATRVAICRENDLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDTNFKLSNCIGTVYRDGQVAFSKDGYSVISPIGNKLSIFDLRNNTSKTLDIDCNYNIKR
                                                                                                                                                                                                 FRKAQIGPP----
                                                                                                                                                                                                                                                                                    LGNW--KNKCFYTTNTECDVTDEIVKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-292 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          palmitate (Cys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.98;
                                                                                                                                                                                                     EVHLEAEDKAIVIHISPGTKDSVMWALD---GLSFTYSLLI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 95.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92.5; DB Pred No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SPGTKDSVMWALDGLSFTY----SLL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70;
                                                                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                                                                                                                                              96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  825/3; 865,
                                                                                                                                                                                                                                                                                                                                                                                                                                            9
```

Š

POKVEYDIIDDNFILRWNRSDESYGNYTFSFDYQ-KTGMDNWIKLSGCQNITSTKCNFSS 65

33;

, 0

Indels

38;

Gaps

12;

```
R;Cofano, F.; MULLE, J... 1990
J. Biol. Chem. 265, 4064-4071, 1990
A;Title: Affinity purification, peptide analysis,
A;Title: Affinity purification, peptide analysis,
A;Title: Affinity purification, peptide analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change
C;Accession: A34368; A3468; A34423; A34508; A36224; I48941
R;Kumar, C.S.; Muthukumaran, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.
J, Biol. Chem. 264, 17939-17946, 1989
A;Title: Molecular characterization of the murine interferon gam
A;Reference number: A34368; MUID:90036866
A;Accession: A34368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-94, E',96-477 <GRA>
A;Residues: 1-94, E',96-477 <GRA>
A;Cross-references: GB:M26711; NID:g194126; PIDN:AAA37896.1; PI
R;Hemm1, S.; Peghini, P.; Metzler, M.; Merlin, G.; Dembic, Z.;
Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989
A;Title: Cloning of murine interferon gamma receptor cDNA: expr
A;Reference number: A34508; MUID:9009370
A;Accession: A34508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J05265; NID:g197964; PIDN:AAA39178.1; R;Gray, P.W.; Leong, S.; Fennie, E.H.; Farrar, M.A.; Pingel, Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989
A;Title: Cloning and expression of the CDNA for the murine in A;Reference number: A34423; MUID:90046824
A;Accession: A34423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Restidues: 1-94,'E,'96-477 <HEM>
A;Cross-references: GB:M28233; NID:g194131; PIDN:/
R;MUNTO, S.; Maniatis, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M25764; NID:g197962; PIDN:AAA39177.1; PID:g309393 R;Cofano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Appella, J. Biol. Chem. 265, 4064-4071, 1990
                                                                                                                                          C; Superfami
C; Keywords:
                                                                                                                                                                                                                                                                                                             A;Title: Characterization of the 5' flanking region A;Reference number: I48941; MUID:95197006 A;Accession: I48941
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M28995; NID:g194123; PIDN:AAA37895.1; PID:g309329 R;Raval, P.; Obici, S.; Russell, S.W.; Murphy, W.J. Gene 154, 219-223, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Expression cloning of the murine interferon gamma A;Reference number: A36224; MUID:90083245 A;Accession: A36224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-477 <COF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-477 < KU
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-28 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 10-477 < MUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                 A; Status: translation not shown; translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status:
                                                                                                                                                                                                A;Cross-references: EMBL:U05960; NID:g454092; PIDN:AAA80980 1;
                                                                                                                                                                     Superfamily: interferon gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary
                                                                                                                                          cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -477 <KUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor precursor - mouse
                        8.6%;
Score 92; DB
Pred. No. 1.4;
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAA37898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                            and
                                                         Length 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA sequence of the mouse
                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y.H.; Mariano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g309330
.; Aguet, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g309394
J.T.; Ferna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g309331
                                                                                                                                                                                                                                                                                                                                                                            encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aguet,
                                                                                                                                                                                                   PID:g454093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fernandez-Luna,
                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ħ
                                                                                                                                                                                                                                                                                                                                                                               mouse inte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900
                                                                                                                                                                                                                                                                                                                  Pred.
score
and is
 J. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
 SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-240-675-2_COPY_27_229
1072
1 GKNLKSPQKVEVDIIDDNFT
                                                                                                                                                                                                                                                                                                                                                                                                                            83857 segs, 30454973 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKNLKSPQKVEVDIIDDNFI.....WKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
                                                                                                                                                                                                                                                                           Length
 2000, 04:38:50 ; Search time 34.71 Seconds (without alignments) 178.115 Million cell updates/sec
                                                                                                                                                                                                                                                                             멂
INR1_SHEEP
INR1_MOUSE
CRF4_HUMAN
INGS_HUMAN
INGS_HUMAN
INGS_HUMAN
PWP2_CAEEL
TF_BOVIN
INGR_MOUSE
CD45_HUMAN
6DC5_SOYBN
INR2_BOVIN
INR2_HUMAN
INR2_HUMAN
INR2_HUMAN
INR2_WEARI
INR2_SHEEP
YCFO_MARPO
ILSS_MOUSE
TF_RABIT
INR2_SHEEP
YCFO_MARPO
ILSS_MOUSE
TF_RABIT
INR2_SHEEP
TF_RABIT
INR2_SHEEP
TF_RABIT
INR2_SHEEP
TF_RABIT
INR2_SHEEP
TF_RABIT
INR2_SHEEP
TF_RABIT
INR3_NOUSE
CYRB_MOUSE
CYRB_MOUSE
CYRB_MOUSE
CYRB_HUMAN
YCO6_SPVKA
YCF0_SPIOL
MTC3_CHYNI
HEMO_RABIT
HEMO_RABIT
                                                                                                                                                                                                                                                                                                                                                                summaries
                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                              83857
                                                                                                                                                                                                     P17181
Q04790
Q28589
P33896
Q08334
P38484
P15260
P915341
                                                                                                                                                                                                                                                                           Description
                                                                                                        4 homo sapien
4 homo sapien
6 homo sapien
6 homo sapien
7 mus musculu
8 paracentrot
8 homo sapien
7 mus musculu
8 paracentrot
8 homo sapien
9 homo sapien
9 waricella-z
5 saccharomyc
                                                                                                                                                                                                                                   ovis aries
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
```

388888888888888888888888888888888888888	CCCCCRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	RN RT RA	ROOOG DD DAA	RES	
MIN PRINTERS	MO PHO PHO	SEQUENCE OF THE SEQUENCE OF TH	O1- O1- INT INT EUX EUX (1)	NULT 1	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
EVEN ON THE EVEN ON THE EVEN ON THE SIMILARITY: SIMILA	FIED SIC PART 19EE	SEQUENCE FROM MEDLINE; 90124 Uze G., Lutfal "Genetic trans into mouse cel. cell 60:225-23 [2] SEQUENCE FROM MEDLINE; 92129 Lutfalla G., G. "The structure J. Biol. Chem.		1 AN LHUMAN	77 76 75.5 75.5 75.5 75.7 75 75 75 75 75 75 75 75
ON THE SURF PHOSPHORYLA ARITY: BELO ARITY: BELO CARTY: BELO SS-PROT entr the Swiss I cean Bioinfo non-profit and this st requires a in email to 171; AAA527 9459; CAA429 9459; CAA429 9459; A3264 112; SI7112.	WIION BY 5059042. 70. Yan 70. Witt oding to a inter Biol. 14 NN: RECER TRIGGER NG JAKS, STHEMSE JULAR LOC	N.A. 4632. 111a G 115s: 111s: 134(19 34(19 376. 3376. 3376. 3376.	(Rel. (Rel. (Rel. LPHA/B LPHA/B ULPHA/B (Huma (Huma etazoa Imates	STA	67777777 6.000000++2
SURFACE OF MOS SURFACE OF MOS CONTAIRD ON TYP CONTAIRS 70 FIFE BELONGS TO THE BELONGS Institute of the contained for the	TYK2.  H., Do te M., and ty rieron 4:8133. PTOR FC S TYROS S TYROS CATION:	, Greff af faf lonin 0) er K he hu	15, Cre 15, Las 39, Las 39, Las Con D) Chord Catar	TANDARD;	504 3898 695 1447 254 376 998 1450 1997
TO ON THE STATE OF	Domans , Kris tyrosi tyrosi n rece s-enece FOR IN COSINE COSINE S. N: TYP	Ö 2 2	EPI		4444444444
) H O K	Comanski P., Handa F. Krishnan K., Krole Tyrosine phosphoryle Treceptor by pl35ty 8142(1994). TOR INTERFERONS ALPH SINE PHOSPHORYLATIC TYPE I MEMBRANE F	I.; ional d expr d expr oudhon interf (1992)	d) equence unnotation OR ALPHA ( ); Craniation	ALIC	Y241_MYCGE MYOC_HUMAN POLG_HCVA FSHR_SHEEP DCC_HUMAN HAC_BT4 EPB3_HUMAN MPSF_CHUMAN MPSF_CHUMAN MPSF_CHUMAN ENDB_ECOLI
IFN RESIDUES ONECTIN TYPE I SINE RESIDUES ONECTIN TYPE I CLASS II CYTON CLASS II CAN CLASS II CA	Handa (., Kro )sphory )y p135 (ONS AL IORYLATIONS A	uman i ssion D., Vi	epde	IGNMENTS	MYCGE HUMAN HCVA SHEEP JUMAN HUMAN HUMAN CHICK HUMAN
STANT CELL STANT CELL STANT CELL CYTOKINE CYTOKINE IS produce matics a There are dy as its Usag ee http:/	la R., Sm clewski Tylatuski 195tyk2 ty 15tyk2 ty 15tyk2 ty 15tyk2 ty 15tyk2 ty 15tyk2 ty 15tyk2 ty 15tyk2 ty	interfe of its ielh E.	e) N I	AA.	
CELLS. Y TYK2 IN THE INE FAMI and the sare no ists con ists con ists con ists con in the ince	malley D J.; of the of the yrosine D BETA. A NUMBE A R ALPHA	cDNA cDNA , Uze	URSOR		
	ZOZ DO	lpha r	(IFN-		P4748; Q99977 P35371; P43140; P01905 P1805; P5475; P52346; P5346;
L S S S S S S S S S S S S S S S S S S S	S es S	ecep	ALPHA		0.4000000000
Ch Collin	n in o	e.",	A-REC		ycoj omo omo omo omo alli sch
mme on no	1t TYPE		č.		lasm hole arie sapi sapi sapi
ation in its way rcial					ma ien era es es ien ien ien ien ien ien ien ien iien i

P0155690 P266690 P061727 P1356990 P061727 P1357248 P1252248 P125224 P1

marchantia ovis aries

mus musculu oryctolagus human rotav

4 saccharomyc
4 mus musculu
4 mus musculu
5 mus musculu
5 mus musculu
6 swinepox vi
6 syinecia vi
3 spinacia vi
5 chlorella v
8 oryctolagus

```
RESULPT INRLIED IN INR
                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 203
                                                                                                                                                     SSULT 2

INR1_BOVIN STANDARD; PRT; 560 A

O04790;
01-OCT-1993 (Rel. 27, Created)
01-FEB-1994 (Rel. 28, Last sequence update
01-NOV-1997 (Rel. 35, Last annotation upda
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN
INTERFERON (FINAR.
BOS taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
TISSUE-LUNG:
MEDLINE; 93076908.
MEDLINE; 93076908.
MOUCHEI-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
MOUCHEI-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
"Specific antiviral activities of the human alpha interferons
determined at the level of receptor (IFNAR) structure.";
FEBS Lett. 313:255-259(1992).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation
                                                                                                                                             Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                     LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                     LTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
458
79
199
466
481
50
50
50
110
110
311
311
311
311
416
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436
457
557
2200
466
481
481
481
481
81
81
1100
1172
254
416
416
416
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
63525
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ດ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВY
                                                                                                                                                                                                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId-VAR_002717.
G -> A (IN REF. 2).
0F6744CBA1ADBE73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1072; DB 1;
Pred. No. 1.1e-88;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERFERON-ALPHA/BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                         560
                                                                                                                                                             Pecora;
                                                                                                                                                                            Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY
(BY
                                                                                                                                                           Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROBABLE)
                                                                                                                                                             Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
    RESULT 3
INR1_SHEEP
ID INR1_S
AC Q28589
                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                          Š
                                                                                                                                                             밁
                                                                                                                                                                                        Qy
                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                    δÃ
   INR1_SHEEP
Q28589; Q95206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM;
                                                                                                   206
                                                                                                                                 180
                                                                                                                                                                                             121
                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                         ω
```

Š

STANDARD;

560

δÃ B δÃ 밁 Š

```
Query Match
Best Local S
Matches 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim J.-K., Langer J.A.;

"Cloning and characterization of a bovine alpha interferon receptor.";

Biochim. Biophys. Acta 1173:314-319(1993).

-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X68443; CAA48484.1; -. EMBL; L06320; AAA02571.1; -. PIR; S33770; S33770. PIR; S27387; S27387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 93305725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNITS THEMSELVES.
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                              FSSLKL-NYYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                              NLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN
LRLQSRVGCYSPVYCINTTERHKV
                                        LLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                     FSSVELENVFEKIELRIRAEEGNNTSTWYEVEPFVPFLEAQIGPPDVHLEAEDKAIILSI
                                                                                                                                                                                                                                                      NLK-PENVEIHIIDDNFFLKWNSSSESVKNVTFSADYQILGTDNWKKLSGCQHITSTKCN
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Transmembrane;
1 24
25 560
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437
458
844
220
220
55
55
109
172
172
173
133
377
                                                                                                                                                                                                                                                                                                                                                             66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      63818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                        Score 708; DB
Pred. No. 4.6e
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERFERON-ALPHA/BETA RECEPTOR
  229
                                        203
                                                                                                                                                                                                                                                                                                                                                                 DB 1;
.6e-56;
                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                       145
                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                               4.
```

```
01-NOV-1997 (Rel. 35, C
01-NOV-1997 (Rel. 35, L
15-FEB-2000 (Rel. 39, L
INTERFERON-ALPHA/BETA F
                                                                                                                                                                                                                                                                                                                                                                                                                          ribonucleic acid for ovine receptors during the estious cycle understancy.";
Endocrinology 138:4757-4767(1997).
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROINCLUDING JAKS, TYX2, STAT PROTEINS AND IFN-R ALPHA-AND BET
    CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
                                                                          CARBOHYD
CARBOHYD
                                                                                                                                              DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                          entitles
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.; "Molecular cloning of ovine and bovine type I interferon receptor subunits from uter; and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of an ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INTERFERON ALPHA/BETA IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                              modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 98006426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97135690.
                                                                CARBOHYD
                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                     SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINE
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINE
CONCEPTUS AT DAY 15 OF PREGNANCY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOM
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY
                                                                                                                                                                                                                                                    PF00041; fn3; 1.
                                                                                                                                                                                                                                                           X95939; CAA65183.1;
U65978; AAB84231.1;
                                                                                                                                                                                                                                                                                         non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cetartiodactyla;
                                                                                                                                                                                                                                         Transmembrane;
                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17:207-215(1996).
     63918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaluzova M. Sheldrick E.L., Flint A.P.F.; interferon receptor and its expression in
                                                                                                                                                                                                                              Glycoprotein; Signal.
. BY SIMILARITY.
     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruminantia; Pecora; Bovoidea; Bovidae;
            POTENTIAL.
S -> G (IN
A -> D (IN
                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                            POTENTIAL.
POTENTIAL.
                                                                                                                                            CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                             BY SIMILARITY.
INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                            POTENTIAL.
                                                     POTENTIAL
                                                                                                                          POTENTIAL
                                                                                                                                      POTENTIAL
G (IN REF. 2).
D (IN REF. 2).
198A1905D4805C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       EXAMINED
                                                                                                                                                                                                                                                                                                                                                                                   DOMAINS
                                                                                                                                                                                                                                                                                                                                                                        OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                       EXCEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS
BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         o.
     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
```

```
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _MOUSE
CARBOHYD
CARBOHYD
                                DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2090 (Rel. 39, Last annotation updat
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN
IFNARI OR IFNAR OR IFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in homospecific or heterospecific background.";
Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
-:- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING
-:- IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PRO
INCLUDING JAKS, TYXZ, STAT PROTEINS AND IFN-R ALPHA-AND BET
SUBUNITS THEMSELVES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P33896;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uze G., Lutfalla G., Bandu M.T., Proudhon D., "Behavior of a cloned murine interferon alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                      PIR; A45283; A45283.
MGD; MGI:107658; IFNAR
                                                                                                                                                                                                                                       EMBL; M89641; AAA37890.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN
                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss institute of Bioinformatics and the EMBL outst
European Bloinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSSLKL-NYYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRLQSRVGCYSPVYCINTTERHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLKS-ENVEIHIIDDNFFLKWNSSSESVRNVTFSADYQILGTDNWKKLPGCQHITSSKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSSVELKDVFEKIELRIRAEEGNNTSTWYEVEPFVPFLKAQIGPPDVHLEAEDKAIILSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                    Transmembrane;
1 26
27 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
27
430
450
78
199
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
429
449
590
220
220
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Ve. Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.68;
                                                                                                                                                                        Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                              EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                      CHAIN.
                                                                                                                                                    INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1693; DB 1;
No. 1e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590
                                                                                                                                                                                     Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ያ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X.E.;
                                                                                                                                                                                                                                                                                                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS
BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQ
멇
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 49.0
Best Local Similarity 51.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 3
01-FEB-1995 (Rel. 3
01-OCT-1996 (Rel. 3
CYTOKINE RECEPTOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                        Fundo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRF4_HUMAN
Q08334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
EMBL; 217227; CAA78933.1; -.
EMBL; U08998; AAA86872.1; -.
PIR; A47003; A47003.
HSSP; P13726; 1DAN.
                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                               J. MOI. EVOI. 41:338-344(1995).
-!- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 96054036.
Lutfalla G., McInnis M.G.,
                                                                                                                                                                                                                                                                                                              rutfalla G., Gardiner K., Uze G.;
"A new member of the cytokine receptor
21 at less than 35 kb from IFNAR.";
Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 93300510.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                              or send an
                                                                            entities requires a
                                                                                                                                                                                                                                   neighbor
                                                                                                                                                                                                                                               Structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 HPSLKKHSNYSTVQCISTTVANKM 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 CEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAEDKAILVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTSWKIGVYSPVHCIKTTVENEL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEVKAI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDEAKWLKVPECQHTTTTK
                                                             equires a license agreement (See http://www.isb-sib.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214
314
370
409
413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
314
370
409
413
65776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31, Created)
31, Last sequence update)
34, Last annotation update)
CLASS-II CRF2-4 PRECURSOR.
                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.0%;
                                                                                                                                                                                                                                            3., Antonarakis S.E., Uze G.;
CRFB4 gene: comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 525.5; DB 1;
Pred. No. 1.1e-39;
6; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7EC6DFF370185D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325
                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                      family maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                 its
                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590;
                                                                                                                              EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
1;
                                                                                                                                         a collaboration
                                                                                                                                                                                                                                                                                                                                         chromosome
                                                                            .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                        commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲,
```

```
δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 60
                                                                   Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R.,
A Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
T "Identification and sequence of an accessory factor required for
m "Identification of the human interferon gamma receptor.";
C ell 76:793-802(1994).
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INGS_HUMAN
P38484;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
1NTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA
RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                TISSUE-LUNG FIBROBLAST;
MEDLINE; 94170380.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                IFNGR2 OR IFNGT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRNKAGEWSEPVCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSWKIGVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENEYETWIMKNVYNSWIYNVQYWKNGIDEKFQITPQYDFEVLRNLEPWITYCVQVRGFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
20
250
250
188
102
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
325
220
249
249
325
37
49
68
102
161
161
161
173
325
37011
                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.

A -> D (IN REF. 2).

FLGHP -> VGRME (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 214; DB
Pred. No. 4.2e
99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB
AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOKINE RECEPTOR CLASS-II CRF2-4. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2)
423 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                 GAMMA. REQUIRED
AN INTEGRAL PART
IS LIKELY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2)
                                                                         OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                              for
                                                                                                                                                                PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                      POR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
```

```
RESULT INCOME RESULT OF THE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
CARBOHYD
CARBOHYD
DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS. MEDILNE; 93183911.
Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gar "Alignment of disulfide bonds of the extracellular domain interferon gamma receptor and investigation of their role biological activity.";
                                                                                                                                                                                                                                                                                                                                                                     INGR_HUMAN STANDARD; PRT; 489 AA p15260; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U05875; AAA16955.1; -. EMBL; U05877; AAA16956.1; -.
                                                                                                                                                                                  Aguet M., Dembic 2., Me
Molecular cloning and
                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 89003065.
                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                        IFNGR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPEVHLE - - - AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEKENT-SSWYEVDSFTPFRKAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYQKTGMDNWIKLS-----
                                                                                                                                             55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFKYTDSK-----WFTADIMSIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCTQITATECDFTAASPSAGFPMDFNV----TLRLRAELGALHSAWVTMPWFQHYRNVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
248
269
269
110
110
137
219
231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337
247
268
337
56
85
110
110
137
2119
                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.48;
24.78;
                                                                                                                                                                                                        Merlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     institutions as long
                                                                                                                                                                                      expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.1e
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERFERON-GAMMA RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_002718.
18C61B10AD90E509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                      of
f
                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                         update)
PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                      human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                           (CDW119).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA
                                                                Garotta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in no w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    way
ial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
```

```
Š
                                                                                           밁
                                         융
                                                                                                                                                  Query Match
Best Local S
Matches 45
                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Winkler F.K., Robinson J.A.;
"Neutralizing epitopes on the extracel (IFNgammaR), alpha-chain characterized and X-ray crystal structure of the A6 J. Mol. Biol. 273.882-897(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Zauoddy P.J., Narula S.K.; "Crystal structure of a complex between interferon-gamma an soluble high-affinity receptor."; Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Mol. Biol. 273:882-897(1
-!- FUNCTION: RECEPTOR FOR
INTERFERON-GAMMA DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J03143; AAA52731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 32:2423-2430(1993).
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                        CRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
              119
                                                                                                                                                                                                                                                                                                                                                                                                                             mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF
                                         98
                                                                   62
                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

PTM: PHOSPHORYLATED AT SER/THR RESIDUES.

SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
               HI--
                                                                                                            NLKSPQKVEVDIIDDNFILRWNRSDESVGNV-TESFDYQKTGMDNWIKLSGCQNITSTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1JRH;
                                         NISDHVGDPSNSLWVRVKARVGQKE--SAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMI
                                                                 NESSLKLNVYEEIKLRIRA---EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI 118
                                                                                              SVPTPTNVTIESYNMNPIVYWEY--QIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYC
                                                                                                                                                   l Similarity 22.1
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98035727.
                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycopioce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A31555
                                                                                                                                                                                                                      54404
                                                                                                                                                                10.48; 22.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Henke C.,
-SPGTK-----DSVMWALDGLSFTYSLLIWKNSSGVEERIENI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the extracellular interferon gamma receptor haracterized by homolog scanning mutagenesis
                                                                                                                                                                                                                     MW;
                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERFERON GAMMA.
                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
COTENTIAL.
                                                                                                                                                  Score 111; DE
Pred. No. 0.01
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  INTERFERON-GAMMA RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by homolog scanning fab-IFNgammaRl-108 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon-gamma and
                                                                                                                                                                DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OWI
                                                                                                                                                    83;
                                                                                                                                                                              Length 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTORS BIND ONE
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ດ
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lunn C.
                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    commercial
                                                                                                                                                    Gaps
                                          143
                                                                                               85
                                                                                                                           61
                                                                                                                                                    7;
```

ä

```
RESULT
TF_BOVIN
ID TF_B
AC P309
DT 01-J
DT 01-J
                                                                                                                                                                                                                                                                                               RESULT 8
PWP2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                              밁
                                                                                                                 Ş
                                                                                                                                        밁
                                                                                                                                                             δ
                                                                                                                                                                                       밁
                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 38; Conser
TF_BOVIN
P30931;
01-JUL-1993
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to licenseelsb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWP2_CAEEL P91341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gattung S., Scheet P., Kemp K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: COUTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
-i- SIMILARITY: BELONGS TO THE PWP2 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F55F8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U80447; AAB37807.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The sympactic institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                              WORMPEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                   143
                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
                                                                                              121
                                                                                                                                          61
                                                                                                                                                                                                               44
                                                            9
                                                                                                         IWKNSSGVEERIENIYSRHKIYKLSPET
                                                                                                                                         LSISPSGYHLLASDERGVVHFVHLLSEFKIYTFRSNKPIGSLQWSPDATRVAICRENDLQ
                                                                                                                                                        AQIGPPEVHLEAEDKAIVIHI----------
                                                                                                                                                                                                      MDNWIKLSGCQNIT--STKCNFSSLKLNVYEEI--KLRIRAEKENTSSWYEVDSFTPFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QCQLAIPVSSLNSQYCVSAEGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQK-----EDDCCDEI 198
                                                                                                                                                                                        MDTNFKLSNCIGTVYRDGQVAFSKDGYSVISPIGNKLSIFDLRNNTSKTLDIDCNYNIKR
                                                                                             IHEFGKSIENKVYNPFSLSRTYKLSSDS
                                                                                                                                                                                                                                                                                                                                                                                                    PR00320; GPROTEINBRPT.; PS00678; WD_REPEATS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             F55F8.3; CE11192.
                                                                                                                                                                                                                                    8.9%;
nilarity 25.7%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation updat
(YPTOPHAN PROTEIN % HOMOLOG.
                                                                                                                                                                                                                                                                                                          l protein;
188 218
358 388
400 430
486 514
524 554
 (Rel.
                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                    STANDARD;
 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematoda; Secernentea; Rhabditia; Rhabditida; 
bidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                              103899 MW;
                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                   ; Repeat; WD 1
18 WD1.
88 WD2.
80 WD3.
14 WD4.
14 WD5.
 Created)
                                                                                                                                                                                                                                     19;
 sequence update)
                                                                                                                                                                                                                                    Score 95.5; DB 1;
Pred. No. 0.64;
9; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                    PRT;
                                                                                                                                                                                                                                                                                               439F35881B398CD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              repeat.
                                                                                             148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 925
                                    292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.
                                                                                                                                                                  SPGTKDSVMWALDGLSFTY - - - - SLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ጅ
                                    ₿
                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                          Length 925;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .ch/announce/
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                  142
                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                way
                                                                                                                                                                                                                                     4
INGR_MOUSE
ID INGR_M
AC P15261
                                                                                                                                                               В
                                                                                         Š
                                                                                                                   В
                                                                                                                                       Š
                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                        RESULT 10
                                                                      밁
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                          Query Match
Best Local
 INGR_MOUSE
P15261;
                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
DISULFID
DISULFID
LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PR00346; TISSUEFACTOR, PROSITE; PS00621; TISSUE_FACTOR; 1. PFAM; PF01108; Tissue_fac; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S74147; AAB20755.1; PIR; JQ1319; KFBO3. HSSP; P24055; 1A21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last annotation update)
TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-ADRENAL GLAMEDLINE; 92109720.
                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
Palmitate.
                                                                      187
                                                                                            144 WK-NSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 198
                                                                                                                   132
                                                                                                                                          97
                                                                                                                                                                 74
                                                                                                                                                                                       44 MDNWIKLSGCQNITSTKCNFS-SLKLNVYEEIKLRIRAEKENTSS------WYEVDSFTP
                                                                                                                                       FRKAQIGPP-----EVHLEAEDKAIVIHISPGTKDSVMWALD---GLSFTYSLLI 143
                                                                      WKASSTGKKKATTN--TNGFLIDVDKGENYCFHVQAVIL-SRRVNQKSPESPIKCT
                                                                                                                  YLETNLGOPTIOSFEQVGTKLNVTVQDARTLVR----ANSAFLSLRDVFGKDLNYTLYY
                                                                                                                                                                  LGNW--KNKCFYTTNTECDVTDEIVKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTP
                                                                                                                                                                                                               40;
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLAND;
             STANDARD;
                                                                                                                                                                                                                                                                                   35
292
248
271
292
292
153
181
181
238
                                                                                                                                                                                                                                                                        32475
                                                                                                                                                                                                                                                                                                                                                                                                                                       coagulation; Transmembrane; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND PARTIAL SEQUENCE
                                                                                                                                                                                                                          8.6%;
22.7%;
                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                     POTENTIAL.

POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PALMITATE (BY SIMILARITY).

FE471D92BFBCE163 CRC64;
                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
WKS MOTIF.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE FACTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
             PRT;
                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                          92.5;
No. 0.
             477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                          DB
28;
             A
                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                    ::
```

Length 292; Indels

31;

Gaps

9

96

131

239

```
Appella E.;
Appella E.;
"Affinity purification, pepular "
mouse interferon gamma receptor.";
mouse interferon 265:4064-4071(1990).
                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurtheria; Rodentia; Sciurognathi; Muridae; Murinae;
   EMBL;
EMBL;
EMBL;
                                                                                                                                                                                               INTERPERON-GAMMA DIMER.

INTERPERON-GAMMA DIMER.

INTERPERON-GAMMA DIMER.

ISUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ISUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

IP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ISUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ISUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ISUBCELLULAR LOCATION: TYPE I MEMBRANE PAMILY OF RECEPTORS.

ISUBCELLULAR LOCATION: TYPE I TIPLE LIKE DOMAINS.

ISUBCELLULAR LOCATION: TYPE I TIPLE LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90099370.

Hemmil S., Peghini P., Metzler M., Merlin G., Dembic Z., Aguet M., "Cloning of murine interferon gamma receptor cDNA: expression in human cells mediates high-affinity binding but is not sufficient confer sensitivity to murine interferon gamma."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequ
15-JUL-1999 (Rel. 38, Last anno
INTERFERON-GAMMA RECEPTOR ALPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray P.W., Leong S., Fennie E.H., Fernandez-Luna J., Schreiber R.D. "Cloning and expression of the cD!
                                                                              or send an
                                                                                                                                                                                                                                                                                                          mouse interferon-gamma receptor.
Gene 154:219-223(1995).
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-28 FR
MEDLINE; 95197006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cofano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 90154099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kumar C.S., Muthukumaran
Mariano T.M., Pestka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Munro S., Ma
Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 90083245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFNGR1 OR IFNGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and expression
                                                                                                                                                                                                                                                                                                                                        Characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Biol.
 M28995;
M26711;
M28233;
M25764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S., Maniatis T.;
ession cloning of the
Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90046824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90036866
                                                                                                                                                                                                                                                                                                                                                          Obici S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moore S.K.,
                                                                            email to license@isb-sib.ch).
AAA37895.1; ALT_INIT.
; AAA37896.1; -.
; AAA37898.1; -.
; AAA39177.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264:17939-17946(1989).
                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A. 86:9901-9905(1989).
                                                                                                                                                                                                                                                                                                                                     Russell S.W., Murphy W.J.; f the 5' flanking region an
                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanaka S., Yuhki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ດ
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t sequence update)
t annotation update)
ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine interferon gamma receptor cDNA.";
.A. 86:9248-9252(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86:8497-8501(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Farrar M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for the murine interferon
                                                                                                                                                                                                                                                                                                                                          region and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noe
                                                                                                                                                                                                                                                                                                                                                                                                                                                  and cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Landolfo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pingel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ү.н.,
                                                                                                                                                                                                                                                                                                                                          encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç
```

```
RESULT
ID 45. HU
PAC PAC
PAC P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 46
                                    TISSUE-LYMPHOCYTES;

MEDLINE: 88061067.

Streuli M., Hall L.R., Saga Y., Sch

"Differential usage of three exons

mRNAs encoding human leukocyte comm

J. Exp. Med. 166:1548-1566(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DOMAIN
                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                          Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
LEUKOCYTE COMMON ANTIGEN PRECURSOR (EC 3.1.
                                                                                                                                                                                                                                                                                                                                                                                               CD45_HUMAN
P08575;
                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                         PTPRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR: A35468: A35468.
PIR: A36224: A36224.
HSSP: P15260: 1JRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:107655; IFNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             munoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 CNETLCELNISVSTLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL; J05265; AAA39178.1

IL; J05960; AAA80980.1

IL 3A3368; A34368.

IL 3A3423; A34423.

IL A34508; A34508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKLNVYEEIK------LRIRAE-KENTSSWYEVDSFTPFRKAQIGPP--EVHLEAEDKA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETTYC-LKVKAALLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVLVFHPEVVVNGESQGTMFG-DGSTCYTFDYTVYVEHNRSG-----EILHTKHTVEKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVIHISP-----GTKDSVMWALDG---LSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NIYGQIMYPDVSAWARVKAKVGQKESDYARSKEFLMCLKGKVGPPGLEIRRKKEEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PINVLIKSYNLNPVVCWEYQNMS---QTPIFTVQVKVYSGSW--TDSCTNISDHCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ-KTGMDNWIKLSGCQNITSTKCNFSS
                                                                                                                                                                                                                                                                      OR CD45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 23.4
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                   (Human).
                                                                                                                                                                   N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277
277
277
277
477
477
477
208
208
243
243
204
204
211
                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
ABFC66E9BAA0B20A CRC64;
                                                                                              Y., Schlossman S.F., Salto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92; DB
Pred. No. 0.57
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERFERON-GAMMA RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
                                                              common
                                                                                                                                                                                                                                                                                                               ion update)
 (EC 3.1.3.48) (L-CA) (CD45 ANTIGEN)
                                                                               generates
                                                                                                                                                                                                                                                                                                                                                                                                                  1304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation;
                                                                                 least five
                                                                                                                                                                                                                                Mammalia;
                                                                                 different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 89017162.

Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;
Charbonneau H., Tonks N.K., Walsh K.A., Fischer E.H.;

"The leukocyte common antigen (CD45): a putative receptor-linked protein tyrosine phosphatase.";

Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
            CARBOHYD
CARBOHYD
                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00700; PRTYPHPHTASE.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y00638; CAA68669.1; HSSP; P18052; 1YFO. MIM; 151460; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 90316093.

Streuli M., Krueger N.X., Thai T., Tang M., Saito H.;

"Distinct functional roles of the two intracellular phosphatase like domains of the receptor-linked protein tyrosine phosphatases LCA and
                                              CARBOHYD
                                                           CARBOHYD
                                                                       CARBOHYD
                                                                                                         CARBOHYD
                                                                                                                                                         CARBOHYD
                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                       PFAM; PF00041; fn3; 2.
PFAM; PF00102; Y_phosphatase;
Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS
                                     CARBOHYD
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                             Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHICH ARISE BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. DATABASE: NAME-PROW; NOTE-CD guide CD45 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd45.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O J. 9:2399-2407(1990).

FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN RECEPTOR. THE FIRST PTPAGE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE THE FIRST ONE.

CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: THERE ARE 8 DIFFERENT VARIANTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN TYROSINE
 splicing;
                                                                                                                                                                                1304
575
597
1304
479
571
919
1235
1235
1235
 78
90
190
190
190
190
232
233
276
276
276
468
468
                                                                                                                                                                                                                                                                                                                            Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORTHOPHOSPHATE
                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III (POTENTIAL).

FIBRONECTIN TYPE-III (POTENTIAL).

PROTEIN-TYROSINE PHOSPHATASE.

PROTEIN-TYROSINE PHOSPHATASE.
POTENTIAL.
                                                                                                                                 POTENTIAL.
                                                                                                                                                                   C->S: LOSS POTENTIAL.
                                                                                                                                                                                                                                                                                                                          Phosphorylation; ase; Signal.
                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                      LEUKOCYTE COMMON
                                                                                                                                                                                SSOT
                                                                                                                                                                                 ဝ္ဇ
                                                                                                                                                                                                                                                                                       MON ANTIGEN. (POTENTIAL).
                                                                                                                                                                                ACTIVITY
                                                                                                                                                                                                                                                                                                                                        B-cell;
                                                                                                                                                                                                                                                                                                                                        T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-CA
                                                                                                                                                                                                                                                                                                                                       Repeat;
```

```
RESULT
6DCS_SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6DCS_SOYBN STAN
P26690;
01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (EC 1.-.-).
Glycine max (Soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudlootyledons;
core eudloots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
                                                                      HSSP: P14550; ZALR.
PRINTS; PRO0069; ALDKETRDTASE.
PROSITE; PS00062; ALDKETO_REDUCTASE_3;
PROSITE; PS00063; ALDKETO_REDUCTASE_1;
PROSITE; PS00798; ALDKETO_REDUCTASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Induced plant responses to pathogen attack. Analysis and heterologous expression of the key enzyme in the biosynthesis ophytoalexins in soybean (Glycine max L. Merr. cv. Harosoy 63)." Eur. J. Biochem. 196:423-430(1991).

FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORMATION OF 4.2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOSYNTHESIS OF
                                                                                                                                                                                                                 EMBL; X55730; CAA39261.1; PIR; S14222; S14222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. HAROSOY
MEDLINE; 91177016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                     PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHILADAL SUBUNIT: NONOMER.
SUBUNIT: NONOMER.
INDUCTION: BY PATHOGEN ATTACK.
INDUCTION: BY PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCEOLLIN TYPE PHYTOALEXINS.
PATHWAY: THIS IS THE KEY ENZYME
PHYTOALEXINS IN SOYBEAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEKYANITVDYLYNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESVGNVTFSFDYOKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNIETFTCDTQNITYRFQCGNMIFDNK---EIKLENLEPEHE-YKCDSEILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDSVMWALDGLSFTYSL----LIWKNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGT------
PF00248; aldo_ket_red; 1.
noid biosynthesis; Oxidoreductase; NADP.
NCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529
1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Α
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147253 MW; 1F357BC5632618B2 CRC64;
                                                                                                                                                                                                                                             .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 90.5; DB
Pred. No. 2.8;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GNNTC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315
                                                                               ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဝ္ဗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   esis of 63).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
```

Query Match

Score

90;

B

Ļ

Length 315

Gaps

7;

```
á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INT2_BOVIN STANDARD,

INT2_BOVIN STANDARD,

Q95141;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

15-FEB-2000 (Rel. 39, Last annotation update)

INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC)

INTERFERON ALPHA/BETA RECEPTOR) (INTERFERON ALPHA/BETA RECEPTOR-
   DOMAIN
TRANSMEM
DOMAIN
DOMAIN
REPEAT
REPEAT
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _BOVIN
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.; "Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                            CHAIN
                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pregnancy.";
Endocrinology 138:4757-4767(1997).
-!- FUNCTION: RECEPTOR FOR INTERFERONS
-!- FUNCTION: W GTOWN! TRANSDUCTION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                             Receptor;
                                                                                                                                                                                                                               EMBL; U75304; AAB84233.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98006426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                      KINASE, JAK1.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYDKERMNQNLHIFDWALTEQDHHKISQISQSRLISGPTKPQLADLW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRKGASRGPNEVMENDVLKEIAEAHGKSI-----AQVSLRWLYEQGVTFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRK-AQIGPPEVH-----LEAEDKAIVIHISPGTKDSVMWALD-GLSFTYSLLIWKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGLTKAIGVSNFSVKKLQNLLSVATIRPVVDQVEMNLAWQQKKLREFCKENGIIVTAFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITSTKC----NFSSLKLN------VYEEIKLRIRAEKENTSSWYE-----VDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSLKTLQLEYLDL----YLIHWPLSSQP-GKFSFPIEVEDLLPFDVKGV--WESMEECQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFD----YQKTGMDNWIKLSGCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos.
                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                            27
   246
267
367
362
362
230
58
                                                                                                                                                                                         Glycoprotein; Repeat;
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKHKIYKLSPETTYCLKVKAALLTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
 BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.5:
8; Mismatches
                                                                                    CYTOPLASMIC
2 X 5 AA TAN
                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                         INTERFERON-ALPHA/BETA RECEPTOR
                                                                                      MIC (POTENTIAL)
TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA AND BETA.
INTERACTING WIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Vertebrata;
Pecora; Bovo
                                                                                        REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76;
                                                                                                                                                                                                         Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovoidea; Bovidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                      ဝှု
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLY
                                                                                    S-L-E-D-
                                                                                                                                                                                                                                                                                                                                                a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                         BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
INRZ_HAMAN
INRZ_HOWAN

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
Submitted [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-FEB-2090 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA-REC)
(TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INR2_HUMAN P48551;
                                                                                                                                                                                                                                                                                                                                                                               receptor subunit generated by altern of a cytokine receptor gene cluster. EMBO J. 14:5100-5108(1995).
                                Cohen B.,
                                                  TISSUE-BLOOD;
                                                                  SEQUENCE
                                                                                                   "Cloning and expres interferon alpha be J. Biol. Chem. 270:
                                                                                                                                                     Domanski P., Witte M., Kellum M., Rubinstein M., Pitha P., Colamonici O.R.;
                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG MEDLINE; 95394915.
                                                                                                                                                                                                                                          Cell 77:391-400(1994).
                                                                                                                                                                                                                                                          Novick D., Cohen B., I "The human interferon molecular cloning.";
                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (SHORT FORM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lutfalla G., Holland S.J., Cinato E., Rogers N.C., Smith J.M., Stark G.R., Kerr I.M., Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFNAR2 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mutant U5A cells are complemented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEPKDPRKIN-RSPLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTK---DSVMWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF--ILRWNRSDESYGNVTFSFDYQKTGMDNWIK-LSGCQNITSTKCNFSSLKLNVYEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALLTSWKIGVYSPVHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEELOFYLAF -----IEEHAGNSVKRHOPQITGNITKNFNYVIDKLIPNTNYCISVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDGLSFTYSLLIWKNSSGVEERIENIYSRHK------IYKLSPETTYCLKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFQSVLSWELKNHSIVPTHYTLWYTIMSKREDMKVVKDCINVTRSFCDLTDVWVNTTDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPQVVGFRENAKLVICMGSFFLVPDKPLDPPEF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 23.4
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96067138.
                                                                                                                                                                                                                                                                                                            94236684.
                                                               FROM N.A.
              Kim S.H., N
(OCT-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ens (Human).
; Metazoa; Chordata; Craniata; Vertebrata;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
101
191
                                                                                                                                   expression of a long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                   beta receptor that is required 70:21606-21611(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
101 P
191 P
59584 MW;
                                                                  (LONG
                Novick D., Rubinstein M.; ) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                        Rubinstein I
n alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194
                                                                FORM)
                                                                                                                                                                                                       FORM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                   by alternative
e cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
66A2C6D896B4DAD6 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89.5; D
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                                                                            receptor: characterization
                                                                                                                                   form
                                                                                                                                                                                                         FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Monneron
Gardiner P
                                                                                                                                                                                                                                                                                                                                               PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515
                                                                                                                                                                                                                                                                                                                                                                                                               an interferon-alpha
tive processing of a
                                                                                                                                   of the
                                .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EIVGFTNHISVNVKFQFDSPGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                   ed for
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ď.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                     Hackett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                   subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reboul
                                                                                                                 signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                   new
                                                                                                                                                                                                                                                                                                                                                                                                                                 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                   member
```

48;

Gaps

10;

171

```
THEWS

TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novick D., Cohen B., Tal N., Rubinstein M.;
"Soluble and membrane-anchored forms of the human IFN-alpha/beta receptor.";
J. Leukoc. Biol. 57:712-718(1995).
-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. THE LONG
                                    CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
VARSPLIC
                                                                                                                                                                        TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U29584
EMBL; X89772
MIM; 602376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISCUSSION OF VARIOUS FORMS, MEDLINE; 95279874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                      Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                   IGNĀL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. THE LONG AND SOLUBLE FORMS ARE DIRECTLY INVOLVED IN SIGNAL TRADUCTION DUE TO THEIR INTERACTION MITH THE TYR KINASE, JAK1. THE LONG FORM ALSO INTERACTS WITH THE TRANSCRIPTIONAL FACTORS, STAT1 AND STAT2. BOTH FORMS ARE POTENT INHIBITORS OF TYPE I IFN ACTIVITY.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
ALTERNATIVE PRODUCTS: THREE ISOFORMS; A LONG FORM/IFNAR2-2 (SHOWN ALTERNATIVE PRODUCTS: THREE ISOFORMS; A LONG FORM/IFNAR2-3/P40; ARE PRODUCED BY ALTERNATIVE SPLICING.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPPORS.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPPORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L42243;
L42238;
L42239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   L41943
L41942
X77722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L42240;
L42323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L41944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L42240
                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB46417.1; JO
AAB46417.1; JO
AAB46417.1; JO
AAB46417.1; JO
AAB46417.1; JO
AAB46417.1; JC
AAB46417.1; JC
AAB46418.1; JC
AAB46419.1; JC
AAB464
                                      27
2444
265
265
207
207
2116
1188
1192
238
240
281
                                      243
264
515
93
227
58
87
116
1188
192
239
331
                                                                                                                                                                                                                                                                                                           515
                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED
JOINED
JOINED
JOINED
JOINED
JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND PARTIAL SEQUENCE
SA -> FS (IN ISOFORM 2-3).

MISSING (IN ISOFORM 2-3).

NEHNELAWDFEPLLEPLEANDMVEVIZINRKKKVWDYNYDDE

SDSDTERAPR -> ROGLAKGWNAVALHRCSHNALGSETPE

LKQSSCLSFPSSWDYKRASLCPSD (IN ISOFORM 2-
                                                                                                                 POTENTIAL.
                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                       CHAIN: EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                               INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                 BETA
    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
IL10RA OR IL10R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I10R_MOUSE
Q61727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                          TRANSMEM
DOMAIN
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-C57BL/6 X A. MEDLINE; 94068585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Euthería; Rodentia;
                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                    EMBL; L12120; AAA16156.1; -. MGD; MGI:96538; IL10RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCLKVKAALLTSWKIGVYSPVHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E-----EELQFDLSLVI------EEQSEGIVKKHKPEIKGNMSGNFTYIIDKLIPNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHK-----IXKLSPETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTVLEGFSGNTTLFSCSHNFWLAIDMSFE------PPEFEIVGFTNHINVMVKFPSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFRSILSWELKNHSIVPTHYTLLYTIMSKPEDLKVVKNCANTTRSFCDLTDEWRSTHEAY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NF--ILRWNRSDESVGNVTFSFDYQKTGMDNWIK-LSGCQNITSTKCNFSSLKLNVYEEI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCVSVYLEHSDEQAV-IKSPLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLRIRAEKENT-----SSWYEVD-SFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 8.3%;
l Similarity 22.7%;
46; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332
10
151
515
                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ટ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515
10
151
57758
        575
241
262
262
575
225
225
2113
113
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           £1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-HEMATOPOIETIC;
                                                                                                                                                                                                    Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 89; DB
Pred. No. 1.2;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM 2-1).
F -> V (IN REF. 2 AND 4).
M -> V (IN REF. 3).
M -> V (TO REF. 3).
    CYTOPLASMIC POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194
                                                                                                                                       INTERLEUKIN-10 RECEPTOR. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
1.2;
                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
Mus.
```

a collaboration MBL outstation -

```
밁
                                       Ş
                                                                                                        δ
                                                                                                                                                 밁
                                                                                                                                                                               Ş
                                                                          β
                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                         Query Match 8.2%; Score 87.5; DB 1; Length 575; Best Local Similarity 20.0%; Pred. No. 1.8; Matches 47; Conservative 38; Mismatches 89; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
168 ------PET------TYCLKVKAALLISWKIGVYSPVHCIKTTVE 200
                                                                                             112 EDKAIVIHISPGTKDSV-MWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS--- 168
                                                                      123 VDEVIL-----TVDSVTLKAMDGIIYGTIHPPRPTITPAGDEYEQVFKDLRVYKISIRK 176
                                                                                                                                           23 GTELPSPSYVWFEARFFQHILHWKPIPNQSESTYYEVAL----KQYGNSTWNDIHICRKA 78
                                                                                                                                                                                                                                           1 GKNLKSPOKVEVDIIDDNFILRW----NRSDESVGNVTESFDYQKTGXDNWIKLSGCQNI 56
                                                                                                                                                                                                                                                                                                                                                                                 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;
                                                                                                                                                                                                                                                                                         89; Indels 61; Gaps
                                                                                                                                                                                                                                                                                         10;
```

Search completed: June 1, 2000, 04:38:52 Job time: 14315 sec

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                      Pred. No.
score great
and is der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB DB
                                                                                                                                                                                                                      Score
                               84.5
84.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq
                                                                                                                                                                                                                                                                                  greater than
                                                                                                                                                                                                                                                                        derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 1000000
                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                      is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                10:
12:
13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-240-675-2_COPY_27_229
1072
1 GKNLKSPQKVEVDIIDDNFI.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKNLKSPQKVEVDIIDDNFI........WKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                 sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                       sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                           sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                     sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                               sp_fungi:*
                                                                                                                                                                                                                                                                                                                sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                     sp_plant:*
                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲
   484
6048
6831
7160
11143
22033
2215
2215
2215
239
6875
26926
429
1220
2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000, 04:38:06; Search time 69.16 Seconds
(without alignments)
203.511 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                      B
                                                                                                                 4555411
                                  44040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 0
5 8
                                                                                           054711
Q95209
                                                                                                                           001190
061190
063953
09YGC8
014936
023020
023550
023551
           Q9YHV9
Q12465
                                                              Q15467
Q99624
                                                                                                                                                                                                                      Ħ
                                                    Q28733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  summaries
                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225878
09ygc8 gallus gall
014936 homo sapien
023020 caenorhabdi
023550 caenorhabdi
023551 caenorhabdi
016614 homo sapien
054711 mus musculu
095209 oryctolagus
088307 mus musculu
015467 homo sapien
029624 homo sapien
029673 oryctolagus
010466 homo sapien
029673 oryctolagus
010466 homo sapien
029673 oryctolagus
010465 saccharomyc
09yhv9 gallus gall
012465 saccharomyc
09yhv9 gallus gall
                                                                                                                                                                                                                      Description
                                                                                                                                                                          Q9yhw0 gallus gall
Q61190 mus musculu
Q63953 mus musculu
```

82.5 82 82 81 81 81 80.5 80.5 80.5 79.5 79.5 79.5 79.5 79.7 79.7 79.7 79
7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.
406 817 1093 11009 11720 13726 2340 9340 9340 9340 9340 9340 9340 9340 9
51115155111112112
Q58459 Q58459 Q58863 Q58863 Q584577 Q94578 Q60705 Q60705 Q40707 Q35663 Q92257 Q35663 Q35683 Q3588 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q35883 Q3
Q58459 methanococc Q07784 gallus gall Q70784 gallus gall Q70535 rattus norv Q58863 methanococc Q08773 saccharomyc Q94537 drosophila Q94538 drosophila Q94538 drosophila Q94577 homo sapien Q35664 mus musculu Q32861 brassica ca Q9x257 thermotoga Q35633 mus musculu Q35983 mus musculu Q35983 mus musculu Q52319 mus musculu Q62319 mus musculu Q9xwd9 caenorhabdi Q1531 caenorhabdi Q82310 caenorhabdi Q5205 mus musculu Q55205 mus musculu Q590754 foot and-mo P91305 caenorhabdi

## ALIGNMENTS

```
RESULT
OPYHWO
PAC OPYHWO
OPYHW
                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
밁
                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LIVER;

REBOUL J., GARDINER K., MONNERON D.
"Comparative genomic analysis of t)
receptor gene cluster.";
Genome Res. 0.0-0(1999).
EMBL; AF082664; AAD13669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9YHWO PRELIMINARY; CONTROL OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
208
                                                                                                       175
                                                                                                                                                                                                                                                                             117 VIHISPGTKDSV--MWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 NLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ-----KTGMDNWIKLSGCQNIT 57
                                                                                                 KVKAALLTSWKIGVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STKCNESSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLKSPQDIQVYAVNTNFTLMWNYTGDGT-NVTFSAQYQCFDDLQTSEPEWKELSGCQNVS
KVQATVPLEDKGGLFSPIHCIKTT
                                                                                                                                                                                                              KINISPPEANQVRKMW-LISVFFKYNVVIWDNSSNV-EKVRSILPIDVINDLAPETTYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                        HTECDFSSAITAYYDTHHIRIRAERREAKSPWSSIFEMIPYEIAQIGPPEIALQSINGAI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     score 415.5; DB 13;
pred. No. 1e-29;
s6; Mismatches 65;
231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F99BC099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D., UZE G., LUTFALLA G.;
the interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
```

```
RESIDENT OF THE PRINCIPLE OF THE PRINCIP
           ACCOUNT ACCOUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U53696; AACC3062.1; -
MGD; MGI:109380; I110rb,
PFAM; PF00041; fn3; 1.
SEQUENCE 349 AA; 39774 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q63953 PRELIMINARY;
Q63953;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-NOV-1999 (TREMBLrel. 12, L
INTERFERON GAMMA RECEPTOR 2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q61190 PRELIMINARY; rn1, Q61190; Q61190; Q61190; TIEMBLrel. 01, Created) 01-NOV-1996 (TIEMBLrel. 01, Last sequence update) 01-NOV-1996 (TIEMBLrel. 12, Last annotation updat CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CY IL10RB OR CRFB4 OR CRF2-4.
SEQUENCE FROM N.A.
STRAIN=129SV/J;
MEDLINE; 97128072.
EBENSPERGER C., RHEE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 97199375.
GIBBS V.C., PENNICA D.;
"CRF2-4: isolation of cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.
                                                                                                                                                                                                                                               HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
"A novel member of the interferon receptor family complements
functionality of the murine interferon gamma receptor in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 186:97-101(1997)
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 94170381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFNGR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 QVQGFLLDQNRTGEWSEPICERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
                                                                                                                                                                                       76:803-810(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVKAALLTSWKIGVYSPVHCIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIENEPET-----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSPYDSEVLRNLEPWTTYCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPEMQIESLAESLHLRFSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH-----CKRTASTQCDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
       MUTHUKUMARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
(INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 215; DB 11;
Pred. No. 7.4e-12;
3; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4AC1802A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332
   ი
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ⋛
   LEMBO D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
II CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
Mus.
       DONNELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

```
OR SEGULT COLOR OF SEGULT COLOR OF SEGUET COLO
멍
                                                        8
                                                                                                                                       밁
                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RA DR RT DR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9YGC8 PRELIMINANI,
Q9YGC8;
Q9YGC8;
Q1-MAY-1999 (TrEMBLrel. 10, C
Q1-MAY-1999 (TrEMBLrel. 10, L
Q1-MAY-1999 (TrEMBLrel. 10, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding the second chain of the mouse Scand. J. Immunol. 44:599-606(1996).
EMBL; U69599; AAC52938.1; JOINED.
EMBL; U69594; AAC52938.1; JOINED.
EMBL; U69595; AAC52938.1; JOINED.
EMBL; U69596; AAC52938.1; JOINED.
EMBL; U69596; AAC52938.1; JOINED.
EMBL; U69597; AAC52938.1; JOINED.
EMBL; U69598; AAC52938.1; JOINED.
EMBL; S69336; AAD30165.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor gene cluster.";
Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1;
EMBL; AF082666; AAD13671.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55
79
                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT
VSS--LSVYGAYVLRVRTEWEDEHSDWAVVRFKPMADTVIGPPSVNVKSESGTLHVDFTG
                                                                                                                                                                                                   PQKVEVDIIDDNFILRWNRSDESVGNVTFSFD----YQKTGMDNWIKLSGCQNITSTKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ
                                                            FSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS- 122
                                                                                                                                       PRNARISSYNFRSYLLWDPPGVRKGNLSYTVQAKSIFPKQNFNN-----VTTNLNVTECD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTPGKGSLVIHFSPPFD----
                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                              Similarity 26.(
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.6%;
                                                                                                                                                                                                                                                                                                                       16.7%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and promoter analysis hain of the mouse inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ĭ.
                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                              Score 179; DB
Pred. No. 1.3e
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 199; DB
Pred. No. 1.9e
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               7433D364 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBF24E9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UZE G., LUTFALLA G.; interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lysis of the gene interferon-gamma
                                                                                                                                                                                                                                                                                                                    DB 13;
.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹
                                                                                                                                                                                                                                                                                      84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1fngr2
                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aves;
                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                      ٥
```

```
RESULT 6
Q23020
PRELIMINARY;
ID 023020
PRELIMINARY;
AC Q23020; Q27232;
AC 01-NOV-1996 (TremBlrel. 01
DT 01-NOV-1996 (TremBlrel. 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                              ద
                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q14936;
Q14936;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U19247; AAC52064.1; -...

EMBL; U19241, AAC52064.1; JOINED.

EMBL; U19242; AAC52064.1; JOINED.

EMBL; U19243; AAC52064.1; JOINED.

EMBL; U19244; AAC52064.1; JOINED.

EMBL; U19245; AAC52064.1; JOINED.

EMBL; U19246; AAC52064.1; JOINED.

EMBL; U19246; AAC52064.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TERMBLIE). 01, Created)
01-NOV-1996 (TERMBLIE). 01, Last sequence update)
01-NOV-1998 (TERMBLIE). 08, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 97246734.
MERLIN G., VAN DER LEEDE B.-J.M.,
BANNWARTH W., ROMQUIN N., VIEGAS-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The gene for the ligand binding receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89003065.
AGUET M., DEMBIC Z.,
                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEMBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenetics 45:413-421(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195
                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                       NLKSPQKVEVDIIDDNFILRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKC
                                                                                                                                                                DI-----
                                                                                                                                                                                               HISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQ-GVIPEWNKTGERSQELCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKAALLTSW-KIGVYSPVHCIKTT
                                                                                                                                                                                                                                        NISDHVGDPSNSLWVRVKARVGQKE--SAYAKSEEFAVCRDGKIGPPKLDIRKEEKQIMI
                                                                                                                                                                                                                                                                          NFSSLKLNVYEEIKLRIRA---EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI 118
                                                                                                                                                                                                                                                                                                                   SVPTPTNVTIESYNMNPIVYWEY--QIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAADREHDKWSLKQYYGSWIYRILYWK--KGSNKKVIHIDTKHNSEILSQLEPWTIYCIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHK---IYKLSPETTYCLK
                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                        -----FHPSVFV----NGDEQEVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MERLIN G
                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
  9,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B.-J.M., MCKUNE K., KNEZEVIC N., VIEGAS-PEQUIGNOT E., KIEFER H.,
                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                            Score 107; DB
Pred. No. 0.06
39; Mismatches
  Created)
Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217
                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
    sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the human interferon-gamma
                                                             6048 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of.
                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the human
                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                            -YDPETTCYIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGUET
                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                            171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :
:
                                                                                                                                                                                                                                                                                                                   85
                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
    RROCOS COTTOC
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                            맑
                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15423; CAA33463.1;
EMBL; Z7399; CAA98081.1; ALT_INIT.
EMBL; Z73897; CAA98081.1; JOINED.
HSSP; Q63450; 1A06.
PFAM; PF00041; fn3; 31.
PFAM; PF00047; 19; 13.
PFAM; PF00069; pkinase; 1.
PRINTS; PR00014; FNTYPEIII.
MYOSIn; Kinase, 568449 MW; 197;
SEQUENCE 6048 AA; 668449 MW; 197;
                                                                                                             Q23550 PRELIMINARY;
Q23550;
01.NOV-1996 (Tremblrel. 0
01.NOV-1998 (Tremblrel. 0
01.NOV-1999 (Tremblrel. 1
UNC-22 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93387664.
BENIAN G.M., L'HERNAULT S.W., MORRIS M.E.;
"Additional sequence complexity in the muscle gene, unc-22, and encoded protein, twitchin, of Caenorhabditis elegans.";
Genetics 134:1097-1104(1993).
                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BENIAN G.M., KIFF J.E.; NECKELMANN N., MOERMAN D.G., "Sequence of an unusually large protein implicated in myosin activity in C. elegans."; Nature 342:45-50(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1130 KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
MEDLINE; 90044042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, TWITCHIN.
                                                                                                                                                                                                                                                                                                                   1211 VIEKKGKHGRDWQ 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       173 CLKVKAALLTSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 56
                                                                                                                                                                                                                                                                                                                                                                                            ------GTPDVVDWDADRVS-----LEWEPPKSDGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                   IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR ZK617.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.1%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                    01,
08,
12,
                                      yda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1977C602 CRC32;
                                                                                                                                                                                                                   6831
                                                                                                                                                                                                                   ጀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATERSON R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its
```

10;

10;

```
δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA DR DR DR DR DR DR DR DR DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A WHITE S.;

L Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

R EMBL; 273897; CAA98064.1; -.

R EMBL; 273899; CAA98064.1; JOINED.

R HSSP; P02751; IFNA.

R HSSP; P00041; fn3; 31.

R PFAM; PF00047; 19; 17.

R PFAM; PF00069; pkinase; 1.

DR PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.1%;
Best Local Similarity 22.8%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q23551 PRELIM
Q23551;
01-NOV-1996 (TrEMB
01-NOV-1998 (TrEMB
01-NOV-1999 (TrEMB
2K617.1B PROTEIN.
                                                                                                                                                                                                                                     WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A., BONFIELD J., BURTON J., CONNELL M., COPSEY J., COOPER J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., JUGHSTON L., LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VADUIN M., VAUGHAN K., WATERSTON R., WATERSTON A., WEINSTOCK L. WILKTERON-GEDON T.
WHITE S.;

Submitted (MAY-1996) to the EMBL/
EMBL; 273899; CAA98082.1; JOINED.
EMBL; 273897; CAA98065.1; -
EMBL; 273899; CAA98065.1; JOINED.
                                                                                                                                                                                                WATSON A., WEINSTOCK L.,
"2.2 Mb of contiguous nuc
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94150718. WILSON R., AINSCOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HARRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2K617.1B
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                    Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIEKKGKHGRĐWQ 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLKVKAALLTSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSTKCNFSSLKLNYYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVIHISPGTKDSVMWALDGLSFTYSLLIW----KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01,
(TrEMBLrel. 08,
(TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GTPDVVDWDADRVS----LEWEPPKSDGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç
                                                                                                                                                                                                           L., WILKINSON-SPROAT J., WOHLDMAN P.,
nucleotide sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 97.5; DI
Pred. No. 14;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a; Rhabditida;
Caenorhabditis.
                                                                                                                                                                                                           III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -APITOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                        æ.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
PROBLEM STORY OF STOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SODROR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
```

```
Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02751; IFNA.
PFAM; PF00041; fn3; 31.
PFAM; PF00047; 17.
PFAM; PF00069; PK1nase; 1.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 7160 AA; 789211 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q16614 PRELIMINARY; PRT; 1143 AA. Q16614; Q16614; Q1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update) T200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR
EMBL;
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 87275816.
RALPH S.J., THOMAS M.L., MORTON C.O
"Structural variants of human T200
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2185
                                                                                                                                                                                                                               antigen (CD45) gene.";
J. Immunol. 141:2781-2787(1988).
                                                                                                                                                                                                                                                                                                                                                 EMBO J. 6:1251-1257(1987).
                                                                                                                                                                                                                                                                                                                                                             antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2323 VIEKKGKHGRDWQ 2335
                                                                                                                                                                                                                                                                                                     TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
                                                                                                                                                                                                                                                            "Complete exon-intron
                                                                                                                                                                                                                                                                                       MEDLINE; 89009812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CD45, LC-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP---CAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLKVKAALLTSWK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GTPDVVDWDADRVS----LEWEPPKSDGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 22.8
44; Conservative
                                                                                                                                                                                                                                                                        STREULI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%;
22.8%;
                                                                                                                                                                                                                                                         organization
                                                                                                                                                                                                                                                            SCHLOSSMAN S.F., SP
organization of the
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDD567FE CRC32
                                                                                                                                                                                                                                                                                                                                                                         .C., TROWBRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.5;
No. 15;
                                                                                                                                                                                                                                                                          SAITO
                                                                                                                                                                                                                                                           human leukocyte common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                         (leukocyte-common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APITOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2292
```

```
OS4711
ID OS4711
AC OS4711
DT 01-JUN
DT 01-JUN
DT 01-WOY
DE (SP250)
GN SORILL
DE EMBL:
DR HERWAN
RA SUESEN
RA HERWAN
RA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M23481;
EMBL; M23483;
EMBL; M23484;
EMBL; M23484;
EMBL; M23485;
EMBL; M23485;
EMBL; M23486;
EMBL; M23486;
EMBL; M23488;
EMBL; M23488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       054711
054711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00041; fn3; 2.
PFAM; PF00102; Y_bhosphatase; 2.
PRINTS; PR00700; PRTYPHPHTASE.
Signal; Alternative splicing; Hydrolase.
SIGNAL 1 23
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SORTILIN-RELATED RECEPTOR, LDLR CLASS A REPEATS-CONTAINING PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                          Olycoprotein.
                                                           PFAM; PF00041; fn3; 4.
PFAM; PF00057; ldl_recept_a; ll.
PFAM; PF00058; ldl_recept_b; 5.
                                                                                                                             MGD; MGI:1202296; Sorll.
PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                     EMBL; AF031816; AAC16739.1; HSSP; P01130; lAJJ.
                                                                                                                                                                                                                 SUESENS U., FENGER U., Mech. Dev. 0:0-0(1997)
                                                                                                                                                                                                                                  HERMANS-BORGMEYER I., HAMPE W., SUESENS U., FENGER U., HERBARTH
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y00062; CAA68269.1;
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M23490; AAD15273
EMBL; M23491; AAD15273
                                                                                                                                                                                                                                                                                   TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                               (GP250) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDSVMWALDGLSFTYSL----LIWKNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEKYANITVDYLYNK-----GNNTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGT---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNIETFTCDTQNITYRFQCGNMIFDNK---EIKLENLEPEHE-YKCDSEILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00383; TYR_PHOSPHATASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 11
1143 AA;
    2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD15273...
AAD15273...
AAD15273...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD15273.
AAD15273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD15273.1;
AAD15273.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD15273
    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130897 MW;
    227305 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 90.5; D
Pred. No. 6.1;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                    в.
,
                                                                                                                                                                                                                                                          SCHINKE B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97A3A561 CRC32;
    DC8108CD CRC32;
                                                                                                                                                                                                                                INKE B., METHNER SCHALLER H.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                             Α:,
                                                                                                                                                                                                                                                             NYKJAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
```

```
OR REPUBLIC SOLUTION OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뭕
                                              Ş
                                                                                                       밁
                                                                                                                                                     Ş
                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
  ద
                                                                                                                                                                                                         몽
                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 33; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q95209
Q95209;
Q95209;
O1-FEB-1997
O1-FEB-1997
O1-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D86350; BAA13075.1; --
HSSP; P01130; 1AJJ.
PROSITE; PS01209; LDLRA_1; 10.
PFAM; PF00057; ldl_recept_a; 11.
PFAM; PF00058; ldl_recept_b; 4.
PFAM; PF00041; fn3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1589
                                                                                                                                                                                                               1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sorting receptor are present in a novel mammalian lipoprotein receptor family member.";
J. Biol. Chem. 271:24761-24768(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1474 NLQLSLNREEEGVILGHWAPPVHTHGLIREYIVEYSRSGSKMWASQRAASNSTEIK----
                                                                                                                                                                                                                                                                                                                 1652 APONLQLSLHGEEEGVIVGHWSPPTHTHGLIREYIVEYSRSGSKVWTSERAASNFTEIK- 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein.
SEQUENCE: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LIVER;
MEDLINE; 96394640.

YAWAZAKI H., BUJO H., KUSUNOKI J.,
SCHNEIDER W.J., SAITO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1530 NLLLNALYTVRV-AAVTSRGIGNWSDSKSITTIKGKVIQAPNIHIDSYDENSLSFTLTMD
1809 LTAQTAY 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Elements of neural adhesion molecules and a yeast
                                                 166 LSPETTY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 -- IHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                          62 NESSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                    6 SPOKVEVDIIDDN---FILRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDIKVN-GYVVNLFWSFDAHKQEKKTLSFRGGSALSHKVSNL-TAHTSYEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFILRWNRSDESV------GNV-TFSFDYQKTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                                                                                            ---NLLVNTLYTVRV-AAVTSRGIGNWSDSKSITTVKGKAIPPPNIHIDNYDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIV-----
                                                                                                                                                        PGTKDSVMWALDGLSFTYSL------LIWKNSSGVEER----IENIYSRHKIYK 165
                                                                                                       -----NSLSFTLTVDGNIKVNGYVVNLFWAFDTHKQEKKTMNFQGSSVSHKVGN 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (TrEMBLrel.
7 (TrEMBLrel.
9 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2213 AA; 247764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.3%;
19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1200
                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89.5;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B35F3995 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEIMIYA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KANAKI T., MORISAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vacuolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            density
                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1530
                                                                                                                                                                                                                 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
```

RESULT 088307

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQUEDER RESERVED DE LA COMPANIA DEL COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01130; 1AJJ.
PROSITE; PS01209; LDLRA_1; 10.
PFAM; PF00057; Idl_recept_a; 11.
PFAM; PF00058; Idl_recept_b; 5.
PFAM; PF00041; fn3; 4.
PRINTS; PR00261; LDLRECEPTOR.
PRINTS; PR001014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q15467;
Q15467;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurthoria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB015790; BAA31219.1; -. HSSP; P01130; 1AJJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KANAKI T., BUJO H., HIRAYAMA S., TA
MORISAKI N., SCHNEIDER W.J., SAITO
"Developmental regulation of;LR11 e
DNA Cell Biol 0:0-0(1998).
                                                                                                          J. Leukoc. B101. 57:712-7:
-!- SIMILARITY: BELONGS TO EMBL; X89814; CAA61940.1;
                                                                                                                                                                                               MEDLINE; 95279874.

NOVICK D., COHEN B., TAL N., RUBINSTEIN M.;

"Soluble and membrane-anchored forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                    TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein. SEQUENCE 2215 AA; 247021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Rodentia;
    SEQUENCE
                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                     IFNABR.
                                                                                                                                                                          receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --IHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLLLNALYTVRV-AAVTSRGIGNWSDSKSITTIKGKVIQAPNIHIDSYDENSLSFTLTMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLQLSLNREEEGVILGHWAPPVHTHGLIREYIVEYSRSGSKMWASQRAASNSTEIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFILRWNRSDESV------GNV-TFSFDYQKTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDIKVN-GYVVNLFWSFDAHKQEKKTLSFRGGSALSHKVSNL-TAHTSYEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 19.;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIVER,
                                                                                       Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 (TrEMBLrel. 08, 08 (TrEMBLrel. 08, 09) (TrEMBLrel. 12,
    239
                                                                                                                                                                                                                                                                                                                                                                                                                   (Tremblrel. 01, Created)
(Tremblrel. 01, Last sequence update)
(Tremblrel. 08, Last annotation update)
ALPHA/BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
    3
                                                                                                                            . 57:712-718(1995).
BELONGS TO THE CLASS
                                              26
239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ).
Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
    27336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%;
    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 89.5; D
Pred. No. 17;
33; Mismatches
                           CHAIN
                                           SOLUBLE IFN ALPHA/BETA
  9DA1F03E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANAKA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFEBECF8 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2215
                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
                                                                                                                                   CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAMAZAKI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine brain.";
                                                                                                                                 FAMILY
                                                                                                                                                                                               IFN-alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                              RECEPTOR
                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                   ဝှု
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEIMIYA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                   RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
```

```
Š
                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                       á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q99624
Q99624;
Q1-MAY-1997
Q1-MAY-1997
Q1-NOV-1999
             TITIN (FKAUNDAL).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Oryctolagus.
                                                                Q28733; Q28736; Q28736; Q1-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 12, 01-NOV-1999) (TrEMBLrel. 12, 01-NOV-1999)
                                                       TITIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1996) to the EMI EMBL; 049082; AAB47736.1; -- PFAM; PF01499; Aa_trans; 1. SEQUENCE 504 AA; 55772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
LATIF F., LERMAN M.,
Submitted (FEB-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLIE1.
01-MAY-1997 (TrEMBLIE1.
01-NOV-1999 (TrEMBLIE1.
TRANSPORTER PROTEIN.
SEQUENCE FROM N.A.
                                                                                                                                                                          358
                                                                                                                                                                                                                       304
                                                                                                                                                                                                                                              108
                                                                                                                                                                                                                                                                    245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                        15
                                                                                                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                     LPIYTELKDPSKKKMQHIS-NLSIAVMYIMYFLAALFGYLTFYN--GVESELLHTYS---
                                                                                                                                                                                                                                                                  NFNNTTGNFSHVEI-VKEKVQLQVEPEASAFCTPSYFTLNSQTAYTIPIMAFAFVCHPEV
                                                                                                                                                                                                                                                                                       NITSTKCNFSSLKLNVYEEIKLRIRAEKEN--TSSWYEVDSFTPF----RKAQIGPPEV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YCVSVYLEHSDEQAV-IKSPLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLRIRAEKENT-----SSWYEVD-SFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF--ILRWNRSDESVGNVTFSFDYQKTGMDNWIK-LSGCQNITSTKCNFSSLKLNVYEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHK-----IYKLSPETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTVLEGFSGNTTLFSCSHNFWLAIDMSFE-----PPEFEIVGFTNHINVMVKFPSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFRSILSWELKNHSIVPTHYTLLYTIMSKPEDLKVVKNCANTTRSFCDLTDEWRSTHEAY
                                                                                                                                                                       --KVDPFDVLILCVRVAVLTAVTLTVPIVLFPVRRAIQQML
                                                                                                                                                                                             IYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                           -----HLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCLKVKAALLTSWKIGVYSPVHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-----EELQFDLSLVI------EEQSEGIVKKHKPEIKGNMSGNFTYIIDKLIPNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.38;
22.78;
                                                                                                                                                                                                                                                                                                                          8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                           MINNA J., DUH F.M., KOONIN E., BADI to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03,
12,
                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                  Last sequence update)
                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89; DB
Pred. No. 1.1;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                          Score 87.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194
                                                                                                                                                                                                                                                                                                                                                                         C41A273E CRC32;
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                 6875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                               64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                       BADER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                               7;
```

```
Š
                                                          밁
                                                                                    Ş
                                                                                                                     밁
                                                                                                                                               δ
                                                                                                                                                                                  В
                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                         SO DE RETERMENTA
                                                                                                                                                                                                                                         Query Match 8.2%; Score 87.5; DB 6; Length 6875; Best Local Similarity 21.0%; Pred. No. 1.1e+02; Matches 48; Conservative 24; Mismatches 70; Indels 87; Gaps
                                                                                                                                                                                                                                                                                                                                                      Nature 345:273-276(1990).

RATURE 345:273-276(1990).

EMBL; X64696; CAA45337.1; -.

EMBL; X17329; CAA35207.1; -.

HSSP; P56276; 1TLK.

PFAM; PF00041; fn3; 50.

PFAM; PF00047; fg; 3.

Myosin; Muscle protein.

NON TER
                                                                                                                                                                                                                                                                                                                      Myosin; M
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 4305-5320 FROM N.A.
TISSUE-PSOAS MUSCLE;
MEDLINE: 90238535.
LABEIT S., BARLOW D.P., GAUTEL M., GIBSON T., HOLT J., HSIEH C.L.,
FRANCKE U., LEOWARD K., WARDALE J., WHITING A., TRINICK J.;
"A regular pattern of two types of 100-residue motif in the sequence of titin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92258380.
LABEIT S., GAUTEL M., LAKEY A., TRINICK J.;
"Towards a molecular understanding of titin.";
EMBO J: 11:1711-1716(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-6805 FROM N.A. STRAIN-CE12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CE12;
LABEIT S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
375
                                                                                                                                                                              327
                                                                                                                     267 KCESKRMVWSTYSATVLTPGTTVTRLIEGNEYIFRVRAENKIGTGPPTESKPVIAKTKYD 326
                                                                                         86
                                                                                                                                                   60 KCNFSSLKLNVY--------EEIKLRIRAEKE----NTSSWYEVDSFTPF 97
                                                                                                                                                                                                   2 KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTESFDYQKTGMDNWIKLSGC--QNITST 59
VPVNKSAIPER-----RLKVQNLIPGHEYQFRVKA----ENEIGVGEP 413
                                                                            RKAQIGPPEVHLEAEDKAIVI-------HISPGTKDSVMMALDGLSFTYSLL 142
                                                         RPGRPDPPEVTKVSKEEMTVVWSPPEYDGGKSITGYYLEKKEKHSVRW------ 375
                                                                                                                                                                                                                                                                                                                      6875 68
6875 AA;
                                                                                                                                                                                                                                                                                                                                      6875
                                                                                                                                                                                                                                                                                                                         759127 MW;
                                                                                                                                                                                                                                                                                                                         E5D3B61F CRC32;
                                                                                                                                                                                                                                           9
```

Search completed: June Job time: 14306 sec

Ļ

2000, 04:38:14

```
Con in
```

A\_Geneseq\_36:Y04994 A\_Geneseq\_36:W56309 A\_Geneseq\_36:W22602 A\_Geneseq\_36:R47812

55.00 55.00 54.50

103 103 95

31.51 33.42 39.08 34.81

Mycobacterium species prot-I Clas II S-receptor kinase I Tylactone synthase ORF2 p: I Sequence of amino acid tra:

```
A_Geneseq_36:R66850
A_Geneseq_36:R74752
A_Geneseq_36:W59836
A_Geneseq_36:R20231
            A_Geneseq_36:W02084
A_Geneseq_36:W09297
A_Geneseq_36:W87468
A_Geneseq_36:R29171
A_Geneseq_36:R74148
A_Geneseq_36:W4336
A_Geneseq_36:W87463
                                                                                                                                                                                       A_Geneseq_36:R57474
A_Geneseq_36:R87511
A_Geneseq_36:R41127
A_Geneseq_36:R41227
A_Geneseq_36:R76075
A_Geneseq_36:R92399
A_Geneseq_36:R92518
                                                                                                                                                                                                                                                                                                          A_Geneseq_36:W93941
A_Geneseq_36:W93962
A_Geneseq_36:W52296
A_Geneseq_36:W07702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
Query: US-09-240-675-1_COPY_27_229
Query length: 203
Database: A_Geneseq_36:*
                                                                                                      A_Geneseq_36:R23784
A_Geneseq_36:W22776
A_Geneseq_36:R67755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database sequences: 188963
Database length: 23686106
Search time (sec): 60.370000
                                                                                                                                                                                                                                                                        A_Geneseq_36:W82404
A_Geneseq_36:R96994
A_Geneseq_36:W59912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: May 31, 2000
                                                                                            A_Geneseq_36:R60610
                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_36:W21806
A_Geneseq_36:R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_36:R28495
A_Geneseq_36:R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL frame*_n2p.model -DEV-x1p
-Q-/ggn2_1/USPTO_spool/US09240675/runat_30052000_164311_24603/app_query.fasta.
-Q-/ggn2_1/USPTO_spool/US09240675-runat_30052000_164311_24603/app_query.fasta.
-Q-/ggn2_1/USPTO_spool/US09240675-moddf.rag -GAPOP-12.000
-GAPOP-12.000
-GAPOP-14.500 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-GAPOP-14.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_36:R28496
A_Geneseq_36:R42635
                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                              _Geneseq_36:W21805
_Geneseq_36:R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -THREADS-1
                                                                                                                                                                                                                                                                                                                                                          _Geneseq__36:W21804
                                                                                                                                                                                                                                                                                                                                                                     _Geneseq__36:R75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of: US-09-240-675-1_COPY_27_229 to: A_Geneseq_36:+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7:05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strd
                                                                                                                                                                                                                                                                                                                                                          340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  χď
  ......
                                    ZScore
795.63
                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                   146
151
127
127
121
121
                                                                                                                                                                                                    121
 1.8e-37
1.9e-37
EScore
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Len
 1321
1321
3135
399
399
409
409
164
438
178
337
337
337
337
337
2264
438
523
2264
2299
2299
2299
382
382
388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! Documentation
                                                                                                                                                                                                                                                          Human brx immunogenic peptide 1.
CRFB4 protein. New recombinant
I CRFB4 protein. New recombinant
I Mouse ETS2 repressor factor (EH
I Human SRE-ZBP analogue GEN 506G
I Mouse IRS-2. New insulin recept
I Amino acid sequence of the mut
I P. falciparum transmission blo
                                                                                                                          Human c-mer protooncogene recept Yeast presequence COX IV-wheat 1910 SLG protein. Isolated cDNA Carbamoylphosphate-synthase hom Human G3BP protein. New ubiquit Rice cultivar IR58024A mitochond Rice mitochondrial protein atp6 Rice mitochondrial protein atp6 Rice mitochondrial protein (37) Maize Id protein. Id gene control Human endothelin-2 vasoconstric Precursor ET-2 sequence. New en
         Camphor Class II acyl-ACP thiod
Camphor class II acyl-ACP thiod
Camphor C14 acyl ACP thioesteral
Camphor thioesterase. New plant
Camphor thioesterase. DNA const
Camphor PCR-generated thioesteral
Camphor C14 acyl ACP thioestera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       out_format :
                                                                                        Human septin-2 protein. Human t
TOMV P30 elicitor. DNA construc
Tobamovirus movement protein. J
                                                                                                                                                                                                                                                                                                                                                                                        Human alpha-interferon receptor Complete interferon-alpha/beta Sequence of a soulble form of t
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of a soulble form of t
IFN receptor extracellular doma
Spliced-deleted interferon alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spliced deleted interferon alph
Soluble interferon alpha/beta r
Mycobacterium species protein
                                                                                                                                                                                                                                                                                                                                                     Human IFN receptor. Compsn. of Transmembranal interferon alpha
                                                                                                                                                                                                                                                                                                                                                                             Human interferon receptor. Mond
                                                                                                                                                                                                                                                                                                                              Human brx protein. Breast cand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfs
```

alignment\_block: US-09-240-675-1\_COPY\_27\_229 x W21805

Align seg 1/1 to: W21805 from: 1 to:

434

CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC

100

34

17

101

AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC

150 50 51 17

34

alignment\_scores

Percent Similarity:

100.000

Quality: Ratio:

340.00

Length: 67
Gaps: 0
Percent Identity: 100.000

```
seq_name: A_Geneseq_36:W21805
New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 2; Fig 7; 46pp; English.

C (W21805) is characterised by a new domain (S) which follows an end-deleted extracellular domain when compared to transmembranal IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd.

C from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNS alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
    W21805 standard; Protein; 434
    W21805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-SEP-1997 (first entry)
Spliced-deleted interferon alpha-receptor
Interferon alpha-receptor; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                   Abramovich C, Ratovitski E, Revel WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                     20-0CT-1994; 075977
24-0CT 1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                          1-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 427
/label- Extracellular_domain
/note- "comprises amino acids 1-427 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            /label- S_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    form
```

seq\_name: A\_Geneseq\_36:R14487

201

Þ

67

ß

67

```
seq_documentation_block:
ID R28495 standard; Prot
AC R28495;
DT 31-MAR-1993 (first e
DE Sequence of a soulble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-240-675-1_COPY_27_229
                                                                                        seq_name: A_Geneseq_36:R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to:
R207-
R28495;
31-MAR-1993 (f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 2; Page 45; 52pp: French.

The transmembrane and cytoplasmic domains of the native IFN receptor have been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliminated. Derivatives obtained by substitution or deletion of this sequence are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   documentation_block:
R14487 standard; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-1991. 7
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen
Tovey MG, Uze G;
WPI; 91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FR2657881-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soluble interferon-alpha/beta receptor. IFN; autoimmune disease; graft rejection; histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                              101
                                                                                                                                                201
                                                R28495 standard; Protein; 436
                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                            51
                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                              ×
                                                                                                                                                                            ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                      AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                              AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                 201
                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 AA;
        (first entry)
a soulble form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 436
                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                  x R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
Identity:
        interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.
        (IFN) receptor
                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                     100
```

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_27_229 x R28495
  PROSERVED
                                                                                                                                                                                                                                             seq_documentation_block:
ID R71723 standard; Protein;
                                                                                                                                                                                                                                                                                                                  seq_name: A_Geneseq_36:R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune of diseases and transplant rejection of diseases and transplant rejection soluble polypeptide with a high affinity for Claim 2; Fig 1; Sepp; English.

DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (030533), was incubated with oligos (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535. RZ8496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor. R28495 (230534 and 030535) R28496 represents the complete receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-1991; F00318.
17-APR-1991; WO-F00318.
23-MAR-1995.
16-SEP-1994;
17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tovey M, Uze G;
WPI; 92-382110/46.
N-PSDB; Q30532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1991; WO-F00318.
(EUB1-) LAB EURO BIOTECHNOLOGIE.
Eid P, Gresser I, Lutfalla G, Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with a high affinity for IFN-alpha and .beta.
Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                       WC9507716-A.
                                                                                                                     IFN receptor extracellular domain.
IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                               6-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGATGGTCGTCCTGCGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ø
                                                                                                                                                                                                                                                                                                                                                                                                                 Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 AA;
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340.00
5.075
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 67
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                436
                                                                                                                                                                                                                                                ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ţo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F, Mogensen
                                                                                                                          immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
```

E03114. EP-402279

```
alignment_block:
US-09-240-675-1_COPY_27_229 x R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: A_Geneseq_36:W21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: R71723 from: 1
                                                                11-MAY 1995.
20-OCT 1994; 075977.
24-OCT 1993; IL-107378.
(YEDA ) YEDA RES & DEV C
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compan of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English. A recombinant soluble form of the human interferon class I protein extracellular domain, given in R71723, was expresse either E. coli or COS cell hosts. The protein was used to immunomodulatory monoclonal antibodies.
New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon Example 3; Fig 7; 46pp; English.
                                        Abramovich C, Ratovitski E, WPI; 95-200634/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
Benizri EJ, Tovey MG;
WPI: 95-131187/17.
N-PSDB: Q86457.
                                                                                                                                                                                                                                                                                                 23-SEP-1997 (first entry)
Spliced-deleted interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                          W21806 standard;
                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                    Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 340.00
Ratio: 5.075
Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                            ß
                                                                                                                                                                                                                                                                                                                                                                                                                                     A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 AA;
                                                                                                                                            transmembranal IFNAR"
                                                                                                                                                                                                    /label= Extracellular_domain
/note= "comprises amino acid residues 1-413
422-427 of transmembranal IFNAR"
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                /label= Intracell
/note= "comprises
                                                                                                                                                                                                                                                                                                                                        Protein; 496
                                                                                                                                                                                          .496
                                                                                 CO LID
                                                                                                                                                                           Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                      IFNAR.
                                                                                                                                                                                                                                                                                                 alpha-receptor
                                                      Revel M;
                                                                                                                                                                                                                                                                                                                                          ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identity: 100
                                                                                                                                                                acids 481-557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
               interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
```

```
alignment_scores:
Quality:
Ratio:
  seq_name: A_Geneseq_36:R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                 y - UCT-1990; F00758.

20-OCT-1989; FR-013770.

A (CNRS ) CNRS CENT NAT RECH SCI.

I Mogensen KE, Uze G, Lutfalla G, Gresser I;

N-PSDB; 011701.

New human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-240-675-1_COPY_27_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
              New human alpha-interferon receptor protein - useful for testir interferon agonists and in treatment or diagnosis Disclosure; fig 4, 30pp; French.
This recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and discending the testing of IFN agonists and for treatment and discending the testing of IFN agonists and for treatment and discending the testing of IFN agonists and for treatment and discending the testing of IFN agonists and for treatment and discending the testing of IFN agonists and for the testing of IFN agonists and for treatment and discending the testing of IFN agonists and for the testing of IFN agonists and for the testing of IFN agonists and for the testing of IFN agonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (W21806) is characterised by a double deletion when compared to transmembranal IFWAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also T73521) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFWAR splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNs, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, or for diagnostic representations.
                                                                                                                                                                                                                                                       W09105862-A.
                                                                                                                                                                                                                                                                                                                                                                         Human alpha-interferon receptor protein. Human alpha IFN; IFN agonists; antiviral;
  nosis of
                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R11958 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel splice-deleted interferon alpha-receptor (IFNAR) form (W21806) is characterised by a double deletion when compared
                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yProTrpValLeuSerAlaAlaAlaGlyGlyLySAsnLeuLySSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                       targetting.
  viral diseases and tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 340.00
: 5.075
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĄΑ,
                                                                                                                                                                                                                                                                         1. .27
/label=
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from:
                                                                                                                                                                                                                                                                         signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x W21806
IFN agonists and for t
nd tumours. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                      557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ţ0:
                                                                                                                                                                                                                                                                                                                                                                           anti tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 67
: 0
: 100.000
                                                                                                                                                                                                                                                                                                                                                                         agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                    diag-
```

```
Pacity of the tent of the tent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_229 x R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        នួននួនន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: A_Geneseq_36:R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                          FR2657881-A.
09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
Eld P, Gresser I, Lutfalla G
Tovey MG, Uze G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
R14488 standard; Pr
               New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. plastlosure; Page 47; S2pp; French.

The invention covers derivatives of the interferon alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also 014239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q14240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete interferon-alpha/beta receptor.
..FN; autoimmune disease; graft rejection; histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                     91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
      See also
557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
458. .55
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eı= transmembrane
.557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ڻ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                            Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                   'nj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
```

```
alignment_block:
US-09-240-675-1_COPY_27_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID R28496 standard; Pr
 seq_name: A_Geneseq_36:R28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: R14488
                                                             water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune diseases and transplant rejection claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (030533), was incubated with oligos 030534 and 030535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind the transmembrane and cytoplasmic domains.
                                                                                                                                                                                                                                                                                                           17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
EID P, Gresser I, Lutfalla G, Me
IFN in the same way as antibodies so are immunosuppressants e.g. treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids. Sequence 57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                              WPI; 92-382110/46.
N-PSDB; Q30533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                              Tovey M, Uze G;
                                                                                                                                                                                                                                                                                                                                                   17-APR-1991;
17-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 340.00
: 5.075
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                G, Meyer F, Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.000
                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
```

alignment\_scores: Ratio: Percent Similarity:

Quality:

340.00 5.075 100.000

Percent Identity:

100.000

alignment\_block: US-09-240-675-1\_COPY\_27\_229

x R28496

```
alignment_block:
US-09-240-675-1_COPY_27_229 x R42635
                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: A_Geneseq_36:R42635
                                                                                                                                                                                                                                                                                                                                           EP-563487-A.

06-CCT-1993.

1 MAR-1992; 400902.

PA 31-MAR-1992; EP-400902.

PA (EUDI-) LAB EURO BIOTECHNOLOGIE SA.

PA (EUDI-) LAB EURO BOTECHNOLOGIE SA.

PANOIT P, Maguire D, Meyer F, Plavec I, T
                                                                                                                  Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                           Align seg 1/1 to: R42635 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: R28496 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
                                                                                                                                                                                                                                 Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis

Disclosure; Fig 3; 21pp; English.

Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection;

cell proliferation; allograft rejection; systemic lupus erythematosus;

psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;

immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R42635 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ຜ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
               ATGATGGTCGTCCTGGGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
67
                                                                                                                                                                                                           557
                                                                                                                                                                                                           ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .436
/label= extracellular_domain
/note= "soluble, immunogenic form of IFN-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $
                                           ;
0
                                            557
                                                                                                                  : 67
: 0
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                     Tovey
                                                                                                                                                                                                                                                                                                                                                                                      ត្ត
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x R75356
                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                     seq_name: A_Geneseq_36:R75356
                                                                                                                                                                                                                                                                                                                                                                       D 23-MAR-1995.

D 23-MAR-1994; E03114.

F 16-SEP-1994; EP-402279.

R 17-SEP-1993; EP-402279.

A (EUBI-) LAB EURO BIOTECHNOLOGIE SA.

Benizri EJ, Tovey MG;

WRI; 95-131187/17.

R N-PSDB; Q86458.

Compsn. of monoclonal antibodies against interferon receptor reseful as immuno:modulator, eg. for treating AIDS pisclosure; F1g.3A-2B; 105pp; English.

The amino acid sequence of human interferon class I receptor is constant of this receptor (R7123) has been used to raise communomodulatory monoclonal antibodies.

So Sequence 557 AA;
                                                                                                                                                                                                               Align seg 1/1 to: R75356 from: 1 to:
                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R75356 standard; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-1995 (first entry) Human IFN receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09507716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                        17
                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          سو
                                           AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                     CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                  MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                     ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                      yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                            inLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                         : 340.00
: 5.075
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .436
/label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular_domain
                                                                                                                                                                                                                                                                                         Length: 67
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                  557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulator; AIDS
                                                         150
                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                            50
                                                                                        34
                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150
```

A 201

51

ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67

```
seq_name: A_Geneseq_36:W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-240-675-1_COPY_27_229 x W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) pisclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-0CT-1994; 075977.
24-0CT-1993; IL-107378.
(YEDA) YEDA RES 6 DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU9475977-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W21804 standard;
W21804;
                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abramovich C, Ratovitski E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembranal
                                                                                                                                                         101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibit, modulate or modify the activities of intand beta in cells, tissues and organisms, or for
201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interferon alpha-receptor; IFNAR.
                                      51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                    17
                                                           AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                 ProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                             CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                              ATGATGGTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                          AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                   lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95-200634/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon alpha-receptor
                                                                                                                                                                                                                                                                                                                                                                  W21804 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437. .457
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Revel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 67
: 0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferons alpha
for diagnostic
                                                                                                                       50
                                                                                                                                                                                                    34
                                                                                 1289
                                                                                                                                                                                                                                                                                                                                                                    53
```

```
seq_documentation_block:
ID w93941 standard; Prot AC w941 standard; Prot Ac w94
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: A_Geneseq_36:W93941
                                                                                                                                                  seq_name: A_Geneseq_36:W93962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: W93941 from: 1 to: 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-675-1_COPY_27_229 x W93941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1243 rArgGly......SerArgThrTrpLysArgSerGlyArgSerSerS 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1230 AspGlyArgProSerTrp......ProSerAlaArgArgArgCysSe 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein, brx
Claim 1b; Page 58-62; 69pp; English.
This invention describes a novel human breast cancer gene encoding a nuclear receptor-binding auxiliary protein, brx. The brx encoded protein nuclear receptor-binding auxiliary protein, brx. The brx encoded protein has anti-cancer, anti-proliferative and mitogenic activity and acts as a transcription factor and tumour suppressor. Levels of expression of Brx can be detected using the primers, probes and antibodies (contained in the kit) to determine a predisposition to breast and ovarian cancer and other proliferative disorders of immune tissues. Vectors containing the Brx gene can be used for prevention and treatment of cancers and proliferative diseases of mammalian reproductive and immune tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Driggers PH, Rubino DM, WPI; 99-254688/21. N-PSDB; X24044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brx protein; breast cancer; nuclear receptor-binding auxiliary protein; anti-cancer; anti-proliferative; mitogen; transcription factor; human; tumour suppressor; ovarian cancer; proliferative disorder; treatment; immune tissue; prevention; reproductive tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AAAGTAGAGGTCGACATCATAGATGACAACTT.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-SEP-1998; U19782.
23-SEP-1997; US-059621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                 GlnLysGlnLeuGluArgGluGlnGluHis...ValArgArgGluAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....TATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erArgArgAlaHisSerGlnTyrAspLeuGluArgLeuArgAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                          ArgLeuSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.00
1.923
52.703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ħ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Segers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1429
                                              <u>ω</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent
                                                                                                                                                                                                                                              1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
5
41.892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1273
```

```
seq_name: A_Geneseq_36:W52296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: W93962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-240-675-1_COPY_27_229 x W93962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                         22-JAN-1998,
17-JUL-1997; U12455.
17-JUL-1996; US-683743.
(UYME-) UNIV NEW JERSEY.
KOTENKO SV. PESTKA S;
WPI; 98-110590/10.
N-PSDB; V19874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein, brx

protein, brx

Disclosure; Page 29; 69pp; English.

Disclosure; Page 29; 69pp; English.

This invention describes a novel human breast cancer gene encoding a nuclear receptor-binding auxiliary protein, brx. The brx encoded protein nuclear receptor-binding auxiliary protein activity and acts as a transcription factor and tumour suppressor. Levels of expression of Brx transcription factor and tumour suppressor. Levels of expression of Brx transcription factor and tumour suppressor and antibodies (contained in the primers, probes and antibodies (contained in the primers) probes and antibodies containing the
                                                                                                                                                                                                                                                                                                                                                                                                  .documentation_block:
 rejection
Claim 2; Page
This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can be detected using the primers, probes and antibodies (contained the kit) to determine a predisposition to breast and ovarian cancer other proliferative disorders of immune tissues. Vectors containing Brx gene can be used for prevention and treatment of cancers and proliferative diseases of mammalian reproductive and immune tissues. Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1999.
23-SEP-1998; U19782.
23-SEP-1997; US-059621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brx protein; breast cancer; nuclear receptor-binding auxiliary protein; anti-cancer; anti-proliferative; mitogen; transcription factor; human; tumour suppressor; ovarian cancer; proliferative disorder; treatment; timmune tissue; prevention; reproductive tissue; immunogenic.
                                                                                                                                                                                                                                                               CRFB4 protein.

CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection; vaccine; photosensitivity; inflammation; autoimmune disease; septic shock; immune response; organ rejection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Driggers PH, Rubino DM, Segers J; WPI; 99-254688/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9915544-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brx immunogenic peptide
Brx protein; breast cancer; nu
                                                      New recombinant DNA - comprises sequences encoding interleukin-10 and CRFB4 linked to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                              Homo sapiens.
W09802542-A1.
                                                                                                                                                                                                                                                                                                                                                                              W52296 standard; Protein; 325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RUBI/) RUBINO D M. (SEGE/) SEGERS J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DRIG/) DRIGGERS P H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1999
                                                                                                                                                                                                                                                                                                                                             23-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 CATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rArgGly.....SerArgThrTrpLysArgSerGlyArgSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGlyArgProSerTrp.....ProSerAlaArgArgArgCysSe 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.00
3.263
57.576
     79pp: Eng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to:
English.
uman CRFB4 sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30
 DNA encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
2
54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
     is used
     'n
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x W52296
     seq_name: A_Geneseq_36:W07702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc encoding the interleukin-10 (IL-10) receptor (III0R) and a sequence (S2) cencoding the interleukin-10 (IL-10) receptor (III0R) and a sequences. CC cells containing (I) may be used to identify agonists/antagonist of CIL-10. Agonists are potentially useful, e.g. for preventing allograft crejection, as vaccine adjuvants, for treatment of photosensitivity, and inflammation, autoimmune disease and septic shock, while antagonists are contentially useful for increasing immune responses against tumours, viruses, bacteria and parasites (especially intracellular pathogens) and control or preventing organ rejection. A vector containing (I) is used to crestore, e.g. by gene therapy, II-10 sensitivity to a cell that expresses a dysunctional III0R and is able to bind II-10 but not to transduce a control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: W52296
                                                                                                                           12-DEC-1996:
04-JUN-1996;
05-JUN-1995;
Sgouras D N;
WPI; 97-043139/04.
N-PSDB; T47200.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse ETS2 repressor factor ETS2 repressor factor; ERF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W07702 standard; W07702;
                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
Athanasiou MA, Beal GJ, Blair DG, Fisher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant DNA (I) of the invention. (I) comprises a sequence
                                                                                                                                                                                                          WO9639517-A1.
                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                    tumour suppressor; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>წ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATTCGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // ymetValProProProGluAsnValArgmetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrAlaGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 AA;
                                                                                                                              U10177.
US-469412.
                                                                                                                                                                                                                            21. 98
/label= DNA_binding_domain
/note= "ets-like DNA binding domain"
466. 525
/label= Active_repressor_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.50
1.922
59.259
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 54
Gaps: 1
Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; oncoprotein; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                            transcriptional repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ERF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                              광
,
                                                                              Mavrothalassitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                ဌ
```

```
alignment_block:
US-09-240-675-1_COPY_27_229/rev x W07702
                                                                                                                                                                                                     Align seg 1/1 to: W07702 from: 1 to: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding ETS2 repressor factor - useful for reducing tumourigenicity, esp. oncogene associated tumour cells Disclosure; Page 70-72; 101pp; English.

Murine ETS2 repressor factor (ERF) (M07702) is a member of the ETS (family and acts as a transcriptional repressor in mammalian cells. (Its amino acid sequence was deduced from the murine ERF gene (C (T47198). Human ERF (see also W07700) has also been identified. (C ERF has tumour suppressor activity. Chimeric molecules comprising the ERF repressor domain in combination with a heterologous tumourigenicity associated with inappropriate expression of transcription factors.
32 AGGGTCGTCGCCCCAGGAGGA 11
|||:::::: |||||||||
383 aGlyGluLysalaProGlyGly 390
                                                                                                61.00
3.389
75.000
                                                                                                                                                                                                                                                                                                                          Length: 24
Gaps: 0
Percent Identity: 45.833
```

+

52.00 52.00 8

.36 30.

```
Database: Issued_Patents_AA:*
Database sequences: 145308
Database length: 14437401
Search time (sec): 65.150000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search information block:
Query: US-09-240-675-1_COPY_27_229
Query length: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: May 31, 2000 7:06 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_n2p.model -DEV-xlp
-Q-/Cgn2_1/USPTO_spool/US09240675/runat_30052000_164312_24612/app_query.fasta.1
-DB-Issued_Patents_AA -QFMT-fastan -SUFFIX-modif.rai
-GRPOP-12_000 -GRPEXT-4_000 -MINMATCH-0.100 -LOOPCL-0.000
-LOOPEXT-0.000 -QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000
-XGAPEXT-0.500 -FGRPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELATEXT-7.000 -START-1
-MATRIX-blosum62 -TRANS-buman40.cdi -LIST-45 -DOCALIGN-200
-THR_SCORE-pct -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext
-MINLEN-0 -MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO_XLPXY -WAIT -THREADS-1
                                                      jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-471-869-2 - 56.50 104.08 12.16 172-6
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-673-269-2 - 55.50 104.08 12.16 173-6
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-673-269-2 - 55.50 110.69 10.32 178
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-40-845D-2 - 55.00 115.64 13.30 264
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-440-845D-2 + 55.00 115.64 13.30 264
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-440-845D-2 + 55.00 112.05 14.56 38-2
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-671-978A-10 + 55.00 107.04 16.51 64
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-671-978A-10 + 55.00 107.04 16.51 64
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-671-978A-10 + 55.00 107.04 16.51 18.07
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-3 - 55.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-442-852-4 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-842-859-4 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-942-859-4 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-14 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-14 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-14 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-8 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-8 + 54.00 104.70 22.57 632
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-8 + 53.50 84.32 42.82 45.50
jn2_6/ptodata/1/iaa/S_COMB.pep:US-08-804-227C-8 + 53.50 101.56 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 678 31.48 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-240-675-1_COPY_27_229 to: Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \text{Ptodata/1/laa/SB_COMB.pep:US-08-307-588-4+} 3. \text{Ptodata/1/laa/BCCUMB.pep:PCT-US94-1427-3} \text{Ptodata/1/laa/BCCUMB.pep:PCT-US94-1427-3} \text{Ptodata/1/laa/SB_COMB.pep:US-08-683-74-4+} \text{Ptodata/1/laa/SB_COMB.pep:US-08-459-412A-7} \text{Ptodata/1/laa/SB_COMB.pep:US-08-317-310A-64-} \text{Ptodata/1/laa/SB_COMB.pep:US-08-323-170B-2+} \text{Ptodata/1/laa/SB_COMB.pep:US-08-252-626A-2+} \text{Ptodata/1/laa/SB_COMB.pep:US-08-505-218-4+} \text{Ptodata/1/laa/SB_COMB.pep:US-08-505-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'ptodata/1/1aa/5A_COMB.pep:US-08-095-734-2 -
'ptodata/1/1aa/5B_COMB.pep:US-08-444-623-2 -
'ptodata/1/1aa/6_COMB.pep:US-08-471-869-2 -
726-306A-152 + 52.
726-306A-152 + 52.50 104
701A-2 - 52.50 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EScore Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LI + 340.00
2 + 340.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.50 12
61.00 1
59.00 1
58.00 1
57.50 115
56.50 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129.61 1.80
0 123.02
00 114.78 2.97
00 101.47 6.89
0 119.10 7.14
119.10 6.40
104.08 12.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4e-38
1.4e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     us-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/1aa/6_COMB.pep:US-09-003-708A-6 +
/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-552-142A-9
/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-910-973-9 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11,
Patent No. 5
                           101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US95-05741-9
                                                                                                                                                             Align seg 1/1 to: US-08-328-256-11 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/328, FILING DATE: 24-OCT-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: IL 107378 FILING DATE: 24-OCT-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, ROGER L. REGISTRATION NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                      CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                            ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 Seventh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABRAMOVICH, Carolin RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVEL, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BROWDY AND NEIMARK
9 Seventh Street, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ication US/08328256
                                                                                                                                                                                                                                                               : 340.00
: 5.075
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/328,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carolina
                                                                                                                                                                                                                                                             Length: 67
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                               434
                                                                            17
ω
4
                                      100
                                                                                                                     50
```

34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn

```
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-2
                                                                           alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-307-588-2
                                                                                                                                                                                                                                   ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-307-588-2
                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                               Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                  Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence
                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-539
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25 (EPO).
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 05-DEC-1994
NIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
1 ATGATGGTCGTCCTCCTGGGCGCGCGACCCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08307588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Foley & Lardner
                                                                                                                                                                                                                                                                                                    436 amino acids
                                                                                                                                                                                                                                                                                                                                                      (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEYER, Francois
MAGUIRE, Deborah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLAVEC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BENOIT, Patrick
                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/307,588
                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                   Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                         17283/117/GUPL
                                                                                                                                                                      Length:
                                                                                                                                      100.000
                                                                                                                                                      67
                   50
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12
                                                                                                    alignment_scores:
Quality:
                                                                                                                                                                                 ; MOLECULE TYPE: US-08-328-256-12
                                                                                                                                                                                                                                                        TELEFAX: 2047...
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 496 amino acids
                                                          Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g_documentation_block:
Sequence 12, Applicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION UNMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ABRAMOVICH, Carolina APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-01-
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVEL, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                 REVEL-13
3ER: 25,618
                                                                                                                                                                                                                                                                                                                       12:
                                                                Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suite 300
                                                                    100.000
                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
```

```
; MOLECULE TYPE: US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10
                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-328-256-12 from: 1
                                                                                                                                                                                                       TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PROOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY_AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SOLUBLE INTERFEITTLE OF INVENTION: PREPARATION AND NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 25
ELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, Roger L
REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20004
                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABRAMOVICH, Carolina RATOVITSKI, Edward
                                                                                                                                                                                                                                              202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVEL, Michel
                                                                                                               linear
                                                                                            protein
 340.00
                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLUBLE INTERFERON ALPHA-RECEPTOR, PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                       REVEL-13
                                                                                                                                                                                                         10:
                                                                                                                                                                                                                                                                                                     25,618
Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496
 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
```

```
seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-675-1_COPY_27_229 x US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,454
                  INFORMATION FOR
                                                                                                                                APPLICATION NUMBER: US 07/
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 A 201
                                                                                           REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl 17
                                                   TELEFAX:
                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                     LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Application US/08471454
5731169
200797 NIXN UR N FOR SEQ ID NO: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UZE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUTFALLA,
                                                                            (703) 816-4000
                                                                                                                                                                                                 UMBER: FR 89/13770
20-OCT-1989
                                                                                                                                                                                                                                                                                                                   06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilles
                                                      816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROPREPARATION OF THE CORRESPONDING PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Georges
                                                                                                                                                                                                                                                         US 07/900,642
                                                                                                                                  32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
```

FOR THE

LENGTH:

amino acids

amino acid

ATTORNEY/AGENT INFORMATION:

```
; STRANDEDNESS:
; TOPOLOGY: lin;
; MOLECULE TYPE: ]
US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
; Sequence 2, Application
; Patent No. 5861258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-240-675-1_COPY_27_229 x US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
FILING LALL
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
APPLICATION NUMBER: FR 89/13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 s 67
                                                                                                                                                                                                                                                                                                     STREET: 1100 NOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Application US/08466974
5861258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOGENSEN, Knud E. UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUTFALLA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340.00
5.075
                                                                                                                                                                                                                                                                                                                                                                                                         CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georges
                                                                                                                                             US/08/466,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-466-974-2 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 816-410
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICANT: MOGENSEN, K
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, G
APPLICANT: GRESSER, IC
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatii
OPERATING SYSTEM: PC-DOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 A 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                 CITY: ARLINGTON STATE: VIRGINIA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 CCCATGGGTGTTGTCCGCAGCCGCAGCTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGATGGTCGTCCTGGGCGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                  STREET:
                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                    2, Application US/08471453
5. 5886153
                                                                                                                                                                  E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THOMAS E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                        Gilles
                                                                                                                                                                                                                                                  CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                  Georges
                                                                                                                                                                                                                                                                                                                                                                           Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 67
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-471-453-2
                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-471-453-2 from: 1
                                                                                                                                                        Sequence 4
Patent No.
APPLICANT: BENOIT, PATTICK
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL
TITLE OF INVENTION: INTERFERO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/
FILING DATE: 20-OCT-1989
ATTORNEY, AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200797 NIXN UR INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                             201 A 201
                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                              101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                             67 s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 06-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 100
                                                                                                                                                                                                                                                                                                                                                              AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                        4, Application US/08307588
5. 5919453
                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (703) 816-4000
(703) 816-4100
                                                                                                                    BENOIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: FR 89/13770
20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                 MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE
   INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/471,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 67
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :
                                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
```

```
seq_documentation_block:
; Sequence 3, Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: US-08-307-588-4
                                                                                                        seq_name: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-240-675-1_COPY_27_229 x US-08-307-588-4
                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-5399 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 201 A 201
                                                                                                                                                                                                                                                      151 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                             101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: 20007
                                                                                                                                               67
                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                                             17 yProTrpValLeuSerAlaAlaAlaGlyGlyLySAsnLeuLySSerProG
                                                                                                                                                                                                                                                                                                                                                                                                   51 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/307,588 FILING DATE: 05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SAXE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    s 67
                                                                                                                                                                                                                     ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                        lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Foley & Lardner
3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           557 amino acids
Aguet, Michel
Bohni, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: EP 92400902.0
31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17283/117/GUPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             557
                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                           150
                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
```

CORRESPONDENCE ADDRESS:

OF SEQUENCES:

ADDRESSEE:

SSEE: Genentech, Inc. T: 460 Point San Bruno Blvd South San Francisco

California

TITLE OF INVENTION: Receptor Subunit Polypeptides

Hemmi, Silvio

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-683-743-4
                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1_COPY_27_229 x PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                   Patent No.
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 5.25 inch, 360 Kb COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-TOS/MS-DOS SOFTWARE: PATIN (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                     182 TTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                      APPLICANT: Pestka, Sidney
APPLICANT: Kotenko, Serguei
TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TITLE OF INVENTION: CHAIN
                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415/952-98
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluAsnLeuLysProProGluAsnIleAsp***TyrIleIleAspAspAs 17
                                                                                                                                                                                                                                                                                           heSerAlaGluTyrArg 39
                                                                                                                                                                                                                                                                                                                                                                              nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 181
                                                                                                                                               INFORMATION:
                                                                                                                                                                     4, Application US/08683743
5. 5843697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112.00
3.613
79.487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 48.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
```

```
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-469-412A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-683-743-4
                                                                                                                                                                                                seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-683-743-4 from: 1 to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1_COPY_27_229 x US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: I
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
NAME: Jackson MUMBER: 26,742
REGISTRATION NUMBER: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                          cent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                   184 TCATTCGATTAT 195
                                                                                                                                                                                                                                                                                                                                                                                                  134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                          53 ThrAlaGlnTyr 56
                                                                                                                                                                                                                                                                                                                                                         36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                       19 yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT...... 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:

    Application US/08469412A
    5856125

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Jersey
  INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201-343-1684
                                                                                            Blair, Donald G
                                     Athanasiou, Meropi A.
                                                         Beal Jr., Gregory J
                                                                            Fisher, Robert
                                                                                                                   Mavrothalassitis, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.50
1.922
59.259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
Dionyssios N. The ERF Genetic Locus and Its Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/683,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 54
Gaps: 1
Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601-1-050
```

CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor

San Francisco : California UMBER OF SEQUENCES:

```
seq_documentation_block:
    Sequence 64, Application
                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:US-08-317-310A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-469-412A-7 from: 1 to: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1_COPY_27_229/rev x US-08-469-412A-7
                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                       APPLICANT: WHITE, MORRIS F.
APPLICANT: SUN, XIAO JIAN
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             367 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 383
                                                                                                                                                                                                                                                                                                                                        383 aGlyGluLysAlaProGlyGly 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein LOCATION: 1.543 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Garrett-Wackowski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                     32 AGGGTCGTCGCCCCAGGAGGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 TTCCACCTGCGGCTGCGGACAACACCCCATGGGCCCACGGCGACGAGCACT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 05 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/469,412A FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94111-3834
                                                                                                                                                                                                       4, Application US/08317310A
5858701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 543 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                       LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.00
3.389
75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "murine ERF amino acid sequence
(first 8 amino acids from first exon not
included)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 24
Gaps: 0
Percent Identity: 45.833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
```

```
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-317-310A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_27_229/rev x US-08-317-310A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-323-170B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-317-310A-64 from: 1 to: 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08323170B Patent No. 5733772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: LOUIS MYGETS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1045 oThrAlaGlySerSerMet.SerSerGluProGly 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 1045
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM CO-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Cloning and Expression of Plasmodium
TITLE OF INVENTION: faliciparum Transmission-Blocking Target Antigen, Pfs230
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCC 49
APPLICATION NUMBER: US/08/323,170B FILING DATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                     94111-3834
                                                                                                                                                                                                                                                    San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                       Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617)227-5941
                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Williamson, Kim C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.00
2.652
79.310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/317,310A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JDP-022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
1
51.724
```

ICATION NUMBER:

US 08/010,409

```
alignment_block:
_us-09-240-673-1_COPY_27_229 x us-08-323-170B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-323-170B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-252-626A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                836 Lys 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 AAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 GGAGCGATGAGTCTGTCGGGAAT...GTGACTTTTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803 rCysPheGlu...GluMetIleProTyrAsnLysGluIleLysTrpAsnL 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 AAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACA 151
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Graham, Douglas K. APPLICANT: Dawson, Thomas L.
                      CURRENT APPLICATION DATA:
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ISOLATED DNA ITTLE OF INVENTION: Protooncogene NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 TCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCCTCA 101
                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                            STREET: P.O. Dra
CITY: Charlotte
STATE: No. 5585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                     COUNTRY:
APPLICATION NUMBER: US/08/252,626A
                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysGluAsnLysSerLeuGlyAsnLeuValAsnAsnSerValValTyrAsn 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGlyAspIleGlyGlyIleLeuPheProLysAsnIleLysSerThrTh 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                 28234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08252626A
                                                                                                                                                                                                                                     P.O. Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3135 amino acids
                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                  Mullaney, David L.
Snodgrass, Hiram R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Earp, Henry S
                                                                                                                                                                                                                                                            Kenneth D. Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 576-0200
                                                                                                                                                                                          5585269th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.00
1.844
62.745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jonathan
                                                                                                                                                                                                                                                                                                                                             Isolated DNA Encoding C-MER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-41,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 37.255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  015280-113100US
                                        Version #1.30
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x US-08-252-626A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-505-218-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-252-626A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-252-626A-2 from: 1 to: 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equence 4, Application US/08505218 stent No. 5914447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 54/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/505,218
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 TCCTGAGGTGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 lAlaProLeuAsnValThrValPheLeuAsnGluSerSerAspAsnValA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AlaValSerProTrpIleLeuAlaSerThrThrGluGlyAlaProSerVa 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 999 amino acids s
ATTORNEY/AGENT INFORMATION: NAME: KRAUS, ERIC J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 spileArgTrp 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                           UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 ATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT.....GACAACTTTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 GCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION:
                                         APPLICATION NUMBER: US/0 FILING DATE: 03-NOV-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                COUNTRY: UZIP: 22314
                                                                                                                                                                                                                                                                     STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                         : 99 Canal
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sibley, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57510
                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (919) 881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOURAS, ARMAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARAYA,
                                                                                                                                                                                                                                                                                                                               LOWE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.00
2.417
64.865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALEJANDRO
                                                                                                                                                                                                                                                                                                            PRICE, LEBLANC & BECKER Center Plaza, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                            TRANSGENIC PLANTS INCLUDING A HYBRID NUCLEIC ACID SEQUENCE, COMPRISING AN UNEDITED MITOCHOUDRIAL GENE FRAGMENT FROM HIGHER PLANTS AND PROCESS FOR PRODUCING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 35.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5470-81
```

```
pir2:T14516
pir2:D75627
pir2:I38547
pir2:T05823
pir2:T24003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pir2:842701
pir2:T02955
pir2:T29518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pir2:S27387
pir2:A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search information block:
Query: US-99-240-675-1_COPY_27_229
Query length: 203
Database: PIR_63:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database sequences: 168808
Database length: 58629743
Search time (sec): 85.570000
                                                                                                                                                                                                                                                                                                                                                                                                                                                piri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM of:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pir2:A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pir2:A2639:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p1r2:A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p1r2:JQ0405
p1r2:S42718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pir2:A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MODEL-frame+_np_model -DEV=xlp
-MODEL-frame+_np_model -DEV=xlp
-Q-/cgn2_1/USPTQ_spool/US09240675/runat_30052000_164312_24623/app_query.fasta.1
-DB=PIR_63 -QFMT=fastan -SUFFIX-model:rpr -GAPOP=12.000
-GAPEXT=4.000 -MINARCH-0.100 -LOOPCL-0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=45 -DCCALION=200 -THR_SCORE=pct
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09240675 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THREADS-1
                                                                                                                                                                2:A38845
2:A64336
                                                                                                                                                                                                                                                                                                                   2:JQ1733
2:S42281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2:I46480
2:I46479
2:F72653
                                                                                                                                                                                                                                                                                                                                                                                                                        :A44831
                                                                                                                                                                                                                                                                                                                                                                     : $24169
                                                                                                                                                                                                                                                                                                                                                                                              : A42634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :149276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :T08930
                                                                                                                                        : $08459
                                                                                                                                                                                                                                                                     :T25131
                                                                                                                                                                                                                                                                                        S26402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : $11143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :T25677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jun 1, 2000 12:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-240-675-1_COPY_27_229 to: PIR_63:*
        3 Orlg 209 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000 198 000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464.26
438.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2Score
768.68
        144.8.76
1224.61
1224.61
1224.87
1227.53
1227.53
1227.53
1227.53
1227.53
1227.53
1227.53
1227.53
1221.31
1221.31
1221.31
1221.31
1221.31
1221.31
1221.31
1221.31
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
1231.30
        ESCORE Len ! 1.16-35 557 9.96-19 560 2.66-17 590 2.66-17 590 2.66-17 590 2.73 1.40 6.67 1.75 8.27 1.10 6.67 1.75 8.27 1.10 6.67 1.75 8.3 3.40 1.75 8.3 3.40 1.9 7.7 1.01 2.42 4.10 1.75 8.27 1.01 2.42 4.10 1.75 8.3 3.40 2.21 1.01 2.42 4.10 1.75 8.3 3.40 2.21 1.01 2.42 4.10 1.75 8.3 3.40 2.21 1.01 2.42 4.10 1.75 8.3 3.40 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.21 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2.40 4.45 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha/beta receptor interferon alpha receptor type interferon alpha/beta receptor hypothetical protein F23M16.40 trp3 protein - rat hypothetical protein f05C5B.0 i hypothetical 119 5K protein (ulnuclear pore complex protein rhypothetical protein respectively phospholipase C (EC 3.1.4.3) phospholipase C (EC 3.1.4.3)
flagellar protein required for hypothetical protein MJ0288 · whypothetical protein 2 · spirop S-locus-specific glycoprotein S potassium-transporting ATPase, novel cellular protein TSL8.180 hypothetical protein R07B5.3 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable cytochrome P450 monoox
hypothetical protein T25F10.2 -
c-mer tyrosine kinase receptor
calcium channel BI-2 - rabbit
calcium channel BI-2 - rabbit
calcium channel BI-2 - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Documentation
                                                                                                                                                                                                        self-incompatibility locus glyd s-locus glycoprotein type II printed the process of the printed protein type II printed the protein type II printed the protein T22H2.2 - 1 transmission blocking target a DNA-directed RNA polymerase alp
                                                                                                                                                                                                                                                                                                                                                   splicing factor SC35 - human mucin - rat
                                                                                                                                                                                                                                                                                                                                                                                                                   class I histocompatibility ant phosphoenolpyruvate carboxylas PR264/SC35 protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine receptor family II, me
cytokine receptor family class
hypothetical protein F08D12.9 -
PR264 protein - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pir1:PWWT6
pir2:JC2100
pir2:A69763
pir2:T34338
  seq_documentation_block:
interferon alpha receptor
                                                                          seq_name: pir2:S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-557 <UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:A32694
                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                     151
                                                                                                                                     67
                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                           3
4
                                                                                                                                                                                  A 201
                                                                                                                                     s 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ი</u>
```

```
A;Gene: GDB:IFNAR1; IFNAR; IFRC
A;Cross-references: GDB:120078; OMIM:107450
A;Cross-references: GDB:120078; OMIM:107450
A;Cross-references: GDB:120078; OMIM:107450
A;Map position: 21q22.1-21q22.1
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
A;Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C;Keywords: cytokine receptor; 9jycoprotein; transmembrane protein
C;Keywords: cytokine receptor; 9jycoprotein; transmembrane fatatus predicted <TRN1>
F;437-455/Domain: transmembrane fatatus predicted <TRN2>
F;50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydra*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon alpha/Deta receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 **sequence_revision 22-Jun-1990 **text_change 22-Oct-1999
C;Accession: A32694; S17112
R;Uze, G; Lutfalla, G; Gresser, I.
Cell 60, 225-234, 1990
A;Title: Genetic transfer of a functional human interferon alpha receptor into mou:
A;Reference number: A32694; MUID:90124632
A;Accession: A32694; MUID:90124632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1991
A;Description: The structuree of the human interferon alpha/beta receptor gene.
A;Reference number: S17112
A;Accession: S17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality: 340.00
Ratio: 5.075
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-16,'A',18-329,'V',343-557 <LUT>
A;Cross-references: EMBL:X60459; NID:g32671
                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-240-675-1_COPY_27_229 x A32694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914
                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: A32694 from: 1 to: 557
                                                                                                                                         101 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                 57.50
57.50
57.50
57.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
115
114
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.04
39.04
39.48
39.62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 67
: 0
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386
386
454
478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H+-transporting ATP synth
H+-transporting ATP synth
homoserine dehydrogenase I
hypothetical protein M03D
       67
                                                                                            50
                                                                                                                                         150
                                                                                                                                                                                      34
                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                17
```

type 1 precursor -

```
interferon alpha/beta receptor - mouse (Species: Nus musculus (house mouse) C; Species: Nus musculus (house mouse) C; Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C; Accession: A45283; 148423; 148424; 148425; 148426; 148427; 148428; 148429 R; Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A; Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A; Reference number: A45283; MUID:92262522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: lung
A; Experimental source: lung
C; Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: interferon alpha receptor type 1 #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; A;Experimental source: MDBK cells R;Lim, J.K.; Langer, J.A. Blochim. Biophys. Acta 1173, 314-$19, 1993 A;Title: Cloning and characterization of a bovine alpha inte A;Reference number: S33770; MUID:93305725 A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Specific antiviral activities of A; Reference number: S27387; MUID:93076908 A; Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S27387; S33770
R;Mouchel-Vielh, E: Luffalla, G: Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mrNA
A;Residues: 1-421,'V',423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-240-675-1_COPY_27_229 x S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
                                        A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-590 <UZE>
A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:102354,
R;Lutfalla, G; Uze, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: S27387 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
: Uze,
1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209.00
3.800
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 65
Gaps: 2
Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the human alpha interferons are determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID: 9432
                                                                       PID: g194112
NCBIP: 102357)
                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at
```

```
A; Molecule type:
A; Residues: 118-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: I48423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
us-09-240-675-1_copy_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 177/3; 331/1
C;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 426-445 < RE6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DN
A; Residues: 127-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-
A;Reference number: I48423; MUID:95047447
seq_documentation_block:
hypothetical protein F23K16.
                                                              seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 265-375 <RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I48426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                            154
                                                                                                                                                                                                                             104 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                      34
                                                                                                        51
                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                             54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                      snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                      AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                                                                                              ATGGTCGTCCTGCGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCC
                                                                                                   HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg
                                                                                                                                                                                                                                                                                                                                                        MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                              pir2:T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                        to: A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: U06238; NID: g497104; PIDN: AAC01749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: U06237; NID: g497103; PIDN: AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <RE7>
EMBL:U06244; NID:g497114; PIDN:AAA65008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198.00
3.536
86.154
    .40
                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Gaps:
Percent Identity:
  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                           590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
0
55.385
                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŗ
                                                                                                                                                                                                                               153
                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID:g755810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g510265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: g510262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g755813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID: 9755811
```

```
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C;Accession: T09357
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16652
A;Accession: T09357
                                                                                                                                                                                             A;Experimental source: brain C;Comment: This protein participates in store-operated Ca2+ entry into cells. C;Superfamily: TRPC3 protein
                                                                                                                                                                                                                                                                                                                                                   A;Title: Expression and characterization of a trpl homolog from rat. A;Reference number: JC5807; MUID:98042538
A;Accession: JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trp3 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
C;Accession: JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-304 <BEV>
A;Residues: 1-304 <BEV>
A;Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.40
A;Experimental source: Cultivar Columbia; BAC clone F23K16
C;Genetics:
                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-828 < PRE>
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, Biochem. Biophys. Res. Commun. 240, 167-172, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_229 x T09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 4
A; Introns: 129/2; 243/2
alignment_block:
                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: ATSP:F23K16.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: T09357 from: 1 to: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 lnLysVal 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 ThrArgArgLysValArgGluProArgPheCysPheLysThrLeuSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 nThrAlaSerLeuGlyValValSerSerLeuLysMetLysLys.LeuLys 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AsnGlyArgHisHisHisHisAspThrProSerArgHisAspLysHisAs 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 TCTCCTCAAAAAGTA.....GA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTCTGTC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uValAspValLeuAspAspGlyTyr....ArgTrpArgLysTyrGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ....GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAA 93
                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.00
1.775
57.143
                                                 71.00
1.614
60.274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
Gaps: 4
Percent Identity: 32.857
                            Percent Identity: 34.247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                       seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-240-675-1_COPY_27_229 x JC5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pir2:T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: JC5807
```

```
C;Genetics:
A;Gene: CESP:Y105C5B.o
A;Introns: 13/1; 56/3; 155/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, September 1999
A;Reference number: Z20208
A;Accession: T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y105C5B.o - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_229 x T26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL110479; NID:e1542153; PIDN:CAB54363.1; CESP:Y105C5B.o A;Experimental source: clone Y105C5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-194 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: T26391 from: 1 to: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 l...IleAspTyrProLys 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 rTrpIleAlaProCysSerArgLeuGlyLysIleLeuArgSerProPheM 371
                              160 GAGTCTGTCGGGAATGTG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 AsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIleThrVa 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 etLysPheValAlaAlaSerPheIleIlePheLeuGlyLeuLeuValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 LeuValValLeuValValAlaLeuAlaLeuProPheLeuAlaIleGlyTy 354
                                                                                                                                                                       110 AGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGAT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 TTCATTCGATTATCAAAAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 ..CAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG 147
                                                                                                                                                                                                                                                                                                                                                                                   10 GTCCTCCTGGGCCCGACGACCCTAGTGCTCGTCGCCCGTGGGCCCATGGGT :::|||||||
                                                                                                                                                                                                                                                                                          60 GTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCT....
                                                                                                                                                                                                                                                                                                                                                    1 MetLeuLeuArgAlaIleLeuLeuIlePheIleSer...AlaProTrpVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ATGGTCGTCCTCGGGGGGGGGGACGACCCTAGTGCTCGTCGCCGTGGGCCC
GluGlnValAlaAsnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAGGAGCGATGAGTCTGTCGGG......AATGTGACTTT 182
                                                                                                                isIleAsnLeuLeu.....AsnGlyIleArgGlnLysAsnAlaIleAsp
                                                                                                                                                                                                                                 lLeuSerValThrValLysArgAsnMetThrGluTyrGluGlnLysIleH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.50
1.756
69.643
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56
2
32.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
```

```
seq_documentation_block:
hypothetical 119.5K protein
N;Alternate names: ORF 1 protein
C;Species: Micrococcus luteus, Micrococcus lysodeikticus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
C;Accession: JQ0405
R;Shiota, S; Nakayama, H.
Wol. Genet. 217, 332-340, 1989
A;Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: identification A;Reference number: S04781; MUID:89364717
A;Accession: JQ0405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S42718; S37477

R;McMorrow, I.; Bastos, R.; Horton, H.; Burke, B.
Blochim. Blophys. Acta 1217, 219-223, 1994

A;Title: Sequence analysis of a cDNA encoding a human nuclear
A;Reference number: S42718; MUID:94154002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-1106 <SHI>
A;Cross references: EMBL:X15867
A;Note: all the codons between two in-frame stop codons are translated; the translation:
A;Note: the gene encoding this protein overlaps uvrA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_229/rev x JQ0405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                           alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1475 <MCM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S42718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuclear pore complex protein nup153 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:S42718
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z25535; NID:g406224; PIDN:CAA80982.1; PID:g406225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: JQ0405 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                           Align seg 1/1 to: S42718 from: 1 to: 1475
                                                                                                                                 US-09-240-675-1_COPY_27_229/rev x S42718
                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 TCACATTCCCGACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTG 129
                            167 ACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTGTCATCTATGAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 TCATCTATGATGTCGACCTCTACTTTTTGAGGAGATTTTAGATTTTTTCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....CysProProLeuCysTrpProArgAlaGlnGluLeuLeuH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGAGGACGACCA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isHisArgLeuLeuArgArgArgGlyProArgArgArgProArgLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerProThrGlyGluThrProValSerCysPro........... 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProArgArgAlaLeuGlyArgAlaGlyProHisArgArgPro 91
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.00
2.233
46.154
                                                                                                                                                                                                               65.00
2.167
58.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 65
Gaps: 2
Percent Identity: 32.308
                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1106
39.216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complex protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hnu
```

```
seq_documentation_block:
hypothetical protein 715N24.90 - Arabidopsis thaliana
hypothetical protein 715N24.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C:Accession: T08930
                                                                                                               seq_documentation_block:
comC-alpha protein - phage T4
N,AHCratte names: gp comC alpha
C:Species: phage T4
A:Note: host Escherichia coli
C:Date: 03-May-1994 *sequence_revision 03-May-1994 *text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T08930
R;Beven, M.; Zimmermann, W.; Gruenelsen, A.; Wambutt, R.; Bancroft, I.; Mewes, submitted to the Protein Sequence Database, May 1999
A;Reference number: 216518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-571 <BEV>
A;Residues: 1-571 <BEV>
A;Cross-references: EMBL;AL078465; GSPDB;GN00062; ATSP:T15N24.90
A;Experimental source: cultivar Columbia; BAC clone T15N24
                            C:Accession: A45731
R:Sanson, B.; Uzan, M.
J. Bacteriol. 174, 6539-6547, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: pir2:T08930
                                                                                                                                                                                                                                                                                                                             seq_name: pir2:A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4
A;Introns: 76/3; 90/3; 142/3; 311/1; 363/2; 415/2
A;Title: Sequence and characterization of the bacteriophage T4 comCalpha gene produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T08930 from: 1 to: 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1_COPY_27_229 x T08930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Gene: ATSP:T15N24.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1298 Ser 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1281 erAsnAsnThrThrThrSerGlyPheGlyPheGlyAlaThrThrThrSer 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1264 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1248 ThrSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThrSe 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 GTCGACCTCTACTTTTTGAGGAGATTTTAGATTTTTTCCACCTGCGGCTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 GAACAGGAGCGATGAGTCTGTC.....GGGAAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 ProAspAspAspAspProPheSerLysArgArgArgMetGluGlyAlaMe 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CGGACAACACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTG 146
                                                                                                                                                                                                                                                                                                                                                                                             pargLysTyrGlyGlnLysValValargGlyAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnThrLeuSer.GluValAspIleLeuAspAspGlyTyr....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tGluIleThrProLeuValLysProIleArgGluProArgValValValG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....GTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.00
1.750
58.065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....CATGGGCCCACGGCGACGAGC 36
                                                                                                                                                                                                                                                                                                                                                                                                   411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 62
: 4
: 33.871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
```

08-Oct-1999

```
C;Accession: 154418
R;Sood, A.K.; Pan, J; Biro, P.A.; Pereira, D; Srivastava, R.; Reddy, V.B.; Immunogenetics 22, 101-121, 1985
A;Title: Structure and polymorphism of class I MHC antigen mRNA.
A;Reference number: 154418; MUID:85287366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5.848-6.274
C;Superfamily: phage T4 comC-alpha protein
C;Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M89919;
C;Genetics:
A;Gene: comC alpha
                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_27_229 x I54418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M16102; NID:g187693; PIDN:AAA59622.1; PID:g307217 C;Superfamily: class I histocompatibility antigen; immunoglobulin homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sepiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-141 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A45731;
A; Accession: A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-361 <SOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: I54418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: pir2:154418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: A45731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-240-675-1_COPY_27_229 x A45731
                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 ACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCT 165
           94
                                                                                                                                       54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 sArgCysAlaGlyGly.....A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 CGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 CTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTC
                                                                       oTrpLeuThrGluThrTrpAlaGlySerHisSerMetArgTyrPheTyrT 33
                                                                                                                                                                                                                                                                                             ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splieLeuAspGluAsnPheIle.....TrpLeuSerThrAsnGluAla
                                                                                                                                                                                                                      MetLeuValMetAlaProArgThrValLeuLeuLeuLeuSer...GlyPr 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                histocompatibility antigen HLA-B7 alpha chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                 to: I54418 from: 1 to: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.50
1.645
62.295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.50
2.155
58.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUID: 93015705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 61
Gaps: 2
Percent Identity: 24.590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 3
Percent Identity: 34.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g215829; PIDN:AAA32485.1; PID:g215832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -š
   TCTCCTCAAAAAGTAGAGGTCGAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duceman, B
                                                                                                                                                                                                                                                                                                                        cytokine receptor family II, CySpecies: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence C;Accession: G01418 R;Lutfalla, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Pseudomonas aeruginosa
C;Date: 08 Mar-1989 #sequence_revision 08-Mar-1989 #text_change
C;Patcession: A26391
R;Pritchard, A.E.; Vasil, M.L.
J. Bacteriol. 167, 291-298, 1986
A;Title: Nucleotide sequence and expression of a phosphate-regul.
A;Reference number: A26391; MUID:86250607
A;Accession: A26391
A;Rocession: A26391
A;Residues: 1-730 <PRI>A;Residues: 1-730 <PRI
A;Residues: 1
A;Cross-references: EMBL;U08988; NID:g571295; PID:g571296
C;Genetics:
A;Gene: GDB:CRFB4; CRF2-4
                                                                                                                                                                                                              submitted to the EMBL Data A; Reference number: G06935 A; Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_229 x A26391
                                                                                                             A; Molecule type: DNA
A; Residues: 1-273 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M13047; NID:g151492; PIDN:AAA25966.1; PID:g151493 C;Keywords: phosphoric diester hydrolase
                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: lecithinase C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phospholipase C (EC 3.1.4.3) – Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: p1r2:A26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: A26391 from: 1 to: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 alLeuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 TTATCAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 ... TGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 ATCATAGATGACAACTTTATCCTGAGGTGGAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 TCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 CTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 TyrValAspAspThrGlnPheValArgPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pPheGln 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTGAGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ................LysValSerAlaGluValPheAspHisThrSerV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrSerValSerArgPro******GlyGluProArgPheIleSerValGly 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family II, member 4 - human
                                                                                                                                                                                                                                                                                                                                                                                               #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.00
1.824
49.275
                                                                                                                                                                                                                                                                                  Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipophosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a phosphate-regulated gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
4
26.087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144
```

```
seq_documentation_block:
cytokine receptor family class II protein CRF2-4 precursor - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 *sequence_revision 09-Sep-1994 *text_change 10-Sep-1997
C;Accession: A47003
R;Lutfalla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at less
A;Reference number: A47003; MUID:93300510
A;Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-240-675-1_COPY_27_229 x G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Map position: 21q
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21q22.1-21q22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_27_229 x A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: pir2:A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:Z17227; NID:g393378; PID:g393379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 61.50
Ratio: 1.922
Percent Similarity: 59.259
                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: A47003 from: 1 to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: G01418 from: 1 to: 273
                            134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 TCATTCGATTAT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT.....
                                                                                                                                                                  97
                                                                                                                                                                                                                                                 55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCT.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                         19 yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 ThrAlaGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                  3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                               .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.50
1.922
59.259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 1
Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
52
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x T25677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:F08D12.9
A;Map position: 2
A;Introns: 28/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-340 <LET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Le, T.; Waterston, R. submitted to the EMBL Data Library, December 1996 A;Description: The Sequence of C. elegans cosmid F08D12. A;Reference number: Z20068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
hypothetical protein F08D12.9 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U80840; PIDN:AAB37931.1; GSPDB:GN00020; CESP:F08D12.9
A;Experimental source: strain Bristol N2; clone F08D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T25677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T25677 R;Le, T.; Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: T25677 from: 1 to: 340
                                                     188 TCGATTATCAAAAA 201
                                                                                                                                                              138 CCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 TCATTCGATTAT 195
98 alGlyTyrGlnGln 102
                                                                                                        82 p...ArgTrpAsnLeuAsnPheCysGluIleAlaAsnValThrTyrThrV 98
                                                                                                                                                                                                                   66 LeuThrAsnGlnGluIleArgLeuAspValLysThrAspArgPheAs 82
                                                                                                                                                                                                                                                                      88 CTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTAT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 ThrAlaGlnTyr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.50
2.241
71.053
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 38
Gaps: 1
Percent Identity: 31.579
```

```
SWISSPICT_38:CCAA_RABIT +
SWISSPICT_38:CCAA_RABIT +
SWISSPICT_38:SFR2_HUMAN +
SWISSPICT_38:SFR2_HUMAN +
SWISSPICT_38:SZ30_PLAFO +
SWISSPICT_38:SZ30_PLAFO +
SWISSPICT_38:FILL_BACSU +
SWISSPICT_38:FILL_BACSU +
SWISSPICT_38:ATP6_WHEAT +
SWISSPICT_38:DIL_ZYMMO +
SWISSPICT_38:DIL_ZYMMO +
SWISSPICT_38:DIL_ZYMMO +
SWISSPICT_38:DIL_ZYMMO +
SWISSPICT_38:SFR3_HUMAN +
SWISSPICT_38:SFR3_HUMAN +
SWISSPICT_38:SFR3_HUMAN +
SWISSPICT_38:SFR3_HUMAN +
SWISSPICT_38:SFR3_HUMAN +
SWISSPICT_38:SFR3_HUMAN +
SWISSPICT_38:SITZ_HUMAN -
SWISSPICT_38:SITZ_HUMAN -
SWISSPICT_38:SUND_COUST +
SWISSPICT_38:SUND_COUST +
SWISSPICT_38:SUND_COUST +
SWISSPICT_38:SUND_COUST +
SWISSPICT_38:SUND_COUST +
SWISSPICT_38:SUND_COUST +
SWISSPICT_38:SUND_TOWN -
SWISSPICT_38:SUND_TOWN -
SWISSPICT_38:SUND_FOUND -
SWISSPICT_38:SUND_TOWN -
SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SWISSPICT_SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query: US-09-240-675-1_COPY_27_229
Query legth: 203
Database. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_38:INR1_HUMAN
SwissProt_38:INR1_BOVIN
SwissProt_38:INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:IRS2_MOUSE
SwissProt_38:SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_38:CRF4_HUMAN
SwissProt_38:ERF_MOUSE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:COMA_BPT4 + SwissProt_38:PHLC_PSEAE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_38:INR1_MOUSE
SwissProt_38:N153_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 83857
Database length: 30454973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time (sec): 45.030000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database: SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_n2p.model -DEV-x1p
-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24686/app_query.fasta.1
-Q-/cgn2_1/USPTO_spool/US09240675/runat_30052000_164313_24686/app_query.fasta.1
-DB-SwissProt_38 -QFMT-fastan -SUFFIX-modif.rsp -GAPOP=12.000
-GAPOXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPCXT-0.000
-QGAPOXT-4.000 -QGAPEXT-0.050 -XGAPOXT-0.500
-TGAPOXT-0.500 -YGAPOXT-0.000 -YGAPOXT-0.500
-TGAPOXT-6.000 -FGAPOXT-7.000 -YGAPOXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1-ATTRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of: US-09-240-675-1_COPY_27_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
          7 340 00 1 204 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 198 00 1 1
       0 109.05 29.21

0 107.17 33.96

115.35 36.09

115.35 36.09

108.41 38.40

0 96.14 40.81

107.37 44.31

107.37 44.31

107.37 44.31

107.37 47.42

101.28 37.42

101.28 53.89

101.28 53.89

101.28 53.89

101.34 55.40

110.34 56.39

111.34 56.39

111.34 56.39
                                                                                                                                                                                                                                                                                                                                                                                                                                               115.03
115.03
112.77
112.51
111.41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132.43
117.53
117.64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110.31
123.05
102.98
109.43
120.81
114.03
114.03
116.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                        ESCOTE Len
3 1.4e-34
52 3.4e-18
10 1.4e-17
3.61

1475 | p33806 mus musculus (sneep
6.21

141 | Q01438 bacteriophage t4. c
730 | p6200 pseudomonas aerugi
8.82

325 | Q08334 homo sapiens (huma
10.60

551 | p70459 mus musculus (mouse,
11.31

121 | p81122 mus musculus (chic
15.79

2424 | p27884 oryctolagus cunicu
17.04

982 | p28594 anabaena sp. (strai
17.60

221 | Q01130 homo sapiens (human)
8.70

496 | p31260 homo sapiens (human)
1.46

335 | Q08372 plasmodium falcipar
1.98

339 | p72404 streptomyces coelico
1.68

140 | p23452 bacillus subtilis. f
1.64

339 | p15833 spiroplasma virus spv1
1.25

386 | p20599 triticum aestivum (w)
1.25

386 | p3050 homo sapiens (human)
1.64 | p3150 homo sapiens
1.64 | p3106 klebsiella pneumoniae
1.64 | p310 p3006 klebsiella pneumoniae
1.65 | p23157 bomo sapiens (human)
1.64 | p23152 homo sapiens (human)
1.64 | p23152 homo sapiens (human)
1.64 | p23152 homo sapiens (human)
1.66 | p23659 clostridium stercorar
1.67 | p23659 clostridium stercorar
1.68 | p23659 clostridium stercorar
1.69 | p03584 tobacco mosaic virus
1.60 | p2369 tomato mosaic virus
1.61 | p2309 aloniae virus
1.62 | p2369 tomato mosaic virus
1.63 | p2809 aloniae virus
1.64 | p2379 tomato mosaic virus
1.65 | p2369 clostridium stercorar
1.66 | p2369 tomato mosaic virus
1.67 | p28099 aloniae virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I Documentation
557 | P17181 ho
560 | Q04790 bo
560 | Q28589 ov
590 | P33896 mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P17181 homo sapiens (human)
Q04790 bos taurus (bovine).
Q28889 ovis aries (sheep).
P33896 mus musculus (mouse)
               Swissprot_38:VPHE_NPVAC
Swissprot_38:VIE4_FRG3V
Swissprot_38:ENV2_MOUSE
Swissprot_38:DHE4_EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_38:INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
          DOMAIN
DISULFID
DISULFID
                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION BY TYK2. MEDLINE; 95059042.
                                                                                                                                                                                                         Receptor; Transm
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 90124632.
                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNAR1 OR IFNAR
                                                                                                                                                                                                                                Transmembrane;
               28
437
458
79
199
               436
457
557
87
220
```

```
RA COLAMONÍCI O., Yan H., Domanski P., Handa R., Smalley D.,
A Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witte M., Krishnan K., Krolewski J.;
AM Mullersman J., Witter M., Krishnan K., Krolewski J.;
AM Mullersman J., Witter M., Krishnan K., Krolewski J.;
AM Mullersman J., Krishnan K., Krishnan 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 92129376.
Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
"The structure of the human interferon alpha/beta receptor gene.";
J. Biol. Chem. 267:2802-2809(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INR1_HUMAN STANDARD; PRT; 557 AA.

P17181;

01-AUG-1990 (Rel. 15, Created)

01-AUG-1990 (Rel. 15, Last sequence update)

15-FEB-2000 (Rel. 39, Last annotation update)

INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE; 90124632.
Uze G., Lutfalla G., Gresser I.;
Uze G., Lutfalla G., Gresser I.;
"Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";
Cell 60:225-234(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J03171; AAA52730.1; -.
EMBL; X60459; CAA42992.1; -.
PIR; A32694; A32694
PIR; $17112; $17112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.50
54.50
54.50
54.50
                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal; Polymorphism;
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                              POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR ALPHA
CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109
105
105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 61
. 87
. 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.90
67.10
67.56
67.87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P24728
P14358
P11370
P18819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rog virus 3 (fv
70 mus musculus (mc
```

```
alignment_scores:
    Quality:
    Ratio:
    Percent Similarity: 1
 seq_name: SwissProt_38:INR1_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1_COPY_27_229 x INR1_HUMAN
                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
CARBOHYD
CARBOHYD
                                                                                                                              INR1_BOVIN STANDARD; PRT; 560 AA. 004790; 01-007-1993 (Rel. 27, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
     MEDLINE; 93076908.

MOUCHel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;

Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;

"Specific antiviral activities of the human alpha interferons determined at the level of receptor (IFNAR) structure.";

FEBS Lett. 313:255-259(1992).
                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
FEBS
                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                         101
                                                       TISSUE-LUNG
                                                                 SEQUENCE FROM N.A.
                                                                                  Bovinae; Bos.
                                                                                                                      IFNAR1 OR IFNAR
                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                 بر
                                                                                                                                                                                                                                                                                                                                                                                                   \vdash
                                                                                                                                                                                                                             s 67
                                                                                                                                                                                                                                                A 201
                                                                                                                                                                                                                                                                                                                                          ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                      AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                               17
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 340.00
: 5.075
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466
481
50
58
81
110
1172
213
314
416
83
314
416
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent
                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY TYK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) (PROBABLE).
) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                         150
                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                            ω
                                                                                           Bovidae
                           are
```

```
alignment_block:
US-09-240-675-1_COPY_27_229
                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                              Align seg 1/1 to: INR1_BOVIN
                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X68443; CAA48484.1; -.
EMBL; L06320; AAA02571.1; -.
PIR; S33770; S33770.
PIR; S27387; S27387.
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 93305725.

MEDLINE; 93305725.

Lim J. -K., Langer J. A.;

"Cloning and characterization of a bovine alpha interferon receptor.";

"Cloning and characterization of a bovine alpha interferon receptor.";

"Cloning and characterization of a bovine alpha interferon receptor.";

"Cloning and characterization of a bovine alpha and beta. Binding to Type

I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
              154 AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA 198
                                                                                         104
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
49
                                                        32
                                                                                                                        16
                                                                                                                                   54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                 4 ATGGTCGTCCTGGGGGGGGGACGACCCTAGTGGTCGCCGTCGGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNITS THEMSELVES.
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELULAR LOCATION: FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                        AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
::||||||::
||||||||::
snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                      gTrpValLeuProAlaAlaSerGlyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                  MetLeuAlaLeuLeuGlyAlaThrThrLeuMetLeuValAla..
SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln
                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Transmembrane; 1 24 25 560
                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                       560
                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                         209.00
3.800
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                    422
63818
                                                                                                                                                                                                                                                                             ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                                                                                                                from: 1 to:
                                                                                                                                                                                                                                                                               INR1_BOVIN
                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                560
                                                                                                                                                                                                                                                                                                                            69.
                                                                                                                                                                                                                                                                                                                            65
2
. 231
                                                                                                                                                                                  .GlyAr
63
                                                            48
                                                                                                                        32
                                                                                                                                                                                    16
```

```
seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               documentation_block:
                                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Pecora; Bovoidea; Bovidae;
                                     CARBOHYD
CARBOHYD
                                                                                                                                    DOMAIN
DISULFID
                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
(INTERFERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SECTIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
- CONCEPTUS AT DAY 15 OF PREGUNANCY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinology 138:4757-4767(1997).

-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYLE

-i IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBBURITS THEMSELVES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaluz S., Fisher P.A.,
"Structure of an ovine
endometrium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                               EMBL; X95939; CAA65183.1; -.
EMBL; U65978; AAB84231.1; -.
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                       or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities reguires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.; "Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pregnancy.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-ENDOMETRIUM;
MEDLINE; 98006426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                         CARBOHYD
                                                                                                         CARBOHYD
                                                                                                                         DISULFID
                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [FNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [NR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinol. 17:207-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q95206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97135690
                                                                                                                                                                                                                                   Transmembrane;
438
438
438
199
199
108
108
108
108
108
108
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
437
458
844
220
220
220
108
108
172
222
222
2313
                                                                                                                                                                                                        .
560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaluzova M., Sheldrick E.L., Flint A.P interferon receptor and its expression
                                                                                                                                                                                                                      Glycoprotein; Signal.
BY SIMILARITY.
                                                                POTENTIAL.
POTENTIAL.
                                     POTENTIAL.
                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                          POTENT IAL
                                                                                                                                                               POTENTIAL
                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                        INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                       SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
```

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: SwissProt_38:INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                MEDLINE; 92262522.

Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen k.L.;
Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen k.L.;
Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen k.L.;
"Behavior of a cloned murine interferon alpha/Deta receptor expression homospecific or heterospecific background.";
in homospecific or heterospecific background.";
proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
INR1_MOUSE STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
EMBL; M89641; AAA37890.1; -. PIR; A45283; A45283. MGD; MGI:107658; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
15-FBB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 92262522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
                                                              or send an email to license@isb-sib.ch).
                                                                              entitles requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P33896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IFNAR1 OR IFNAR OR IFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --
                                                                                                                                                                                        INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  snValGluIleHisIleIleAspAspAsnPhePheLeuLysTrpAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerSerGluSerValArgAsnValThrPheSerAlaAspTyrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359
377
434
352
560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
377
434
352
522
63918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204.00
3.778
83.077
                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
S -> G (IN
A -> D (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> G (IN REF. 2).
-> D (IN REF. 2).
E7198A1905D4805C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
2
. 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 198
                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                            a collaboration
                                                                                                                                                                                                                                                                                                                                          expressed
                                                                                                                                                                                                                                                                           PROTEINS
                                                                                .ch/announce/
                                                                                                                                              outstation
                                                                                                                ö
                                                                                                                                 g
```

way

```
alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
 alignment_block:
US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                 seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
PROTEIN, hnup153.";
BIOCHIM. BIOPHYS. ACTA 1217:219-223(1994).
-I- FUNCTION: POSSIBLE DNA-BINDING SUBUNIT OF THE NUCLEAR PORE COMPLEX (NPC). THE REPEAT-CONTAINING DOWAIN MAY BE INVOLVED IN ANCHORING COMPONENTS OF THE PORE COMPLEX TO THE PORE MEMBRANE.
-I- SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX. LOCATED TO THE SUBCELLULAR LOCATION INCLEAR PORE COMPLEX. LOCATED TO THE
                                                                                                                                                                                                                    documentation_block:
N153_HUMAN STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153
                                                                McMorrow I., Bastos R., "Sequence analysis of a protein, hnup153.";
                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                     154
                                                                                                                                                                                                                                                                                                                           104
                                                                                             MEDLINE;
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                       Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                        Homo sapiens (Human).
Homo sapiens (Human).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                     NUP153
                                                                                                                                                             NUCLEOPORIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGNAL
                                                                                                                                                                                                                                                                                                                                          AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                      snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                                                                                                              ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                 HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArg
                                                                                                                                                                                                                                                                                                                         AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                SwissProt_38:N153_HUMAN
                                                                                           94154002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                     to: INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
109
181
214
314
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198.00
3.536
86.154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
449
590
220
220
43
109
1109
1109
1314
314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65776
                                                                         Horton H., Burke cDNA encoding a h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Signal POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                       INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent
                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7EC6DFF370185D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identity: 55.385
                                                                                                                                                                                                                                                                                                                                                                                                                     .
6
                                                                                                                                                                                                                     1475
                                                                          human nuclear
                                                                                  ₩.;
                                                                                                                                                                                                                    ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 5
                                                                                                                                                                                                                                                                  65
                                                                          pore
                                                                                                                                                                                                                                                                                                                                                             103
                                                                                                                                                                                                                                                                                                       50
                                                                                                                                                                                                                                                                                                                                           ω
A
                                                                                                                                                                                                                                                                                                                                                                                17
                                                                          complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA
                                                                                                                                                                       ž
1281
                                                                                                                                                                                                                    1298
                                                                                                                                                                                                                                                                                             1264
                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                             001438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                     ω
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM;
                                                                                                                                                                                                                                                                          67
```

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                          seq_name: SwissProt_38:COMA_BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-240-675-1_COPY_27_229/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                            documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1248 ThrSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThrSe
"Sequence and characterization of the bacteriophage gene product, a possible transcription antitermination J. Bacteriol. 174:6539-6547(1929).
                                                                  SEQUENCE FROM N.A. MEDLINE; 93015705. Sanson B., Uzan M.;
                                                                                                                                                    COMCA OR GOF.
Bacteriophage T4.
Viruses; dsDNA viruses,
                                                                                                                                                                                                      01-OCT-1993 (Rel. 27,
01-OCT-1993 (Rel. 27,
01-FEB-1995 (Rel. 31,
COMC-ALPHA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 603948;
                                                                                                                                                                                                                                                                                          COMA_BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein;
                                                                                                                                    4-like phages.
                                                                                                                                                                                                                                                                                                                                                                                                                ACT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                              erAsnAsnThrThrSerGlyPheGlyPheGlyAlaThrThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST NUP1, NSP1, POM 121 AND MAMMALIAN P62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGACAACACC......CATGGGCCCACGGCGACGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTTCCACCTGCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGACTCATCGCTCCTGTTCCACCTCAGGATAAAGTTGTCATCTATGAT 118
                                                                                                                                                                                                                                                                                                                                                                                Ser 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00641; zf-RanBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z25535; CAA80982.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1475
                                                                                                                                                                                                                                                      (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N153_HUMAN
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.00
2.167
58.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447
681
745
816
874
                                                                                                                                                                                                                        Created)
Last seq
Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153889
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
Percent Identity:
                                                                                                                                                                                                                        sequence up
annotation
                                                                                                                                                       RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; Z.
GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x N153_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C4-TYPE.
C4-TYPE.
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLY.
                                                                                                                                                                                                                                                                                            PRT;
                                 of the bacteriophage T4 pription antitermination
                                                                                                                                                      stage; Tailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3CB415A6909DF80E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
6
                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinc-finger;
                                                                                                                                                                                                                                                                                            141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
1
39.216
                                                                                                                                                    phages; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions on
tent is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1264
                                 comC alpha
factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         commercia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       its
```

333333333ggggg

```
alignment_scores:
Quality:
                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: SwissProt_38:PHLC_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  documentation_block:
PHIC PSEAE STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation. SPONENCE 141 AA; 16682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M89919; AAA32485.1; PIR; A45731; A45731.
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                            -1- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO PHOSPHATIDYLCHOLINE.
-1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O - 1,2-DIACYLGLYCEROL + CHOLINE PHOSPHATE.
-1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
HEMOLYTIC PHOSPHOLIPASE C PRECURSOR (EC 3.1.4.3) (HEAT LABILE-
                                                                                                                                                                                                                          Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases -- I- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO
                                                                                                                                                                                                                                                                                                                         Pritchard A.E., Vasil M.L.;
"Nucleotide sequence and expression of a phosphate-regulated encoding a secreted hemolysin of Pseudomonas aeruginosa.";
J. Bacteriol. 167:291-298(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
                                 modified
                                                       use
                                                                                                                                                                                                                                                                 Pritchard A.E.;
                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMOLYSIN) (PHOSPHATIDYLCHOLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sArgCysAlaGlyGly....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spIleLeuAspGluAsnPheIle.....TrpLeuSerThrAsnGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGlyArgProThrLysIleMetThrSerIleGly.....ValLeuLy
                                                         y
               pean Bioinformatics Institute. There are no rest
non-profit institutions as long as its content
and this statement is not removed. Usage by an
requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                86250607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.50
2.155
58.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 50
Gaps: 3
Percent Identity: 34.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₩;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMA_BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96C9EFA8C673C479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHOLINEPHOSPHOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64
by a...ww.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                     for
                                       commercial
                                                       o
```

```
STANDRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                        seq_name: SwissProt_38:CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                        443
             TISSUE-FETAL BRAIN;
MEDLINE; 93300510.

Lutfalla G., Gardiner K., Uze G.;

"A new member of the cytokine receptor
21 at less than 35 kb from IFNAR.";
Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M13047; AAA25966.1; -. PIR; A26391; A26391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                     SEQUENCE FROM N.A.
MEDLINE; 96054036.
Lutfalla G., McInnis M.G., Antonarakis
"Structure of the human CRFB4 gene: con
neighbor.";
                                                                                                                                                                                                                                                                                                                                                                               457
                                                                                                                                                                                                                                                                                                                                                                                                   192
                                                                                                                                                                                                                                                                                                                                                                                                                                             145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hemolysis; Toxin; Hydrolase; SIGNAL 1 38
                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 CTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 TCTAMAATCTCCTCMAAAAGTAGAGGTCGACATCATAGATGACAACTTTA
                                                                                                                                                                                                                                                                                                                                                                              pPheGln 459
                                                                                                                                                                                                                                                                                                                                                                                                                       ProTrpArgAla.....ValCysGlyAspLeuThrSerLeuPheAs
                                                                                                                                                                                                                                                                                                                                                                                                   TTATCAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                            ...TGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alLeuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTGAGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....LysValSerAlaGluValPheAspHisThrSerV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: PHLC_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       730 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.00
1.824
49.275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      730
82655 MW;
                                                                                                                                                                                                                         Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHLC_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEMOLYTIC PHOSPHOLIPASE C. F1D3695824445FBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                         Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to:
                                                                             kis S.E., Uz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Gaps:
                                                                                                                                                                                                                                                                                                                          325 AA
                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
4
26.087
                                                                                                                                                         family
                                                                               Uze G.
                                                                                                                                                         maps
                                                                                                                                                                                                                                     Mammalia
                                                                               its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                          457
                                                                                                                                                                                                                                                                                                                                                                                                                                              191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414
                                                                                                                                                           on
                                                                                                                                                           chromosome
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

ifor com

```
alignment_block:
US-09-240-675-1_COPY_27_229 x CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                      seq_name: SwissProt_38:ERF_MOUSE
                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL,
PIR; A47003; A4700
HSSP; P13726; 1DAN.
                                                                                                                                  documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                           Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z17227; CAA78933.1;
EMBL; U08988; AAA86872.1;
PIR; A47003; A47003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                 Mus musculus (Mouse).
                                                                                                              P70459;
                                                                                                                                                                                                 184
                                                                                                                                                                                                                             134 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
SEQUENCE FROM N.A
STRAIN-129/SVJ;
                                                                                                                         ERF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                            53
                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                         55 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                      w
                                                                                                                                                                                                TCATTCGATTAT 195
                                                                                                                                                                                                                                                            yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                            ThrAlaGlnTyr
                                                                                                                                                                                                                  snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                    TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
221
250
66
188
49
68
102
161
124
269
274
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       209
49
68
102
161
124
273
325
37011
                                                                                                                                                                                                                                                                                                                                                                                                 61.50
1.922
59.259
                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                .CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
                         Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal "POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.
                                                                                                                                                                                                                                                                                                                                                                                                 Percent
                                                                                                                                                                                                                                                                                                                                              from: 1 to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A -> D (IN REF. 2).
FLGHP -> VGRME (IN REF. 2).
MISSING (IN REF. 2).
66706C79F8514B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOKINE RECEPTOR CLASS-II CRF2-4. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                Identity:
                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                        551
                                                                              update;
                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                 54
1
. 630
                                                                                                                                                                                                                   52
```

```
See properties and see of see 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-240-675-1_COPY_27_229/rev x ERF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: SwissProt_38:IRS2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: ERF_MOUSE from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                 documentation_block:
IRS2_MOUSE STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation.
DNA_BIND 27
DOMAIN 166
DOMAIN 290
DOMAIN 362
DOMAIN 420
DOMAIN 420
MOD_RES 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu D., Pavipoulos E., Modi W., Moschonas N., Mavrot "ERF: genomic organization, chromosomal localization analysis of the human and mouse genes."; Oncogene 14:1445-1451(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED IN CELLULAR PROLITERATION (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
-!- PTM: PHOSPHORYLATION REGULATES THE ACTIVITY OF ERF (BY SIMILARITY).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).
                                                                                                                                                                                                                                                                                                                                                                                       391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 PheLysPheLysLeuGlnProProProLeuGlyArgArgGlnArgAlaAl 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q01543; 1FLI.
MGD; MGI:109637; ERF.
PRINTS; PR00454; ETSDOMAIN.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U58533;
EMBL; U58534;
                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AGGGTCGTCGCGCCCAGGAGGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 TTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCACT
                                                                                                                                                                                                                                                                                                                                                                                       aGlyGluLysAlaProGlyGly 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC09474.1;
AAC09474.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.00
3.389
75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
171
293
373
425
529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repressor; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER.
POLY-GLY.
POLY-SER.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
5AC1B72FB2743FE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY ERK2)
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
Ö:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Gaps:
                                                                                                                                                                                                                                                 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551
                                                                                                                                                                                                                                                 ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
0
45.833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mavrothalassitis
  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assitis G.J.;
promoter
```

```
alignment_block:
US-09-240-675-1_COPY_27_229/rev x IRS2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                           Align seg 1/1 to: IRS2_MOUSE from: 1 to: 1321
                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                    _documentation_block:
SFR2_CHICK STANDARD;
                                                                                                                                                                                                                             1029 GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sun X.J., Wang L.-M., Zhang Y., Yenush L., Myers M.G. Jr., Glasheen E., Lane W.S., Pierce J.H., White M.F.; "Role of IRS-2 in insulin and cytokine signalling."; Nature 377:177-177(1995).

-!- FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1)
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 95405472.
Sun X.J., Wang L.-M., Zhang Y., Yenush L.
Sun X.J., Wang L.-M., Plance J.H., Whit
SFRS2.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:109334; IRS2. TREST. PRINTS; PR00628; INSULINESI. PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00169; PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: SKELETAL MUSCLE,
                                                                                                                                                                                                      48
                                                                                                                                                                                        CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA 14
                                                                                                                                                                                                                                                    GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCCATGGGCC
                                                                                                                                                                               oThrAlaGlySerSerMet.SerSerGluProGly 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEART AND SPLEEN.
                                                                                                                                                     SwissProt_38:SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P35568; 1IRS
                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
187
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649
                                                                                                                                                                                                                                                                                                                                                                                                             ₹,
                                                                                                                                                                                                                                                                                                                                     61.00
2.652
79.310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1242
                                                                                                                                                                                                                                                                                                                                                                                                                        28
449
641
939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144
300
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649
                                                                                                                                                                                                                                                                                                                                                                                                             136526
                                                                                                                                                                                                                                                                                                                                Length: 29
Gaps: 1
Percent Identity: 51.724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PH DOMAIN.
PTB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-ASN.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                             POLY-SER.
W; 5069CE9D614960C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY INSR) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY INSR) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY)
                                                                                                                    PRT;
                                                                                                                    221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUNG, BRAIN, LIVER, KIDNEY
                                                         FACTOR SC35) (SC-35)
                                                                                                                                                                                                                                                      49
```

```
seq_documentation_block:
ID CCAA_RABIT STAN
AC P27884: P27803.
                                                                       seq_name: SwissProt_38:CCAA_RABIT
                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vellard M., Sureau A., Soret J., Martinerie C., Perbal B.;

"A potential splicing factor is encoded by the opposite strand of the trans-spliced c-myb exon.";

Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).

-!- FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND INTERACTS WITH SPLICEOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND 3 SPLICE SITES DURING SPLICEOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPS WITH PRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X62446; CAA44306.1; -. PIR; S17327; S17327. PIR; B42701; B42701. HSSP; P19339; ISXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing; Phospborylation.

16 21 RNA-BINDING (RNP2) (BY SIMILARITY).

17 21 RNA-BINDING (RNP1) (BY SIMILARITY).

18 62 RNA-BINDING (RNP1) (BY SIMILARITY).

19 11 16 GLY-RICH (HINGE REGION).

10 11 221 ARG/SER-RICH (RS DOMAIN).

11 221 ARG/SER-RICH (RS DOMAIN).

11 221 ARG/SER-RICH (RS DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>:</del>
                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00030; RNP_1; PFAM; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                          44
                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                             GGTCGTCCTCCT......GGGCGCGACGACCCTAGTGCTCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS I RNA RECOGNITION MOTIF (RNP).
SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: DIFFERENT E
PRODUCED BY ALTERNATIVE SPLICING.
PTM: EXTENSIVELY PHOSPHORYLATED C
DOMAIN (BY SIMILARITY).
                                                                                                                                                AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGA 116
                                                                                                                                                                                                                          CCGTGGGCCCATGGGTGTTGTCCGC.....AGCCGCAGGTGGA
                                                                                                                                                                                                                                                              GlyArgProProAspSerHisHisSerArgArgGlyProProProArgAr
                                                                                                            rgArgSerArgSerArgSerArgSerArg
                                                                                                                                                                                     gTyrGlySerSerGlyTyrGlyArgArgSerArgSerProArgArgArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92212859.
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
62
116
221
25524
                                                                                                                                                                                                                                                                                                                                                                                                                               60.00
2.500
53.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIFFERENT FORMS OF THE PROTEIN MAY BE
                                                                                                                                                                                                                                                                                                                                                                         SFR2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                                                                                                                                                                                                                                                                                                                      from: 1 to:
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ON SERINE RESIDUES
                     2424 AA
                                                                                                                                                                                                                                                                                                                                        221
                                                                                                                137
                                                                                                                                                                                                                                                                                                                                                                                                                                   40
                                                                                                                                                                                                                                                                                                                                                                                                                                   . 000
2000
                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                   43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR
```

```
01-JUL-1993 (Rel.
01-JUL-1993 (Rel.
15-FEB-2000 (Rel.
VOLTAGE-DEPENDENT I
CHANNEL, L TYPE, AI
                                                                                                                                                                                                   INTER 100: "O'(1974).

IN A VARIETY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-GACOXIN-TOXIN (OMEGA-AGA-TVA). THEY ARE HOWEVER INSENSITIVE TO DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-CVIA (OMEGA-CTX-GVIA).

COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1, SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE DATALLARY SUBUNITS BETA AND DELTA SUBUNITS IN ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1. ALTERNATIVE PRODUCTS: IN THE BRAIN, A SHORT ISOFORM BI-1/1A-1 AND A LONG ISOFORM BI-2/1A-2 (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE SPECIFIC: PURKINJE CELLS CONTAIN PREDOMINANTLY P-TYPE VSCC, THE Q-TYPE BEING A PROMINENT CALCIUM CHARNEL ACTIVITY: BRAIN-SPECIFIC: PURKINJE CELLS.

-1. DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPOHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE PROSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SEMILES OF POSITIVEN.

-1. SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS.
EMBL; X57477; EMBL; X57689; EMBL; X57476; EMBL; X57476; EMBL; X57688;
                                                                                                                                                            This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytoplasmic linker of Nature 368:67-70(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 91187110.

MORI Y., Friedrich T., Kim M:-S., Mikami A.,
BOSSE E., Hofmann F., Flockerzi V., Furuichi
Imoto K., Tanabe T., Numa S.;
"Primary structure and functional expression
of a brain calcium channel.";
Nature 350:398-402(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACNATA OR CACNLIA4 OR CACH4 OR CACN3.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                         <del>:</del> <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÷
                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

 I) (BI).

                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
CAA40715.1;
CAA40872.1;
CAA40714.1;
CAA40711.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 26, Created)
. 26, Last sequence update)
. 39, Last annotation update)
. T P/Q-TYPE CALCIUM CHANNEL AL
ALPHA-1 POLYPEPTIDE ISOFORM
   . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha 1-subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mori Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanabe T., Snutch T.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved
                                                                                          http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA-1A SUBUNIT (CALCIUM
RM 4) (BRAIN CALCIUM CHANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakai J., Ruth
T., Mikoshiba F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from complementary DNA
                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        motif
                                                                                                              γ̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                             d for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
;
                                                                                                                                                              a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۵.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANNEL
                                                                                                             ons on its
in no way
commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I-II
```

```
NAMARANA NA
Namarana na
                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ionic channel; Transmembrane; Ion Calcium channel; Glycoprotein; Rep Calcium-binding; Phosphorylation;
                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0167; CACHANNEL. PRINTS; PRO0170; NACHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00520;
                                                                                                                                727
1004
1012
2219
2242
                                                                                                                                                                                                                 1409
1496
1521
1576
1630
1630
1657
1657
1704
1704
1704
1704
1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ion_trans;
                                                  732
1010
1017
2227
2246
2297
2301
2377
2416
                                                                                                                                                                                                               POLY-GLY.
POLY-GLY.
POLY-GLY.
POLY-ARG.
POLY-GLY.
POLY-ARG.
POLY-A
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).

S3 OF REPEAT II (POTENTIAL).

S4 OF REPEAT II (POTENTIAL).

S4 OF REPEAT II (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

S5 OF REPEAT II (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

S1 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S2 OF REPEAT III (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).

S4 OF REPEAT III (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

S7 OF REPEAT III (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

S7 OF REPEAT IV (POTENTIAL).

S1 OF REPEAT IV (POTENTIAL).

S1 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S3 OF REPEAT IV (POTENTIAL).

S6 OF REPEAT IV (POTENTIAL).

S7 OF REPEAT IV (POTENTIAL).

S8 OF REPEAT IV (POTENTIAL).

S9 OF REPEAT IV (POTENTIAL).

S1 OF REPEAT IV (POTENTIAL).

S2 OF REPEAT IV (POTENTIAL).

S3 OF REPEAT IV (POTENTIAL).

S4 OF REPEAT IV (POTENTIAL).

S6 OF REPEAT IV (POTENTIAL).

S7 OF REPEAT IV (POTENTIAL).

S8 OF REPEAT IV (POTENTIAL).

S9 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).

$4 OF REPEAT I (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$5 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

$6 OF REPEAT I (POTENTIAL).
                                                                                                                                                                                                                           EXTRACELLULAR
S6 OF REPEAT I
CYTOPLASMIC (P
                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S6 OF REPEAT IV (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S5 OF REPEAT I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
S2 OF REPEAT II (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).

$1 OF REPEAT I (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

$2 OF REPEAT I (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
S3 OF REPEAT I (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ion transport; Voltage-gated channel;
; Repeat; Multigene family;
ion; Alternative splicing.
                                   PERMEABILITY
        PERMEABILITY
```

```
seq_name: SwissProt_38:CAPP_ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                   documentation_block:
CAPP_ANASP STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          2229
                                                                                                                                                                                                                               2277
                                                                                                                                                                                                                                                                             2261
                                                                                                                                                                                                                                                                                                                         2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGEN
MUTAGEN
MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
CA_BIND
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITE
                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
15-yUL-1999 (Rel. 38, Last annotation
PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
SEQUENCE FROM N.A.
MEDLINE; 9268846:
Luinenburg I., Coleman J.R.;
Identification, characterization and sequence analysis of the gene
"Identification, characterization and sequence analysis of the gene
encoding phosphoenolpyruvate carboxylase in Anabaena sp. PCC 7120.";
                                                                      Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                                                           LeuArgLeuArgArg 2281
                                                                                                                                                                                                                                                     GTGGAACAGGAGCGA 158
                                                                                                                                                                                                                                                                           laHisAlaArgAlaArgAlaArgAlaProAla...ArgLeuLeuProGlu
                                                                                                                                                                                                                                                                                                                        gArgGlyProValAlaArgValArgProAlaArg...AlaProAlaLeuA 2261
                                                                                                                                                                                                                                                                                                                                                 CCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAA
                                                                                                                                                                                                                                                                                                                                                                       GlyArgGlyProGlyArgValSerProGlyValSerAlaArgArgArgAr
                                                                                                                                                                                                                                                                                                                                                                                               TCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                       .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1831
1849
283
1665
772
772
1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2274
419
877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2230
                                                                                                                                                                                                                                                                                                                                                                                                                       CCAA_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.00
1.765
61.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2424
419
877
1104
386
389
392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1831
1860
283
1665
1051
1120
1884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273228
                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAA_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                       from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A -> T (IN ISOFORM CBS).
S -> N (IN ISOFORM CBS).
E->S: REDUCED BETA-SUBUNIT INTERACTION.
L->H: REDUCED BETA-SUBUNIT INTERACTION.
Y->S: REDUCED BETA-SUBUNIT INTERACTION.
E->A: NO EFFECT ON BETA-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARL -> PAAADKERYGPODRRDHGHGRARARDORWSRSPS
EGREHTTHRO (IN ISOFORM BI-1/1A-1).
MISSING (IN ISOFORM BI-1/1A-1).
MISSING (IN ISOFORM CBP315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGPGRVSPGVSARRRRRGPVARVRPARAPALAHARARARAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN ISOFORM CBP107).
MISSING (IN ISOFORM CBP103).
LYROMYAMLHHMPPPLGLGKNCPARVAY ->
RVISPPLGLGKKCPHRVAC (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY). PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
CALCIUM ION SELECTIVITY AND PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
CALCIUM ION SELECTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBP101/CBP109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                       ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F7CC4D0AB4B45604 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Gaps:
Identity:
                                                                                                         on update)
(4.1.1.31)
                                                                                                                                                                                                                                                                                                                                                                                                                       .
6
                                                                                                                                                                    982
                                                                                                                                                                                                                                                                                                                                                                                                                       2424
                                                                                                                                                                    ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
3
36.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY CAPK) (POTENTIAL).
                                                                                                          (PEPCASE) (PEPC).
                                                                         Anabaena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND
                                                                                                                                                                                                                                                                                                  143
                                                                                                                                                                                                                                                                             2276
                                                                                                                                                                                                                                                                                                                                                                        2245
                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERMEABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYKDMYSLL
```

```
alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1_COPY_27_229/rev x CAPP_ANASP
                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                              seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A44831; A44831.

PRINTS; PRO150; PEPCARBXLASE.

PROSITE; PS00393; PEPCASE_2; 1.

PROSITE; PS00781; PEPCASE_1; 1.

PROM; PF00311; PEPCASE; 3.

Lyase; Carbon dioxide fixation; A:

Tricarboxylic acid cycle.

ACT_SITE 155 155

ACT_SITE 628 628 BY S:

SEQUENCE 982 AA; 112679 MW; 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                SEQUENCE FROM N.A., AND SEQUEN MEDLINE; 92237694.

FU X.-D., Maniatis T.;

"Isolation of a complementary factor C735".
                                                                                        SFROE.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Hominidae; Homo.
                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
splicing factor, Argining/SERINE_RICH 2 (SPLICING FACTOR SC35) (SC-35)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                          782
                                                                                                                                                                                                                                                                                                                                                               767
                                                                                                                                                                                                                                                                                                                                                                                                                    752
                                                                                                                                                                                                                                                                                                                                                                                                                                           115 CGACCTCTACTTTTGAG.....GAGATTTTAGATTTTTTCCACCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M80541; AAA22023.1; -.
                      factor SC35
                                                                                                                                                           (SPLICING COMPONENT,
                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                                                                                                   ArgGlyLeuIleTyrGluGlnProAspPheIleAspPhePheHis....
                                                                                                                                                                                                                                                                                                                        GCCCAGGAGGACGACCATCA
                                                                                                                                                                                                                                                                                                                                                            ....GlnValThrProIleGluGluIleSerGlnLeuGlnIleSerSerA
                                                                                                                                                                                                                                                                                                                                                                                        GCTGCGGACAACACCCATGGGCCCACGGCGACGAGCACTAGGGTCGTCGC
                                                                                                                                                                                                                                                                                                         rgProAlaArgArgProSer 788
                                                                                                                                                                                                                                                                              SwissProt_38:SFR2_HUMAN
                                                                                                                                                                                                                                          HUMAN
            256:535-538(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAPP_ANASP
                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.50
2.288
65.000
                                                                                                                                                            35
                                                                              SEQUENCE OF
                                                                                                                                                           KD) (PR264 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                        DNA
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY.
SIMILARITY.
250621FFAAFCC8DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allosteric
                                       that encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 982
                                                                               67-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                           221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib
                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 000
                                        the
                                        mammalian splicing
                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                 782
                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
```

```
Sureau A., Perbal B.;
Sureau A., Perbal B.;
Several mRNAs with variable 3' untranslated regions and different
"Several mRNAs with variable 3' untranslated regions and different
stability encode the human PR264/SC35 splicing factor.";
Proc. Natl. Acad. Sci. U.S.A. 91:932-936(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE: 92212859.
MEDINE: 92212859.
Vellard M., Sureau A., Soret J., Martinerie C., Perbal B
"A potential splicing factor is encoded by the opposite
trans-spliced c-myb exon.";
Proc. Natl. Acad. Sci. U.S.A. 89:2511-2515(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sureau A., Soret J., Vellard M., Crochet J., Perbal B.; "The PR264/C-myb connection: expression of a splicing factor modulated by a nuclear protooncogene."; Proc. Natl. Acad. Sci. U.S.A. 89:11683-11687(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 95354672...
Tacke R., Manley J.L.;
Tacke R., Manley J.L.;
"The human splicing factors ASF/SF2 and SC35 possess distinct, functionally significant RNA binding specificities.";
EMBO J. 14:3540-3551(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-34 FROM N.A. MEDLINE; 93101590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kohtz J.D., Jamison S.F., Will C.L., Zuo P., Luhrmann Garcia-Blanco M.A., Manley J.L.;
"Protein-protein interactions and 5'-splice-site recognity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 67-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                           Nature 365:82-85(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFICITY FOR BETA-GLOBIN MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammalian mRNA precursors.";
Nature 368:119-124(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94187841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Specific interactions between proteins implicated in splice selection and regulated alternative splicing."; Cell 75:1061-1070(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN INTERACTIONS IN SPLICEOSOME ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zahler A.M., Lane W.S., Stolk J.A., "SR proteins: a conserved family of Genes Dev. 6:837-847(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93368668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA BINDING SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING TO U1-70K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                     Specific commitment of different pre-mRNAs
                                                                                            FUNCTION: NECESSARY FOR THE SPLICING OF PRE-MRNA. IT IS REQUIRED FOR FORMATION OF THE EARLIEST ATP-DEPENDENT SPLICING COMPLEX AND INTERACTS WITH SPLICEOSOMAL COMPONENTS BOUND TO BOTH THE 5' AND 3' SPLICE SITES DURING SPLICEOSOME ASSEMBLY. IT ALSO IS REQUIRED FOR ATP-DEPENDENT INTERACTIONS OF BOTH U1 AND U2 SNRNPS WITH PRE-MRNA. INTERACTS WITH OTHER SPLICEOSOMAL COMPONENTS, VIA THE RS DOMAINS, TO FORM A BRIDGE BETWEEN THE 5' AND 3' SPLICE SITE BINDING COMPONENTS, U1 SNRNP AND U2AF. IN VITRO, BINDS SF2/ASF, U1-70K AND THE 35 KD BUT NOT THE 65 KD SUBUNIT OF U2AF. BINDS TO PURINE-RICH RNA SEQUENCES, EITHER 5'-AGSAGAGTA-3' CAN BIND TO BETA-GLOBIN MRNA AND COMMIT IT TO THE 5PLICENCE PATHWAY.
SUBCELLULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: DIFFERENT FORMS OF THE PROTEIN MAY BE PRODUCED BY ALTERNATIVE SPLICING.
PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94134745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maniatis T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94084782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92249775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roth M.B.;
pre-mRNA sp
                                                                                                                                                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing
                                                                                                                                                                                                                                                                                                                                                                                                                   splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perbal B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recognition
                                                                                                                                                                                                                                                                                                                                                                                                                     уd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand
                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of.
                                                                                                                                                                                                                                                                                                                                                                                                                          SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
                                                                                                                                                                                                                                                                                                                                                                                                                        114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
```

```
seq_documentation_block:
ID HXAA_HMMAN STANDA
AC P31260; Q15949;
DT 01-JUL-1993 (Rel. 26,
DT 15-FEB-2000 (Rel. 39,
DE HOMEOBOX PROTEIN HOX-
GN HOXALO OR HOX1H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; C
CC Eutheria; Primates; C
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91288229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_27_229 x SFR2_HUMAN
                                                                                                                                                                                                                                                                                                                                           seq_name: SwissProt_38:HXAA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M90104; AAA60306.1; -.
EMBL; X62447; CAA44307.1; -.
EMBL; X75755; CAA53383.1; -.
EMBL; L03693; AAA60162.1; -.
PIR; S17328; S17328.
PIR; A42634; A42634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation.
DOWAIN 16
DOWAIN 55
DOWAIN 111
DOWAIN 117
CONFLICT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                      P31260; Q15949;
Q1-JUL-1993 (Rel. 26, Created)
Q1-JUL-1993 (Rel. 26, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
HOMEDBOX PROTEIN HOX-Al0 (HOX-1H) (HOX-1.8) (PL)
                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P19339; 1SXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 GlyArgProProAspSerHisHisSerArgArgGlyProProProArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GGTCGTCCTCCT......GGGCGCGACGACCCTAGTGCTCGTCG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                              CGACATCATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rgArgSerArgSerArgSerArgSerArgSerArgSerArgSer 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gTyrGlyGlyGlyTyrGlyArgArgSerArgSerProArgArgArgA 126
                                                                                                                                                                                                                                                                                                                                                                                     ArgTyrSerArg 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00030; RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFR2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rrm;
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.00
2.185
50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
62
116
221
38
25575
                                                                     Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Œ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA-BINDING (RNP2) (BY SIMILARITY).
RNA-BINDING (RNP1) (BY SIMILARITY).
GLY-RICH (HINGE REGION).
ARG/SER-RICH (RS DOWAIN).
R -> G (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9D1B76BDB65701F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .CGTGGGCCCATGGGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                          496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
2
35.185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
```

```
sp_invertebrate:021784 +
sp_invertebrate:016867 +
sp_invertebrate:02149 +
sp_tungi:008912 +
sp_rodent:088277 +
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archea:Q9YEB6 +
sp_mcc.Q62143 +
sp_mhc:Q62143 +
sp_fung1:Q9Y775 +
sp_flant:Q08700 +
sp_plant:Q08700 +
sp_lnvertebrate:Q25994 +
sp_bacteria:Q66774 -
sp_bacteria:Q66774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_invertebrate:002424 +
sp_invertebrate:023047 +
sp_rodent:060805 +
sp_human:09Y5L9
                                                                                                                                                                                                                                                                                                                                              sp_plant:09XID0
sp_plant:023740
sp_plant:09XFW5
sp_human:012866
sp_plant:065711
sp_virus:065450
   sp_virus:Q81166
sp_invertebrate:(
sp_lant:023854
sp_plant:064680
sp_human:075167
o_plant:023292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_mamma1:077699
sp_human:095927
sp_rodent:088970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
Query: US-09-240-675-1_COPY_27_229
Query length: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database sequences: 225878
Database length: 69334122
Search time (sec): 89,94000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_invertebrate:P91232
sp_plant:O64410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_invertebrate:076514 +
sp_human:Q13507 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database: SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_bacteria:Q9X4V6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_human:Q9Y4L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_human:Q9Y5T6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_vertebrate: Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL-frame+_n.p.model -DEV-xlp
-Q-/cgp2_1/USPTO_spool/US09240675/runat_30052000_164313_24664/app_query.fasta.1
-Q-/sgp2_1/USPTO_spool/US09240675/runat_30052000_164313_24664/app_query.fasta.1
-DB-SFTREMBL_12 -QFMT-fastan -SUFFIX-modif.rspt -GAPOP=12.000
-GAPEXT=4.000 -MMANCH-0.100 -LOOPCL-0.000 -LOOPEXT=0.000
-QGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-DELOP-5.000 -BELEXT=7.000 -START=1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE-PCt
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-MAXLEN=1000000 -USER-US09240675 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1_COPY_27_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strd Orig
                                                                                                                                                                                                                                                  + 60.00

- 60.00

- 59.50

+ 59.50

+ 59.50

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.00

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 59.50

- 5
Orig ZSCOTE ESCOTE LIGHT OF THE CONTROL OF THE CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  software, version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Len
      18 Q13507 homo sapiens (human). tr

17 Q77699 bos taurus (bovine). tr

19 Q95927 homo sapiens (human). d

10 Q8970 mus musculus (mouse). ir

10 Q9415 homo sapiens (human). hy

12 Q9415 homo sapiens (human). hy

13 Q9415 homo sapiens (human). hy

14 Q9416 zeamays (maize). cytoch

15 Q23047 caenorhabditis elegans

17 Q23047 caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! Documentation
                                                                                                                                                                                                                                               Q9yeb6 aeropyrum pernix. 108aa | Q62143 mus musculus (mouse). Q8 | Q30849 oryctolagus cuniculus (yeas | Q62140 brassica napus (rape). S | Q9y775 candida tropicalis (yeas | Q08700 brassica oleracea (cauli oleracea) | Q9yfw6 brassica oleracea (cauli oleracea) | Q9yfw6 brassica oleracea (cauli oleracea) | Q25994 plasmodium falciparum | Q80774 streptomyces coelicolor | Q25994 plasmodium falciparum | Q80774 streptomyces granaticolor | Q3x4v6 streptomyces granaticolor | Q3x4v6 streptomyces granaticolor | Q3x4v6 brassica oleracea (cauli oleracea) | Q3
1 008912 saccharomyces cerevisiae 1 008927 rattus norvegicus (rat) 1 081166 hepatitis b virus. core 1 09xyt5 cassiopea xamachana. s 1 023854 brassica campestris (fiel 054680 arabidopsis thaliana (md 1 075167 homo sapiens (human). ki 1 023292 arabidopsis thaliana (md
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q60805 mus musculus (mouse). c: Q9y519 homo sapiens (human). t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9yhw0 gallus gallus (chicken)
1 Q9y5t6 homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             076514 caenorhabditis elegan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_invertebrate:045604
sp_bacteria:034557 +
sp_plant:038704 +
         RRRRCOCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: sp_human:Q9Y5T6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMHA60
      TISSUE-TESTIS;
MEDLINE; 98288806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFNAR1.
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               +
```

```
alignment_block:
US-09-240-675-1_COPY_27_229 x Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: sp_vertebrate:Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: Q9YHW0 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
BRX.

Born.

Homo sapiens (Human).

Homo sapiens (Human).

Therryota; Metazoa; Chordata; Cr

Therryota; Metazoa; Catarrhini;
                                                                                          01-NOV-1999 (TIEMBLIEL 12, Created)
01-NOV-1999 (TIEMBLIEL 12, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
BREAST CANCER NUCLEAR RECEPTOR-BINDING AUXILIARY PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TREMBLIER: 10, Creat. 01-MAY-1999 (TREMBLIER: 10, Last. 01-MAY-1999 (TREMBLIER: 10, LAST. INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative genomic analysis receptor gene cluster."; Genome Res. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF082664; AAD13669.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REBOUL J., GARDINER K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           69 AGCCGCAGGTGGAAAAAATCTAAAAATCTCCCTCAAAAAAGTAGAGGTCGACA :::::|||||||
                                                                                                                                                                                                                                                                                               GGGAATGTGACTTTTTCATTCGATTATCAA 198
                                                                                                                                                                                                                                                                                                                                              laValAsnThrAsnPheThrLeuMetTrpAsnTyrThrGlyAspGlyThr
                                                                                                                                                                                                                                                                        TCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyArgLeuAlaAlaVa,LLeuLeuCysValLeuVa,LValValSerArgCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCATGGGTGTTGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                        sCysAlaGlyGlnThrAsnLeuLysSerProGlnAspIleGlnValTyrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108.50
2.712
66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.50 1
56.50 1
56.50 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MONNERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115.88
111.36
111.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                     Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F99BC099 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D., UZE G., LUTFALLA G.;
the interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 60.
76.79
73.98
73.91
                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569
                                     Vertebrata;
                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1083
217 !
402 !
409 !
                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i 045604 caenorhabditis
034557 bacillus subtilis.
038704 avena fatua. dna-b
039363 brassica napus (ra
                                                                                                                                                                                                                                                                                                                                                                                      168
                                                                                                                                                                                                                                                                                                                                                    58
                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
```

```
seq_documentation_block:
ID 076514
AC 076514
AC 076514
CONTROLOW-1998 (TIEMBLIE
DT 01-NOV-1998 (TIEMBLIE
DT 01-NOV-1999 (TIEMBLIE
CET-1.
OS Caenorhabditis elegan
OC Enhabditina; Rhabditol
RN [1]
OS Caenorhabditis Rhabditol
RN [1]
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
RT "Body Length and Male
RT Body Length and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-240-675-1_COPY_27_229 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE REPRESENTATION OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_invertebrate:076514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q9Y5T6 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1274 GlnLysGlnLeuGluArgGluGlnGluHis...ValArgArgGluAlaG1 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1289 u.........ArgLeuSerGln 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1243 rArgGly.....SerArgThrTrpLysArgSerGlyArgSerSerS
MORITA K., CHOW K.L., UENO N.;

"Body Length and Male Tail Ray Pattern Formation of C. elegans

"Body Length and Male Tail Ray Pattern Formation of C. elegans

Regulated by a Member of TGFb Family.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF074395; AAC26791.1;

EMBL; AF074395; AAC26791.1;

EMBL; PRINTS; PRO019; TGF-beta; 1.

PRINTS; PRO0438; GFCYSKNOT.

SEQUENCE 365 AA; 41781 MW; 54051BEE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RUBINO D.M., DRIGGERS P.H., Submitted (FEB-1999) to the EMBL; AF126008; AAD21311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUBINO D., DRIGGERS P., ARBIT D., KEMI
PAGLIAI K., GRAY K., GUTKIND S., SEGAR
"Characterization of Brx, a novel Dbl
estrogen receptor action.";
Oncogene 16:2513-2526(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCCTCAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTTTCATTCGATTATCAAAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erArgArgAlaHisSerGlnTyrAspLeuGluArgLeuArgAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlyArgProSerTrp......ProSerAlaArgArgArgCysSe 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....TATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1429 AA; 161033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.00
1.923
52.703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILLER B., SEGARS J.H.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGARS J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542BBC25 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 74
Gaps: 5
Identity: 41.892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family member that modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                          are
```

alignment\_scores:

```
seq_documentation_block:

ID Q13507 PRELIMINA
AC Q13507: O00593;

DT O1-NOV-1996 (TREMBLEE
DT O1-NOV-1999 (TREMBLE)
CE ENANSIENT RECEPTOR PO
GN FREDLINE; 96234226.
RA SHUX., JIANG M., PEY
RA ZHUX., JIANG M., PEY
RA ZHUMAN M.A.
RA ZHUX., JIANG M., PEY
RA ZHUX.,
                                                                                                                                                                     alignment_block:
US-09-240-675-1_COPY_27_229 x Q13507
                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-240-675-1_COPY_27_229 x 076514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_human:Q13507
                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: 076514 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         conductance.";

Cell 89:115-1164(1997).

EMBL; 047050; AAC51653.1; -.

EMBL; Y13758; CAA74083.1; -.

PEAN; PF00023; ank; 2.

PEANT; PF01097; TRNSRECEPTRP.

PEQUENCE 848 AA; 97354 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        013507; 000593;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TRANSIENT RECEPTOR POTENTIAL RELATED CHANNEL 3 PROTEIN.
TRPC3 OR HTRP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 97358541.
XU X.Z.S., LI H.S., GUGGINO W.B., MONTELL C.;
"Coassembly of TRP and TRPL produces a distinct conductance".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "trp, a novel mammalian gene capacitative Ca2+ entry."; Cell 85:661-671(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
351 LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaIleGlyTy 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 96234226.
ZHU X., JIANG M., PEYTON M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 GACCCTAGTGCTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAG
:::||||||::: |||||||
                                                      4 ATGGTCGTCCTGGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTTTTTCATT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluProSerSerValArgArg.....LysArgSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspPheTyrVal 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nThrGlyAsnSerGluArgLysAsnArgLysLysGlyArgLysHisHis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AsnThrGluAlaGluSerAsnLeuCysArgArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                     ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                     Q13507
                                                                                                                                                                                                                                                                    63.00
1.537
54.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRNSRECEPTRP.
A; 97354 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.00
1.941
62.963
                                                                                                                     from: 1
                                                                                                                                                                                                                                                                       Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOULAY G., HURST R., STEFANI E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                     с
6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                78AC2E9D CRC32,
                                                                                                                     848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
: 2
: 31.481
                                                                                                                                                                                                                                                                       75
3
33.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        store-operated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agonist-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239
```

```
seq_name: sp_human:095927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_229 x 077699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: sp_mammal:077699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
077699 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WISSENBACH U., PHILIPP S., FLOCKERZI V.;
"Cloning and analysis of TRP channels.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AJ006781; CAA07246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRP3 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel 08, 01-NOV-1998 (TrEMBLrel 08, 01-NOV-1998 (TrEMBLrel 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 AGGTGGAACAGGAGCGATGAGTCTGTCGGG......AATGT 176
                                                                                                                                                                                                                                                              104 AAGTAGAGGTC......GACATCATAGATGACAACTTTATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                               91
                                                                                                                                    75
                                                                                                                                                                                                                                                                                                       41 rTrpIleAlaProCysSerArgLeuGlyLysValLeuArgSerProPheM
                                                                                                                                                                                                                                                                                                                                                     54 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACTTTTTCATTCGATTATCAAAAA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eThrValThr...AspTyrProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTAGAGGTC.....GACATCATAGATGACAACTTTATCCTG
                                                                                        GACTTTTTCATTCGATTATCAAAAA 201
                                                                                                                                 ValPheAsnAlaSerAspArgPheGluGlyIleThrThrLeuProAsnIl
                                                                                                                                                                        AGGTGGAACAGGAGCGATGAGTCTGTCGGG......AATGT 176
                                                                                                                                                                                                                        etLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeuLeu 74
                                                                                                                                                                                                                                                                                                                                                                                            :::|||||||::: |||
LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaTleGlyTy
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGTCGTCCTGGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etLysPheValAlaHisAlaAlaSerPheIleIlePheLeuGlyLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rTrpIleAlaProCysSerArgLeuGlyLysIleLeuArgSerProPheM
                                           eThrVal...IleAspTyrProLys 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 077699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.00
1.512
54.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 75
Gaps: 3
Percent Identity: 33.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B9F9B808 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400
                                                                                                                                    91
                                                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384
```

```
seq_documentation_block:
ID 095927
AC 095927;
PT 01-MAY 1999 (TrEMBLIZE
DT 01-MAY 1999 (TREMBLIZE
DT 01-MAY 1999 (TREMBLIZE
DT 01-MAY 1999 (TREMBLIZE
DT 01-MAY 1999 (TREMBLIZE
DE DJ465N24.2.1 (PUTATIV
GN DJ465N24.2.
OS Homo sapiéns (Human).
OC Eukaryota; Metazoa; C
C Euthería; Primates; C
RN [1]
RP SEQUENCE FROM N.A.
RA WILSON S.;
RA WILSON S.;
RA SUDMICHE (FEB-1999)
DR EMBL; AL031432; CAB37
SQ SEQUENCE 290 AA; 3
                                                                                                                               Seq_documentation_block:
ID 088970
AC 088970;
DT 01-NOV-1998 (TrEMBLre
DT 01-NOV-1998 (TREMBLre
DT 10-NOV-1998 (TREMBLre
DE INSULIN RECEPTOR SUBS
GN IRS2.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; C
OC Eukaryota; Medentia; S
RN [1]
RP SEQUENCE FROM N.A.
RA XU G., ULMER W.T., WC
RT "Partial genomic DNA
RA XU G., ULMER W.T., WC
RT "Partial genomic DNA
RA SUBMitted (SED-1998)
DR EMBL; AF090738; AAC61
FT NON_TER
1
SQ SEQUENCE 734 AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allgnment_block:
US-09-240-675-1_COPY_27_229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_rodent:088970
                                                                    alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: 095927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                                           SEQUENCE FROM N.A.
XU G., ULMER W.T., WOLF B.A.;
"Partial genomic DNA sequence of mouse beta-cell IRS-2.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF090738; AAC61743.1; -...
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; ALO31432; CAB37992.1; -. SEQUENCE 290 AA; 33613 MW; B59EOC18 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TREMBLrel. 10, Last sequence update)
01-MAY-1999 (TREMBLrel. 10, Last annotation update
DJ465N24.2.1 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
DJ465N24.2.
                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INSULIN RECEPTOR SUBSTRATE-2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 GGGTGTTGTCCGCAGCCGC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 rgSerHisSerArgValSerSerArgPheSerSerArgSerArgArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 .....AGGTGGAAAAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 GlySerProGlnGluLysAspSerProSerThrSerArgSerGlyGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rSerArgLeuSerSerArgSerArgSerArgSerPheSerArgSerSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysSerArgSerArgSerArgArgArgHisGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
  61.00
2.652
79.310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.00
2.296
43.548
                                                                                                                                        75251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    095927
  Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                        B3410CAF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
  29
1
51.724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
1
29.032
                                                                                                                                                                                                                                                                                                                       Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
```

alignment\_block: US-09-240-675-1\_COPY\_27\_229/rev x O88970

Align seg 1/1 to: 088970

from:

ب

to: 734

GGAGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCATGGGCC

```
seq_documentation_block:
ID Q9Y4L5;
AC Q9TEMBLrel 12
DT 01-NOV-1999 (TrEMBLrel 12
DT 01-NOV-1999 (TrEMBLrel 12
DT 01-NOV-1999 (TrEMBLrel 12
DT 01-NOV-1999 (TrEMBLrel 12
CE WARTYOTA METAZOA; ChOTDA
CE EUNARTYOTA; METAZOA; ChOTDA
CE EUNARTYOTA; METAZOA; CATATA
RA BASSI M.T., BANFI S., RIBO
RT Thuman gene transcripts.";
RL Submitted (JUN-1999) to th
RN SEQUENCE FROM N.A.
LEHRACH H., POUSTKA A., LU
RA AUFFRAY C., ANSORCE W., BA
RA AUFFRAY C., SUBMITTED
THE EUROPEAN IMAGE CONSOR
RT human gene transcripts.";
RL Submitted (JUN-1999) to th
DR EMBL; AL079314; CAB45280.1
KW Hypothetical protein.
FT NOM_TER
SQ SEQUENCE 232 AA; 26168
                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_229/rev x Q9Y4L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: sp_human:Q9Y4L5
    seq_name:
                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q9Y4L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439
                                                                                                                                                                                                                                                                                                                      AUFFRAY C., ANSORGE W., BALLABIO A., ESTIVILL X., GIBSON K., LEHRACH H., POUSTKA A., LUNDEBERG J.;
"The European IMAGE consortium for integrated Molecular analysis human gene transcripts.",
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL079314; CAB45280.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASSI M.T., BANFI S., RIBONI M., BALLABIO A., "The European IMAGE consortium for integrated human dene transcripte "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                              54
                                                                                                                              39
                                                                                                                                                                          96
                                                                                                                                                                                                                38
                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OThrAlaGlySerSerMet.SerSerGluProGly 466
                                                                                                                                                                                                                                                        CACCTCAGGATAAAGTTGTCATCTATGATGTCGACCTCTACTTTTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGGCGACGAGCACTAGGGTCGTCGCGCCCAGGA 14
                                                                                                                                                                      AGATTTTAGATTTTTCCACCTGCGGCTGCGGACAACACCCATGGGCCCA 47
                                                                                                                                                                                                                                                                                                AspAsnArgAlaAsnGlu...ArgGlyHisGlnThrHis......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAspLeuTyrArgLeuProProAlaSerAlaAlaThrSerGlnGlyPr 455
                                                                    CGGCGACGACTAGGGTCGTCGCGCCCAGGAGGACGACCATCA 2
                                          ArgTyrArgSerArgGlySerSerArgProAspArgSerProAla
sp_invertebrate:P91232
                                                                                                                              .....ThrAspPheTrpGlyAlaArgProProArgLeuProLeuGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.161
43.077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
26168 MW; A8DF2B4D CRC32,
                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                      to: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
2
29.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BORSANI G.
                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                              38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of.
```

```
seq_documentation_block:
ID p91232
AC p91232;
DT 01-MAY-1997 (TIEMBLIED OI) -MAY-1997 (TIEMBLIED OI) -MAY-19815701 -MAY-1981570 -MAY-19815701 -MAY-19815701 -MAY-19815701 -MAY-19815701 -MAY-19
seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: P91232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-240-675-1_COPY_27_229 x P91232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P91232;
01-MAY-1997 (TIEMBLrel. 03, C
01-MAY-1997 (TIEMBLrel. 03, L
01-NOV-1999 (TIEMBLrel. 12, L
COSMID F08D12.
                                                                                                                                                                                                                                                                                              documentation_block:
O64410 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
BONFIELD J., BURTON J., CONNELL M., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KENSHAW J., KIRSTEN J., LAUTER N., LATRETILE P.,
LIGHTNING J., LOYD C., MCMURRAY A., MOTTINORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 M of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
CYTOCHROME P450 MONOOXYGENASE (FRAGMENT).
                 Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 CCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LE T., WATERSTON R.;
Submitted (DEC-1996) to the
EMBL; U80840; AAB37931.1;
PFAM; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 TCGATTATCAAAAA 201
Poaceae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 p...ArgTrpAsnLeuAsnPheCysGluIleAlaAsnValThrTyrThrV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 LeuThrAsnGlnGluGluIleArgLeuAspValLysThrAspArgPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 CTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                alGlyTyrGlnGln
                                                                                                                                                                                                                                                                                                                                                                                              sp_plant:064410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.50
2.241
71.053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7488406A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
. Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340
                                                                                                                                                                                                                                                                                                     270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.579
                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COULSON A.,
```

```
SO TW DR RA
                                                                                                                 alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                   alignment_block:
US-09-240-675-1_COPY_27_229 x 002424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: sp_invertebrate:002424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-240-675-1_COPY_27_229/rev x 064410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                         Align seg 1/1 to: 002424 from: 1 to: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
002424 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
YEGHIAZARYAN K., STRATER T., HACHTEL W.;
SUBMITTED (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ004810; CAA06156.1; -.
MENDEL; 28451; Zeama; 3078; 28451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                           YANDELL M.D., ROSS R.M., SUZUKI Y., WOOD W.B.; "Characteristics of dbl-1, a C. elegans decapentaplegic homologue, support a conserved role for BMP-family signaling in bilaterian development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997 (TIEMBLIEL. 04, Created)
01-NOV-1998 (TIEMBLIEL. 08, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
DECAPENTAPLEGIC PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 TGTCGACCTCTACTTTTGAGGAGATTTTAGATTTTTTCCACCTGCGGCT
                                                                                                                                                                                                     PRINTS; PRO0438; GFCYSKNOT.
SEQUENCE 365 AA; 41768 MW;
                                                                                                                                                                                                                                 Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF004395; AAC27729.1; -. HSSP: P18075; 1BMP. HSSP: P18075; 1BMP. PFAM; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monooxygenase.
NON_TER 270
                                                                                                                                                                                                                                                                                                                                                        STRAIN-N
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DBL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 CAGGAGGACGACCA 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 tSerSerAlaArgIleGlyProAlaArgProGlyLeuGlyAlaLysArgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 GCGGACAACACCCATGGGCCCACGGCGACGAGCACTAGGGTCGTCGCGCC
27 GACCCTAGTGGTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysArgProSerGlnThrPro..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O64410 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.00
2.857
55.263
                                                                                                                 60.00
1.818
61.111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29047 MW;
                                                                                                            Length: 54
Gaps: 2
Percent Identity: 29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D2F4F715 CRC32
                                                                                                                                                                                                       7D3FDF49 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
1
36.842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
               76
```

```
Seq_documentation_block:
ID Q23047
AC Q23047
DT Q1-NOV-1996 (TrEMBLre DT Q1-NOV-1999 (TrEMBLre DT Q1-NOV-1999)
CARPORT OF SEQUENCE FROM N.A.
CARPORT RAMBELINE; Metazoa; N QC EMASTYOTA; Metazoa; N QC EMASTYOTA; Metazoa; N QC EMASTYOTA; MALSON N.A.
CARPORT SEQUENCE FROM N.A.
CARATION M., DEAR S., RA GARDIER A., AINSCOUGH BONFIELD J., BURTON J.
RA GARDIER N., KERSHAW J., LLOYD C.
RA GARDIER J., LLOYD C.
RA GARDIER J., LLOYD C.
RA GARDIEN J., PERCY C.,
RA GARDIEN J., PERCY C.,
RA GARDIEN J., FORCY C.,
RA GARDIER J., LLOYD C.
RA GARDIER J., FORM N.A.
CAPTION N., SMITH A.,
RA SMALDON N., SMITH A.,
RA GARDIER J., FORM N.A.
RA GARDIER J., FORM N.A.
REGUENCE FROM N.A.
REGUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA PAULEY A., GATTUNG S.
SUBMITTED (JUL-1996)
RN SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
RA PAULEY A., GATTUNG S.
SUBMITTED (JUL-1996)
DR SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
RA MATERSTON R.;
SUBMITTED (JUL-1996)
DR SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
RA MATERSTON R.;
SUBMITTED (JUL-1996)
DR SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
RA MATERSTON R.;
SUBMITTED (JUL-1996)
DR SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
RA MATERSTON R.;
SUBMITTED (JUL-1996)
DR PASSP, P18075; 1BMP,
DR PASSP, P18075; 1BMP,
DR PASSP, P18075; 1BMP,
DR PASSP, P18075; PRO438; GRCY
SEQUENCE 379 AA; 4
                                                                                                                                                                                             alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: sp_invertebrate:Q23047
                                                                                                       alignment_block:
US-09-240-675-1_COPY_27_229 x Q23047
                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1996) to the ENBL; U64856; AAB04986.1; -. HSSP; P18075; IBMP. PF00019; TGF-beta; 1. PRINTS; PR00438; GFCYSKNOT. SEQUENCE 379 AA; 43881 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET J., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., ERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., FLOYD C., FIKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 MD of contiguous nucleotide sequence from chromosome III of C.
elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T25F10.2.
Caenorhabditis elegans.
Caenorhabditis elegans.
Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILAR TO BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAULEY A., GATTUNG S., Submitted (JUL-1996) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
27 GACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACTTTTTCATT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nThrGlyAsnSerGluArgLysAsnArgLysLysGlyArgLysHisHis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluProSerSerValArgArg.....LysArgSerAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .........AsnThrGluAlaGluSerAsnLeuCysArgArgThr
                                                   to: Q23047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                             60.00
1.818
61.111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ដូ
                                                         from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                 X.
                                                                                                                                                                                                Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secernentea; Rhabditia; Rhabditida; bditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                 029CB1BB
                                                                                                                                                                                                Identity:
                                                         379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379
                                                                                                                                                                                                                                                                                                                                                                 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ
                                                                                                                                                                                             54
2
29.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COULSON A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
```

spileArgTrpThrLys

402

```
seq_name: sp_rodent:Q60805
                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1_COPY_27_229 x Q60805
                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                               Align seg 1/1 to: Q60805 from: 1 to: 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U4113; 11...
HSSP; P06213; 11...
MGD; MGI:96965; Mer.
R PFAM; PF00041; fn3; 2.
PFAM; PF00047; 19; 2.
PFAM; PF00047; 19; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block:
Q60805 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIE). 01, Created)
01-NOV-1996 (TIEMBLIE). 01, Last sequence update)
01-NOV-1996 (TIEMBLIE). 12, Last annotation update)
01-NOV-1999 (TIEMBLIE). 12, Last annotation update)
C-MER PROTOONCOGENE PRECURSOR (C-MER TYROSINE KINASE RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95303502.
GRAHAM D.K., BOWMAN G.W., DAWSON T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
                                                                                                                               Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U21301; AAA80222.1; ...
HSSP: P06213; 11RK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and developmental expression analysis of the tyrosine kinase."; Oncogene 10:2349-2359(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-B6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-315 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q60805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNODGRASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNODGRASS H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                               93
                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTTTTTCATT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGT
:::::|||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nThrGlyAsnSerGluArgLysAsnArgLysLysGlyArgLysHisHis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspPheTyrVal 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluProSerSerValArgArg.....LysArgSerAlaGl
                                                        lAlaProLeuAsnIleThrValPheLeuAsnGluSerAsnAsnIleLeuA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AsnThrGluAlaGluSerAsnLeuCysArgArgThr 267
                                                                                           ATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTG.
                                                                                                                                                                        GCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAA
                                                                                                                                                                                                                                                                                                                                                   Quality:
.AGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                              21
994 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                            60.00
2.222
69.231
                                                                                                                                                                                                                                                                                                                                                                                                                            20 POT
994 C-א-
110156 MW;
                                                                                                                                                                                                                                                                                                              Percent
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.

C-MER TYROSINE KINASE RECEPTOR

W; 3C2F429D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                              Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANFORD W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⋛
                                                                                                                                                                                                                                                                                                            39
1
33.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARP H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
```

```
Seq_documentation_block:
ID 09YEB6
AC 09YEB6;
AC 09YEB6;
AC 09YEB6;
AC 09YEB6;
AC 09YEB6;
AC 01-NOV-1999 (TYEMBLTel. 12, DT 01-NOV-1999) (TYEMBLTEL. PRC APEO658.

OC AICHABA; CICRETAIN.
OC AICHABA; CICRETAIN.
AC STRAIN-K1;
RX MEDLINE; 99310339.
RA KAWARABAYASI Y., HINO Y., FRA JIN-NO K., TAKAHASHI M., SI RA HOSOYAMA A., FUKUI S., NAGJ RA HOSOYAMA A., FUKUI S., NAGJ RA HOSOYAMA A., FUKUI S., KIKUCHI RA YAMAZKAI J., KUSHIDA N., OK RA NOMURA N., SAKO Y., KIKUCHI RA YAMAZKAI J., KUSHIDA N., OK RA NOMURA N., SAKO Y., KIKUCHI RAT (Complete genome sequence (TICRETAICHE GENOME) BAA79630.1.
SO SEQUENCE 108 AA; 11371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq_documentation_block:
ID 097519;
AC 097519;
DT 01-NOV-1999 (TrEMBLrel. 12
DT 01-NOV-1999 (TREMBLrel. 12
DT 01-NOV-1999 (TREMBLREL. 12
DE TRANSCRIPTIONAL ACTIVATOR
GN SRCAP.
OS Homo Sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Eutheria; Primates; Catarr
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99278407.
RA JOHNSTON H., KNEER J., CHA
RT "Identification of a novel
RT which interacts with CREB-
RL J. Biol. Chem. 274:16370-1
DR EMBL; AF143946; AAD39760.]
SQ SEQUENCE 2971 AA; 31563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-240-675-1_COPY_27_229/rev x Q9Y5L9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_human:Q9Y5L9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: Q9Y5L9 from: 1 to: 2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 99278407.

JOHNSTON H., KNEER J., CHACKALAPARAMPIL I., YACIUK P., CHRIVIA J.;
JOHNSTON H., KNEER J., CHACKALAPARAMPIL I., YACIUK P., CHRIVIA J.;
"Identification of a novel SNF2/SWI2 protein family member, SRCAP,
which interacts with CREB-binding protein.";
J. Biol. Chem. 274:16370-16376(1999).

EMBL: AF143946; AAD39760.1;
EMBL: AF143946; AAD39760.1;
SEQUENCE 2971 AA; 315639 MW; 1C7B94CB CRC32;
                                 "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; AP000060; BAA79630.1; -.
                                                                                                                                    MEDLINE: 9310339.

KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y., JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H., HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H., TAKAMIYA M., MASUDA S., FUWAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y., NOMURA N., SAKO Y., KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         942 PheProProAlaAlaAlaThrThrThrSerThrThrAlaThrAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TIEMBLIE1. 12, CIEA
01-NOV-1999 (TIEMBLIE1. 12, LAST
01-NOV-1999 (TIEMBLIE1 12, LAST
TRANSCRIPTIONAL ACTIVATOR SRCAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (Tremblrel. 12,
01-NOV-1999 (Tremblrel. 12,
01-NOV-1999 (Tremblrel. 12,
108AA LONG HYPOTHETICAL PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 TAGGGTCGTCGCGCCCAGGAGGACG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 TTTCCACCTGCGGCTGCGGACAACACCCATGGGCCCACGGCGACGAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rThrThrAlaValProAlaProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_archea:Q9YEB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.00
3.333
72.000
             11371 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12, Created)12, Last sequence update)12, Last annotation updatPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                             Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 52.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
             BCB1E741 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ጀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
```

```
Title:
Perfect score:
Sequence:
                                                     Scoring table:
                                                                                                                                                                                                                                               OM protein - protein search, using sw model
   Searched:
                                                                                                                                                                                                                  Run on:
                                                                                         US-09-240-675-2_COPY_1_229
1196
1 MMYVLLGATTLYLVAYGPWV......WKIGYYSPVHCIKTTYENEL 229
                                                                                                                                                                    June 1, 2000, 00:40:13; Search time 42.08 Seconds
(without alignments)
128.900 Million cell updates/sec
188963 seqs, 23686106 residues
                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

Minimum DB seg length: 0
Maximum DB seg length: 1000000

Total number of hits satisfying chosen parameters:

188963

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

A\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

23 24 27 28 29 20 31 31 33 33 34	66 67 67 113 113 114 115 116 117 118 119 119 119 119 119 119 119 119 119	Result No. 1 2 3
4 · H · O O · · · · O O O	1196 1196 1196 1191 1191 1191 1222.5 203 184.5 149.5 149.5 131.5 131.5	1196 1196 1196
7.7.7.8899.8 7.7.7.889.33	100 0 100 0	00000 34
942 245 210 210 575 578 578 219 219 253 251 251 251	557 557 557 557 557 553 332 332 332 332 333 333 337 221 221 221 221 221 221 221 221 221 22	•
40000000000	~ · · · · · · · · · · · · · · · · · · ·	49744 1
N-R-GBP human in terferon -10 rece kin-10 r -10 rece -10	<b>もれららのはのだなちちもりじゅんりょう</b>	Description Soluble interferon Sequence of a soul IFN receptor extra Human alpha-interf Complete interfero

45	44	43	42	41	40	39	38	37	36	35
92	92	92	92	92	92	92	92	92	92	92
7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7
295	295	295	295	295	295	295	295	295	265	251
Н	ш	Ь		<b>_</b>	٢	ר	_	دبو	Н	↦
W98950	W59047	W55780	W31532	W17716	R55178	P80713	P80504	P81503	R80063	W55781
Human tissue facto	Human thromboplast	Full length tissue	Human tissue facto	Human tissue facto	Pre-huTFh. Inhibit	Complete sequence	Sequence encoded b	Human tissue facto	Human IFNAB-BPI en	Truncated tissue f

# ALIGNMENTS

														•									
RESU R284 ID AC DT	Оy	Оу Оъ	Оγ	dg VQ	Queri Best Matcl	80 00 00	388	88	88	868	Į P	P T	尿	DR PI	P. :	P R	F.	g g	So		달		RESULT
ULT 2 495 828495 standard; Protein; 436 AA. R28495; 31-MAR-1993 (first entry)	181 ENTYSRHKTYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229 	121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180 	61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120 	1 MMYVLLGATTLVLVAVGFWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60 	Query Match 100.0%; Score 1196; DB 1; Length 436; Best Local Similarity 100.0%; Pred. No. 2.6e-115; Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 436 AA;	(or deriv.) and an immunoglobulin such as IgG1	perivatives obtained by substitution or deletion of this sequence	receptor. Potentially immunogenic epitopes have thus been eliminated.	The transmembrane and cytoplasmic domains of the native IFN receptor	aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.	New water-soluble polypeptide(s) with arrinity for itw-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease,	N-PSDB; Q14239.	Tovey MG, Uze G; WPI; 91-319778/44.	Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;	O5-FEB-1990; FR-001298.		FR2657881-A.	•	Soluble interferon-alpha/beta receptor. IFN; autoimmune disease; graft rejection; histocompatibility.	16-JAN-1992 (first entry)	R14487 standard; Protein; 436 AA.	1 87

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mater soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosyppressants, for treating auto:immune and diseases and transplant rejection

If all 1: Sep; English.

NA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate coligonucleotides as primers and cloned CDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos C 030534 and 030535 R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for toxic side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 229
                                                                16-SEP-1994; E03114.
16-SEP-1993; EP-402279.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE S/
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
N-PSDB; 086457.
Compsn. of monoclonal antibodies against interferon useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English. A recombinant soluble form of the human interferon c protein extracellular domain, given in R71723, was 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1992.
17-APR-1991; WO-F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eid P. Gresser I, Lutfalla G, Mc
                                                                                                                                                                                                  IN receptor extracellular domain. ITN receptor; interferon-alpha; ITN receptor; interferon receptor; interferon-alpha; interferon-beta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of a soulble with a high affinity for Interferon receptor; a
                                                                                                                                                                          Homo sapiens.
WO9507716-A.
                                                                                                                                                                                                                                                                R71723 standard; Protein; R71723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q30532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tovey
                                                                                                                                                             23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                       MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                              ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMVVLLGATTLYLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92-382110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Uze G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e form of the interferon (IFN) receptor for IFN-alpha and -beta. alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                             436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                           ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meyer
                                                                                                                    SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1196; DB 1;
No. 2.6e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                                                                                       immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
crass I receptor expressed in
                                                         receptor
                                                                                                                                                                                                                                                                                                                                                                             229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
```

```
Š
                                                                              g
                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
Š
                         밁
                                                                                                                                                                                                        뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ဥ္ပင္သ
                                                                                                                                   Query Match
Best Local S
Matches 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 229
                                                                                                                                                                                                    New human alpha-interferon receptor protein - useful for testin interferon agonists and in treatment or diagnosis Disclosure; fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and dinosis of viral diseases and tumours. Antibodles raksed against this protein can be used for blocking the receptor when require eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residues 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-1991.
19-OCT-1990;
20-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  either E. coli or COS cell hosts. The protein immunomodulatory monoclonal antibodies. Sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q11701
                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-1990; F00758.
20-OCT-1989; FR-013770.
(CNRS ) CNRS CENT NAT RECH SCI.
MOGENSEN KE, UZE G, Lutfalla G,
WPI; 91-148740/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human alpha-interferon receptor protein. Human alpha IFN; IFN agonists; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9105862-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R11958 standard;
R11958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8-JUL-1991
  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                           61
                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                ب
                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAVVLLGATTLVLVAVGFWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                              MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                         FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    targetting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMYVLLGATTLYLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNYT 60
                           FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229;
                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal
                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1196;
Pred. No. 2.6
0; Mismatches
                                                                                                                                  Score 1196; DB 1;
Pred. No. 3.7e-115;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                 Gresser
                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Was
                                                                                                                                                            Length
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used
                                                                                                                                                                                                                                                                        required,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                raise
                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                  diag-
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                           60
                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

```
RESULT
RE
                 RESULT
R28496
R7
RAC
R7
AC
R7
DT
R7
CDE
R8
CDE
R8
THE R8
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                   跊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-1991.
05-FEB-1990;
05-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.
The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also 014239.
31-MAR-1993 (first entry)
Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                    R28496;
R28496;
31-MAR-1993 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EUBI-) LAB EURO BIOTECHNO
Eld P, Gresser I, Lutfalla
Tovey MG, Uze G;
WPI; 91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete interferon-alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R14488 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    001298.
FR-001298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
458. .55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 437. .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1= transmembrane
.557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557
                                                                                                                                                                                                                          557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1196; DB 1; Pred. No. 3.7e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ጀ
                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                     ACCEPT THE SERVICE OF THE SERVICE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
```

```
RESULT
R42635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune provides as and transplant rejection claim 3; Fig 2; 58pp; English.

CL Alim 3; Fig 2; 58pp; English.

CL DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for CL invalpha and -beta is isolated by PCR, using appropriate coliponarclectides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos CL invalpha and -beta receptor (Q30533), was incubated with oligos CL invalpha and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the CX is ide-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                   EP-563487-A.
06-OCT-1993.
31-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-1992.
17-APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P, Gresser I, Lutfalla G, Me
                                                 (EUBI-) LAB EURO BIOTECHNOLOGIE Benoît P, Maguire D, Meyer F, WPI; 93-312951/40.
                                                                                                                                                                                                                                                     IFW.R; extracellular domain; monoclonal antibody; viral in cell proliferation; allograft rejection; systemic lupus er psoriasis; multiple sclerosis; Behcet's Disease; aplastic immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tovey M, Uze G;
Monoclonal antibody to
neutralising activity a
                                 P-PSDB; R42635
                                                                                                      31-MAR-1992;
                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                          Human interferon receptor
                                                                                                                                                                                                                                                                                                                                            20-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                              R42635 standard;
R42635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q30533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                      EP-400902
                                                                                                                      400902.
                                                                                                                                                                                                       Location/Qualifiers
1. .436
                                                                                                                                                                      /label= extracellular_domain
/note= "soluble, immunogenic
                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                 human
                                                                                                                                                                                                                                                                                                                                                                              557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
interferon
t human typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1196; DB 1;
Pred. No. 3.7e-115;
                                                                                                                                                                                                                                                                                                                                                                              A
                                                     SA.
Plavec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F, Mogensen
              type-I
                                                                     Tovey
                                                                                                                                                                        form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                 receptor
                                                                                                                                                                                                                                                                                                            viral infection;
                                                                     នី
                                                                                                                                                                        of IFN-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229
                                                                                                                                                                                                                                                                                           erythematosus;
having
ed for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
```

0

against

type

interferon,

used

```
RAPSOLD AND BEAUTY OF THE STATE OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                      δ
                                                                             В
                                                                                                                        δ
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 229
                                                                                                                                                                                  Query Match
Best Local Sin
Matches 229;
                                                                                                                                                                                                                                                                                            Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.

The amino acid sequence of human interferon class I receptor is given in R73356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monoclonal antibodies.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human invested are casimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IFN receptor: Interferon receptor; interferon-beta; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy and diagnosis Disclosure; Fig 3; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q86458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9507716-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
61
                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |--1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                           MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                  0;
                                                                                                                                                                               Score 1196;
Pred. No. 3.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interferon-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1196; DB 1;
No. 3.7e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunomodulator;
                                                                                                                                                                                                        DB 1;
1.7e-115;
                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                             Length
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                             120
                                                                                           60
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                  0;
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                 밁
                          Š
                                                         В
                                                                                    Š
                                                                                                                   밁
                                                                                                                                                                            В
                                                                                                                                                                                                          δÃ
 밁
                                                                                                                                                                                                                                                                                                                           New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Example 2; Fig 7; 46pp; English.

C Novel splice-deleted interferon alpha-receptor (IFNAR) form 1 (W1805) is characterised by a new domain (5) which follows an end-deleted extracellular domain when compared to transmembranal (FINAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. (from human myeloma U266 cells. Soluble, non-membrane bound IFNAR (splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN (antagonists or by regulating the activity of the multiple IFN (antagonists or by regulating the activity of the multiple IFN (tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 228; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1997 (first entry)
Spliced-deleted interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W21805 standard;
W21805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abramovich C, Ra
WPI; 95-200634/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-1994;
24-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU9475977-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
 181
                            181
                                                           121
                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                   61
                                                                                                                                                 5
                                                                                                                                                                               ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                        TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                   FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENIYSRHKIYKLSPETTYCLKYKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                               MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
ENTYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                           TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                   FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratovitski E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Extracellular_domain /note= "comprises amino acids transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                       99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ၀
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-receptor
                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                       Score 1191; DB 1;
Pred. No. 8.4e-115;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acids 1-427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    form
                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                         180
                                                                                                                                                                               60
                                                                                                                                                                                                             60
                                                              180
                                                                                                                                                                                                                                            0
```

RESULT W21806

```
RESULT
W21804
ID W2
AC W2
DT 23
DE Tr
KW In
OS HO
FH Ke
                                                                                                                                                                                            Ş
                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                δõ
                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibiting, modulating or modifying the activities of interferon(s) Example 3; Fig 7: 46pp; English.

Novel splice-deleted interferon alpha-receptor (IFNAR) form 2 (W21806) is characterised by a double deletion when compared to transmembranal IFNAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also T73521) obtd. From human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNs, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, Sc Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO
(ABRA) ABRAMOVICH C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1997 (first entry) Spliced-deleted interferon Interferon alpha-receptor;
                                      23-SEP-1997 (first entry)
Transmembranal interferon a
Interferon alpha-receptor;
                                                                                   W21804 standard; Protein; W21804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abramovich C, Ratovitski E,
WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1995.
20-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W21806 standard;
W21806;
             Homo sapiens.
Key
                                                                                                                                                                                                  181
                                                                                                                                                                       181
                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                      ш
                                                                                                                                                                                                                           MYVLLGATTLYLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                    ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                       ENTYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                     FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                  FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
228; Conser
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420. 496
/label Intracellular_domain
/note "comprises amino acids
transmembraņal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .419
/label- Extracellular_domain
/lote- "comprises amino acid residues
422-427 of transmembranal IFNAR"
Location/Qualifiers
1. .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                             99.6%;
                                           alpha-receptor.; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       496
                                                                                                 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-receptor form IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                 Score 1191; DB 1;
Pred. No. 1e-114;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ
                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of.
                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                             22-JAN-1998.
17-JUL-1997; U12455.
17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
KOtenko SV, Pestka S;
WPI; 98-110590/10.
N-PSDB; V19874.
New recombinant DNA - com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU9475977-A.
11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES 6 DEV CO L
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting, modulating or modifying the activities of interferon(s Disclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
Claim 2; Page -; 79pp; English.

This sequence is the human CRFB4 sequence, DNA encoding it is used recombinant DNA (I) of the invention. (I) comprises a sequence (Sl) encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence
                                                                                                                                                                                                                                                  CRFB4 protein.
CRFB4; interle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abramovich C, Ratovitski E, WPI; 95-200634/27
                                                                                                                                                                                             Homo sapiens. W09802542-Al.
                                                                                                                                                                                                                       septic shock; immune response;
                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                               23-JUN-1998
                                                                                                                                                                                                                                                                                             W52296 standard;
W52296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mammalian soluble interferon alpha-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
                                                         rejection
                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRFB4 linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                         ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                             TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                       interleukin-10; IL-10; IL-10 receptor; allograft rejection;
s; photosensitivity; inflammation; autoimmune disease;
shock; immune response; organ rejection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Extracellular_domain 437. .457
                                                                   DNA - comprises sequences encoding interleukin-10 to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1191; DB 1;
Pred. No. 1.2e-114;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                         Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Revel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forms - used ror ies of interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                              in the
    (S2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc encoding CRFB4, both operably linked to expression control sequences.

Cc Cells containing (I) may be used to identify agonists/antagonist of CC II-10. Agonists are potentially useful, e.g. for preventing allograft CC rejection, as vaccine adjuvants, for treatment of photosensitivity, CC inflammation, autoimmune disease and septic shock, while antagonists are contentially useful for increasing immune responses against tumours, Viruses, bacteria and parasites (especially intracellular pathogens) and CC for preventing organ rejection. A vector containing (I) is used to restore, e.g. by gene therapy, II-10 sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind II-10 but not to transduce a containing and intracellular pathogens, can inhibit II-10 activity in cells. Antibodies specific for CRFB4 are used to measure and localise CRBF4, for diagnosts of defective II-10 activity. CC Fragments of (I) are used as primers or probes to assay CREB4-specific CC RNA. Agonists/antagonists may be administered parenterally, orally or rectally especially by intravenous injection or directly into a tumour or callograft.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 66
Novel interferon gamma receptor beta chain p
treatment of inflammatory bowel disease and
Claim 3; Fig.2A; 86pp; English.
The IFN-gamma receptor beta-subunit encoded
                                                                                                                                                               W09516036-A.
15-JUN-1995.
07-DEC-1994; U14277.
09-DEC-1993; US-164596.
                                                                                                                                                                                                                                                                                                                                                                                        IFN-gamma receptor beta-subunit.
Interferon-gamma receptor beta s
interferon-gamma-antagonist.
                                                                               (HEMM/) HEMMI S.
Aguet M, Boehni R,
WPI; 95-224321/29.
                                                                   N-PSDB; Q90808
                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R75782
                                                                                                                               (AGUE/) AGUET M.
(BOEH/) BOEHNI R.
                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 EVLRNLEPWITYCVQVRGFLPDRNKAGEWSEPVCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>Α</u>
                                                                                                                                                                                                                            /label-
                                                                                                                                                                                                                                                                                            /label= Extracelular_domain
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                            /label-
                                                                                                                                                                                                                                                                                                                         label Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.6%;
                                                                                                  Hemm1
                                                                                                                                                                                                                                                          Transmembrane_anchoring_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ⋧
                                                                                                                                                                                                                                                                                                                                                                                                         subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222.5; DB :
encoded by a cDNA clone
                                 chain polypeptide
ase and liver damac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213
                                 damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ន្តន្តន្តន្ត
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.NOV-1998 (first entry)
20.NOV-1998 (first entry)
20.YOY-1998 (first entry)
20.YOY-7 cytokine receptor polypeptide.
20.YOY-7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
20.YOY-7; cytokine receptor family; CRF2; prostate tissue; nervous tissue;
type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
type 2 cytokine receptor family; cRF2; prostate tissue; nervous tissue;
agonist; cell proliferation; cell differentiation; renal disease; human;
neural disease; pancreatic disease.
                                                                                                   Novel human Zcytor? DNA encodes a type 2 cytokine receptor - useful for treating renal, neural, pancreatic and prostatic diseases Claim 1; Pages 55-59; 72pp; English.

This represents the Zcytor? cytokine receptor. Zcytor? is a ligand-binding receptor polypeptide and is a novel member of the type 2 cytokine receptor family (CRF2). An expression vector containing the Zcytor polynucleotide, operably linked to transcription promoter, a sequence encoding a transmembrane and intracellular domain, or both, and a transcriptional terminator can be used to transform host cells for the recombinant production of the polypeptide. The sequences can be used to study the Zcytor? gene and to isolate ligands binding to it. Zcytor? is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from mouse B-cells is given in R75782. Recombinant betapref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may may be used to treat pathological conditions associated w IFN-gamma production.
                                   also be used in the treatment of renal,
                                                  preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Agonists of Zcytor7 can be used to stimulate proliferation and differentiation of cell in these organs. The antagonists and agonists
                                                                                                                                                                                                                                                                                                                 N-PSDB; V57515.
                                                                                                                                                                                                                                                                                                                                                Adams RL, Fa. Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9837193-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W79159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                         ( OMYZ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIYSRHKIY -- KLSPETTYCLKVKAAL-LTSWKI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YENVTVGPPKNISVTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
69; Conser
                                                                                                                                                                                                                                                                                                                                                                 1997; US-943087.
1997; US-803305.
ZYMOGENETICS INC.
L, Farrah TM, Jelmberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%; ilarity 30.1%; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 30..250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "extracellular (ligand-binding) domain; sequence claimed in claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 203; DB 1;
Pred. No. 4.9e-13;
8; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                     ΑC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                       K
ho
                                                                                                                                                                                                                                                                                                                                                                     ភូ
                                   neural,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant beta-subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                   prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                   cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
```

```
Š
                                         밁
                                                                        Ş
                                                                                                                      밁
                                                                                                                                                          8
                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                          Query Match 12.7%; Score 151.5; DB 1; Length 337; Best Local Similarity 24.6%; Pred. No. 1e-07; Matches 61; Conservative 44; Mismatches 94; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 15.4%; Score 184.5; DB 1; Length 553; Best Local Similarity 26.3%; Pred. No. 8.4e-11; Matches 55; Conservative 38; Mismatches 95; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suppressing tumours in mammals with accessory factor 1 (AF-1) -
for interferon gamma, specifically induction of class I HLA
antigens, including use of AF-1 DNA in gene therapy
Disclosure; Fig 21A; 114pp; English.
The sequence is that of human interferon-gamma accessory factor-1.
Incorporation of AF-1 into immune and tumour cells re-establishes
normal function with elimination of malignant cells.
Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYNE-) UNIV NEW JERSEY.

COOK JR, Donnely RJ, Emanuel S,

Pestka S, Schwartz B, Soh J;

WPI; 95-106679/14.

N-PSDB: 084697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-1995.
22-AUG-1994; U09438.
20-AUG-1993; US-110119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-1995 (first entry)
Human IFN-gamma accessory factor-1.
Interferon-gamma; AF-1; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R71035 standard; Protein; 337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R71035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 QCVTN----HTLVLTWLEPNTLYCVHVES 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204 : : | | | | | | | : :
                                         175 YYVHYWE--KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI 232
                                                                                 165
                                                                                                                    120 GALHSAWVTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRESSPEDIADTSTAE----EC 174
                                                                                                                                                            109 ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LYLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                                                                                      69
                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                      12 VLVAVGPWVLSAAAGG---KNLKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFS 62
                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
  HCIKTTVE 226
                                                                                                                                                                                                                                       FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                               YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV 218
                                                                                                                                                                                                 YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL 119
                                                                                                                                                                                                                                                                                 LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kotenko S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mariano TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
```

뮍

233 SCYETMAD 240

Search completed: June 1, 2000, 00:40:15 Job time: 20021 sec

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match
Listing first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
score grea
and is der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
    seq length: 0 seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
1: /cgn2_6/ptodata,
2: /cgn2_6/ptodata,
                                                                                                                                                                                                                                                                                                                   100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June 1, 2000, 04:17:54; Search time 23.82 Seconds (without alignments) 138.798 Million cell updates/sec
                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-240-675-2_COPY_1_229
1196
1 MMYVLLGATTLYLVAVGPWV......WKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145308 segs, 14437401 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/5COMB.pep:*
/cgn2_6/ptodata/1/laa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0%
45 summaries
 US-08-328-256-11
US-08-328-256-12
US-08-328-256-12
US-08-328-256-12
US-08-471-454-2
US-08-471-453-2
US-08-471-453-2
US-08-471-453-2
US-08-471-4277-2
PCT-US94-14277-2
PCT-US94-14277-2
PCT-US94-14277-2
PCT-US94-14277-2
PCT-US94-14277-2
US-08-943-087-18
US-08-943-087-18
US-08-943-087-26
US-08-943-087-27
US-08-943-087-27
US-08-943-087-28
US-08-943-087-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
Sequence 11, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 6, Appl Sequence 6, Appl Sequence 11, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 26, Appl Sequence 27, Appl Sequence 28, Appl Sequence 30, Appl Sequence 31, Appl Sequence 41, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
```

	US SE		
Query I Best Lo Matche	-08 Pates GENUALITION OF CONTRACTOR OF THE PROPERTY OF THE P		0 C C C C C C C C C C C C C C C C C C C
Match ocal s 22	I 1 Jence 11, Applent No. 564374 NERAL INFORMAT APPLICANT: RA ITTLE OF INVEN COMPUTER: D.C. COUNTRY: USA EXITE 20004 COMPUTER READA MEDIUM TYPE: COMPUTER READA APPLICATION FILING DATE: FILING DATE: PRIOR APPLICAT APPLICATION REFERENCE/DO APPLICATION REFERENCE/DO APPLICATION REFERENCE/DO APPLICATION REFERENCE/DO APPLICATION REFERENCE/DO APPLICATION REFERENCE/DO TELEYA: 2486 FORMATION FOR SEQUENCE CHARA LENGTH: 434 TYPE: amino STRANDEDNESS TOPOLOGY: 1 MOLECULE TYPE: MOLECULE TYPE:		1184 1174 11684 11689 11689 114 1462 1170 1170 1170 1170 1170 1170 1170 117
Simila 9; Cc	6-11 1, Applica 1, App		88888991111115 1111111111111111111111111
larity Conserv	Application US/08328: Application US/08328: Application US/08328: Application US/08328: CASTON: ARAMOVICH, Caroli: AGURES: IS ACTURES: IS ARAMOVICH, Caroli: INVENTION: BROWDY AND NEIMA LICATION AND NEIMA LICATION APTA: IS PACED NATA: IS E PACTOCKET NUMBER: US/08/3 AGION NUMBER: REFEL- ATION NUMBER: REFEL- ATION NUMBER: 20-628-5197 CCLARACTERISTICS: INICATION STAR INFORMATION: BROWDY, ROGET L. LICATION STAR INFORMATION: BROWDY, ROGET L. INFORMATION: BROWDY, ROGET L. INFORMATION: CARAGETERISTICS: INCATON SEQ ID NO: CHARACTERISTICS: INCATON SEQ ID NO: CHARACTER		44004000000000000000000000000000000000
100. 100. ative	tion US/083282 ; , Michel , Michel OVICH, Carolin ITSKI, Edward N: SOLUBLE IN N: PREPARATIO ES: 12 DRESS: WAY AND NEIMAR WAY AND NEIMAR PC Compatible M: PC-DOS/MS- ntin Release # PC LOS/MS- ON DATA: BER: US/08/32 4 - CCT - 1994 4 - CCT - 1994 DATA: BER: REVEL-1 WHER: REVEL-1 TINDMER: 25 INFORMATION: ROGET L FORMATION: ROGET L STINFORMATION: 11: NISTICS: INFORMATION: 13 - 3528 11 INFORMATION: 17 NUMBER: 25 INFORMATION: 18 - 197 37 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528 31 - 3528		553 553 553 553 553 553 553 553 553 553
0 0 0 0 1: 1:	S/08328 el el el caroli Edward LUBLE I EDWARD D NEIMA Street, DOS/MS (-DOS/MS (-DOS/		
Sc Pr	1 1 1 1 1 1 1 0 2 5 N	₽	US-08-9
₹ @ C	56 N.W., N.W., S.	LIGN	3-94 3-94 3-94 3-94 3-94 3-94 3-94 3-94
e 119 1. No. Smatc	< > >	ALIGNMENTS	-943-087-46 -943-087-56 -943-087-59 -943-087-59 -943-087-50 -943-087-50 -943-087-58 -943-087-58 -943-087-10 -943-087-10 -943-087-10 -943-087-10 -943-087-10 -943-087-10 -943-087-10 -943-087-10 -943-088-10 -110-683-4 -477-166-4
96; . 2.4 .ches	ON ALP USE Suite	ຂີ	56-44
DB e-1	#1 #1		00004000004 <b>4</b>
1; 26; 0;	.30		
Lengt Indel	RECEPTOR		٠
rth 4	់ អ		n bess n
134; 0;	ú		Sequence
Gaps			444 C C C C C C C C C C C C C C C C C C
ικ			Appl Appl Appl Appl Appl Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli

δõ

MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT

60

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                               Ş
                                                                                                                                                  ; MOLECULE TYPE: protein US-08-307-588-2
   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                 Query Match
Best Local
                                                                Matches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Relicurrent APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 05-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: SAXE, Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/EP93/00770 FILING DATE: 30-MAR-1993
                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                  TELEPHONE:
MYVYLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, Application US/08307588
). 5919453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BENOIT, Patrick MEYER, Francois
                                                                                                                                                                                                                                                                 : (202)672-5300
(202)672-5399
                                                                  Conservative
                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1994
                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     us/08/307,588
                                                                                                                                                                                                                                                                                                  28,665
FR: 17283/117/GUPL
                                                                                                                                                                                                                                                     2:
                                                                  0
                                                                Score 1196; DB 2;
Pred. No. 2.4e-126;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 500
                                                                                            Length
                                                                  Indels
                                                                                                   436;
                                                                  0,
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                  0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-08-328-256-12
                       Ş
                                                   밁
                                                                              δõ
                                                                                                                                                                               ; MOLECULE TYPE: US-08-328-256-12
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5643749
GENERAL INFORMATI
                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12,
                                                                                                                          Best
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/328
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 496 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SOLUBLE INTERPERON ALPHA-RECEPTOR, ITS TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                               TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                  NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: RE'
REFERENCE/DOCKET NUMBER:
61
             61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                          Local
                                                                                                                                                                                                           TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                   TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                             229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                          Similarity
                                                                                                                                                                                                                                   : 496 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABRAMOVICH, Carolina RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVEL,
                                                                                                                                                                                                          ss: single
linear
                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michel
                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/328,256
                                                                                                                                                                                                                                                                                                                                                               REVEL-13
                                                                                                                                                                                                                                                                                 12:
                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                     25,618
                                                                                                          Score 1196; DB 1;
Pred. No. 3e-126;
D; Mismatches 0;
                                                                                                             Indels
                                                                                                                                       Length
                                                                                                                                       496;
                                                                                                             0
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                             0,
```

```
밁
                                                                                    8
                                                                                                                                         B
  S
                                                       Ş
                                                                                                             Ş
                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                       ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-328-256-10
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08328256 Patent No. 5643749
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SOLUBLE INTERFER
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: REVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
 181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                      61
                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 24-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                             TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                         FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                   FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                                                                                                                                                                    229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVEL, Micher RABRAMOVICH, Carolina ABRAMOVICH, Carolina RATOVITSKI, Edward SCLUBLE INTERFERON ALPHA-RECEPTOR, ALPHA-RECEPTOR, SCHUBLE NATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                  202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JMBER: IL 107378
24-OCT-1993
                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us/08/328,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVEL-13
                                                                                                                                                                                                  0
                                                                                                                                                                                                             Score 1196; DB 1;
Pred. No. 3.6e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                          25,618
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                             Length 557;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                 0;
                                                                                                                                                                                                 Gaps
                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                         60
                                                                                                                                                                                                  0
                             밁
                                                    Ş
                                                                                   B
                                                                                                            οy
                                                                                                                                         멍
                                                                                                                                                                  9
                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-471-454-2; Sequence 2, Ap.; Patent No. 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 816-410
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LUTFALLA,
APPLICANT: GRESSER,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DO SOFTWARE: PATENTIN RelaCURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
  181
                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Application US/08471454 5731169
                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRESSER, Ion
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUTFALLA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995
                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges
```

```
PRIOR APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY,AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
                                                                                                                           61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                           1 MAYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                          FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                               MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                       100.0%; Score 1196; DB 1; 100.0%; Pred. No. 3.6e-126; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/471,454
                                                                                                                                                                                                                                                                                                                                         Length 557;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR THE
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                       0
```

```
Š
                                                                                                                                                             ₽
                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                 밁
          S
                                                           밁
                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                             Query Match
---- rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                                                   121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
     181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                             61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                    1 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                                                                                                                                        FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                              HITTHE THE TEACH TO THE TEACH THE TEACH TO T
                                                        TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                          229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08466974
5861258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UZE, Gilles
LUTFALLA, Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIXN UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA FRAGMENT CODING FOR THE GENE
THE ALPHA INTERFERON RECEPTOR AND
PREPARATION OF THE CORRESPONDING I
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1196; DB 2; 100.0%; Pred. No. 3.6e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/466,974
                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960-7
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND PROCESS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN
                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                    Š
                                                                                                                                                          밁
                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                  Matches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/900,64
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: ER 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-JUN-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                        121
                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (/U3) TELEFAX: 200797 NIXN UR
                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                      1 MYVYLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITY: ARLINGTON
FATE: VIRGINIA
ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                                                   TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                       FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                           FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT

    Application US/0847145;
    5886153

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUTFALLA, Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA FRAGMENT CODING FOR THE GENE FOR THE THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREPARATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 07/900,642
1-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/471,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                  Score 1196; DB 2;
Pred. No. 3.6e-126;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                Length 557;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                               Gaps
```

60

```
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-588-4
                                                              밁
                                                                                      S
                                                                                                                       밁
                                                                                                                                                  S
                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Applic
Patent No. 5919453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EP 9
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D. 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3000 A SO
                                                                                                                         61
                                                                                                                                       61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 30-MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                            TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08307588
                                                                                                                                                                                                                                                                                                                                                                                 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Foley & Lardner
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAVEC, Ivan
TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BENOIT, Patrick MEYER, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGUIRE, Deborah
PLAVEC, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernhard D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1993
                                                                                                                                                                                                                                            100.0%; Score 1196; DB 2;
100.0%; Pred. No. 3.6e-126;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP 92400902.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/307,588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17283/117/GUPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25 (EPO)
                                                                                                                                                                                                                                                                          Length 557;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                              0
                                                                                                                         밁
                                                                                                                                                                                  В
                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                          å
                                                                                                                                                                                                                                                                                                                                    Ş
                                                            US-08-683-743-4
            Sequence 4, Application US/08683743
Patent No. 5843697
GENERAL INFORMATION:
```

```
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US94-14277-3
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Applicati GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/164
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,65
REFERENCE/DOCKET NUMBER: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: patin (Genentech)
CURRENT APPLICATION NUMBER: PCT/US9.
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
181 PSLKKHSNYSTXQCISTTVANK 202
                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                        61
                                                                                                                                                        88 NFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                             -
                                                                                                                                                                                                                                             28 KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LICANT: Hemm1, Silvio
                           LTSWKIGVYSPVHCIKTTVENE 228
                                                                                                                                                                                                            SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
                                                                                                     SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
                                                                                                                                        EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
                                                                                                                                                                                                                                                                                98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94080
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                           202 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aguet, Michel
                                                                                                                                                                                                                                                                                                41.0%; Score 490.5;
48.5%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subunit Polypeptides
                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                              1.9e-47;
                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                   202;
                                                                                                                                                                                                                                                                                ۲.
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                             60
                                                                                                                                                                                                                                             87
```

```
õ
                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                             PCT-US94-14277-2
                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,743
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                             Sequence 2, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201-343-1684
NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: U/U/COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                               TITLE OF INVENTION: Receptor Subunit Polypeptides NUMBER OF SEQUENCES: 8
                                                                                              APPLICANT:
                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     116 PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          176 EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT 213
                                                                                                                                                                                                                                                        187 HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                     131 PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                                                                                                                                                                                      59 YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 WVLSAAAGGKNLKS------PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 30.3 nes 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      72 NWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAOIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 411 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                      3 WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza,
                                                                            Bohni, Ruth
Hemmi, Silvio
                                                                                                              Aguet, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kotenko, Serguei
/ENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.6%;
               Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 222.5; DB:
Pred. No. 5.6e-17;
0; Mismatches 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                       PCT-US94-14277-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-14277-2
                                                                                                                                                                                                                                                   Sequence 6, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                        COUNTRY:
                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
```

```
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                  APPLICANT: Aguet, Michel APPLICANT: Bohni, Ruth APPLICANT: Hemmi, Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                          ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                  TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Love, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/
FILING DATE: 09-DEC-199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YENVTVGPPKNISVTPGKGSLVIHFSPPFD----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    South San Francisco 
California
                                                                                                                                                                                                                                                                                                                                                                                           Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: 415/225-5530
415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.0%;
                                                                                                                                                                                                                                                                             Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 203; DB 4;
Pred. No. 9.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
```

```
RESULT 13
US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08943087 Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acid
                                              CURRENT APPLICATION DATA
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         APPLICANT: FAXIAH, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 KPYRVYCLQTERQLILKNKKIRPHGLLSNVSCHETT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 866
LECOMMUNICATION THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
                                                           OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                               COMPUTER:
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Love, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                         APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                     ZIP: 98102
                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DITETRCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LARPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i: 223 amino acids amino acid
                                                                                                                                                                                                     Seattle
                                                                                                                                                                                    WA
                                                                                                                                                                                                                     1201 Eastlake Avenue East
                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415/952-9881
                                                                                                                                                                                                                                                                                                                                             Jelmberg, Anna
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                Lok, Si
Kho, Choon J.
                                                         SYSTEM: DOS
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                               Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                            IBM Compatible
                                                                                                                                                                                                                                          ZymoGenetics, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.1%;
                                                                                                                                                                                                                                                                                                                                                              Anna C.
                                                                                                                                                                                                                                                                                                                                Theodore E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 192; DB 4;
Pred. No. 8.5e-14;
7; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
COMPUTER: IBM COMPUTER: COMPUTER: IBM COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/943,087
APPLICATION UMBER: US/08/943,087
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/8
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 QCVTN----HTLVLTWLEPNTLYCVHVES 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 QIGPPEVALTIDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                                                    COUNTRY: UZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                                                                    Seattle
                                                                                                                                                                                                                                                                                            OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                          T: Farrah, Theresa M.
INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                     WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08943087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 amino acids
                                                                                                                                                                                                                                      E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                              Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                               Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                               Whitmore,
                                                                                                          E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.48;
                                                                                                                                                                                                                                                                                                                                               Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/803,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 184.5;
Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4e-12;
es 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
```

Gaps

7;

밁 S

REGISTRATION NUMBER: 32,743
REFERENCE/COCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627

96-24C1

TELEFAX: 206-442-6678

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/8
FILING DATE: 20-FEB-1997

08/803,305

ORNEY/AGENT INFORMATION:

```
; TOPOLOGY: 11s; MOLECULE TYPE: FRAGMENT TYPE: US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.4
Best Local Similarity 26.3
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                          APPLICANT: FAITAH, THERESA M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
                                                                                                                                                                                                                     STREET: 1201 E
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 QCVTN----HTLVLTWLEPNTLYCVHVES 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 QIGPPEVALTIDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LYLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
CLASSIFICATION: 536 IOR APPLICATION DATA:
                                      FILING DATE:
                                                      APPLICATION NUMBER:
                                                                                                                                                                                    COUNTRY: UP
                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08943087
                                                                                                                                                                                                                                                       E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                  Jelmberg, Anna C.
Adams, Robyn L.
Whitmore, Theodore
                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Score 184.5; DB 2; 26.3%; Pred. No. 2.4e-12; tive 38; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                      Theodore E.
                                                    US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
```

```
ş
                                                                      밁
                                                                                                  δÃ
                                                                                                                                        밁
                                                                                                                                                                       Š
                                                                                                                                                                                                           멍
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
"""ches 55; Conservat
 밁
                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACT
LENGTH: 553 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
196 QCVTN----HTLVLTWLEPNTLYCVHVES 220
                                  178 ERIENIYSRHKIYK--LSPETTYCLKVKA 204
                                                                     136 QIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195
                                                                                                    127 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                        11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                        76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                       68 TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                         18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lunn, Paul G
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/803,305 FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206-442-6678
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                   protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                               15.4%; 26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16:
                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96-24C1
                                                                                                                                                                                                                                                                                               Score 184.5; DB 2
Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                               Length 553;
                                                                                                                                                                                                                                                                               21;
```

Gaps

7 ;

7;

Search completed: June Job time: 15449 sec ۳ 2000, 04:17:55

```
OM protein . protein search, using sw model
June 1, 2000, 04:35:14; search time 64.83 Seconds (without alignments) 207.099 Million cell updates/sec
                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

Perfect score:	Title:
	US-09-240-675-2_COPY_1_229

Run on:

Sequence: 1 MMVVLLGATTLVLVAVGPWV......WKIGVYSPVHCIKTTVENEL 229

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 168808 segs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_63:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

4 4 4 5 4 3	440	333 387 6	33331
82.5 5.5		83.55 5556	87 87 87 86 . 5
თ თ თ ა ა ა ა	, o o o o	7.1 7.0	7.3 7.3 7.3
378 406 1068	5255	2131 623 306	639 1083 1120 26926 429
ผผพ		งงษง	N L N N N
T04239 B64432 S01519	JT0569 JS0734 T04591	S01446 VGBE68 A25698	JC1391 T23031 S67208 I38344 S59773
hypothetical prote capsular polysacch hypothetical prote	chondromodulin I p endo-1,4-beta-xyla ferulate-5-hydroxy	hypothetical prote glycoprotein E - h probable protein k s-locus-spoolfic a	dnaK-type molecula hypothetical prote hypothetical prote titin, cardiac mus 26S proteasome reg

# ALIGNMENTS

RESULT  1 A12554  Interferon alpha/beta receptor precursor - human  C:Species. Homo aspiens (man)  C:Date: 22-un-1990 **ext_change 22-Oct-1999  C:Accession: A12594 .517112  R:Cute. G: Lutfalla .G: Gresser, I.  Celi 60, 25-224, 1990  C:Accession: A12594 .517112  A:Title: Generic transfer of a functional human interferon alpha receptor into mouse  R:Geterone number: A12694; MUID:90124632  A:Accession: A12594  A:Accession: The structure of the human interferon alpha/beta receptor gene.  A:Accession: The structure of the human interferon alpha/beta receptor gene.  A:Accession: S17112  A:Accessi			
4 0 4 0 9	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	% W D	77707777777777777777777777777777777777
4 0 4 0 9	1 61 61 121 121 181	Query Ma Best Loc Matches	RESULT 1 A32694 Interferon alpha/beta receptor precursor - human C;Species: Homo sapiens (man) C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_chan C;Species: Lutfalla, G; Gresser, I. R;Uze, G; Lutfalla, G; Gresser, I. Cell 60, 225-34, 1990 A;Title: Genetic transfer of a functional human interferon a. A;Reference number: A32694 A;Molecule type: mRNA A;Residues: 1-557 <uze> A;Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; R;Lutfalla, G. submitted to the EMBL Data Library, July 1991 A;Residues: 1-587 <uze> A;Reference number: S17112 A;Reference number: S17112 A;Accession: S17112 A</uze></uze>
4 0 4 0 9	WARTE TO THE TERM TO THE TERM TENDES WE THE TE	igth 557; lels 0;	hange 22-0c halpha rece na/beta rece na/beta rece na/beta rece na/beta rece
		aps	4 0

```
interferon alpha/beta receptor - mouse (Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C; Accession: A4528; 148423; 148424; 148425; 148426; 148427; 148428; 148429 R; Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 A; Title: Behavior of a cloned murine interferon alpha/beta receptor expressed A; Reference number: A45283; MUID: 92262522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S27387; S3770
R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
                                                                                 A; Residues: 1-590 <UZE>
A; Residues: 1-590 <UZE>
A; Cross-references: GB: M89641; NID: g194111; PIDN: AAA37890.1;
A; Cross-references extracted from NCBI backbone (NCBIN: 102354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: lung
C; Keywords: antiviral; cytokine receptor; transmembrane protein
F; 1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: MD R; Lim, J.K.; Langer, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-560 < MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Specific antiviral activities of the human alpha A; Reference number: S27387; MUID:93076908 A; Accession: S27387
                A; Title: Sta
A; Reference
                                                          Gene 148,
                                                                                                                                                                   A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F; 25-560/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:L06320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-421,'V',423-560 <LIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: S33770; MUID:93305725
A;Accession: S33770
                                                                               R; Lutfalla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X68443; NID: g431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon alpha receptor type 1 precursor
C;Species: Bos primigenius taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  веят Local
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 MYVLLGATTLVLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNEILRWNRSDESVGNYTF 61
           Structure of the murine interferon alpha/beta nce number: I48423; MUID:95047447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMWALDGLSFTYSLLIWKNSSGVEE 178
                                                          343-346,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPVYCINTTERHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVPFLEAQIGPPDVHLEAEDKAIILSISPPGTKDSIMWAMDRSSFRYSVVIWKNSSSLEE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155; Conserv
                                                                               Uze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon alpha receptor type 1 #status predicted
                                                            1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.4%; Score 782.5; DB 2; 67.1%; Pred. No. 6.5e-61; tive 31; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID: g163187; PIDN: AAA02571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bovine alpha interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA48484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shown
                                receptor-encoding gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID: 9432
                                                                                                 PID:g194112
NCBIP:102357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                         'n
                                  high-frec
                                                                                                                                                                                                                                                           homospe
A; Reference number: G06935
A; Accession: G01418
A; Status: preliminary
```

Š 밁 Ş 밁 δÃ

δ 몽

밁

R; Lutfalla, G.

translated

from

GB/EMBL/DDBJ

06-Jun-1997

#text\_change 17-Jul-1998

```
RESULT 4
601418
cytokine receptor family II, member 4 -
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision (C;Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 177/3; 331/1 C; Keywords: cytokine re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 473-590 <RE7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 426-445 <RE6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 397-424 < RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 265-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; A;Accession: I48426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 118-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Accession: I48423;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Gene: IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1;
                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                           181 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                             121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLAVVGAAALVLVAGAPWVLPSAAGGENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTF
                                                                                                                                                                                 STYYVEKIPELLPETTYCLEVKAIHPSLKKHSNYSTVQCISTTVANKM
                                                                                                                                                                                                                                                                                                                                                              SAEYRTKDEAKWLKVPECQHTTTTKCEFSLLDTNVXIKTQFRVRAEEGNSTSSWNEVDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
                                                                                                                                                                                                                                                                        IPFYTAHMSPPEVRLEAEDKAILVHISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTI
                                                                                                                                                                                                                                                                                                                                                                                                        SFDYOKTGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 600.5; DB 1; ; Pred. No. 6.4e-45; 40; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from GB/EMBL/DD3J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB/EMBL/DDBJ
                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                 229
                                                                                                                                                                                                                              229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g510262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g755813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g755812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID: g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID:g755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g755810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID: g510265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲.
                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۳.
```

```
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene family maps on chromosome A;Reference number: A47003; MUID:93300510
A;Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:CRFB4; CRF2-4
A;Cross-references: GB:138168; OMIM:123889
A;Map position: 21922.1-21922.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                밁
                                                                                                                                            Ş
                                                                                                                                                                                  멍
                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokine receptor family class II protein CRF2-4 precursor -
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          뭐
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U08988; NID:g571295; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-273 <LUT>
                                                  밁
                                                                              S
                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 21q
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:Z17227; NID:g393378; PID:g393379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 30.3 Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
                                                  176
                                                                                 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 WVLSAAAGGKNLKS------PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD
                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                   w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSLGSWLGGCLLVSALGMVPPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                  WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGMQVEVLDDSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEVHLEAEDKAIVIH-ISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRIFODKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP 115
                                                EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT
                                                                               HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
                                                                                                                PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                 YRIFQDKCMNTTLTECDFSS---LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                                                NWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                 WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A47003
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                  18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%;
                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 227.5; DB 2;
Pred. No. 1.2e-12;
2; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                  Score 222.5; DB 2
Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g571296
                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 273;
                                                                                                                                                                                                                                                                                                                   Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                   œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 at les
밁
                    ρy
                                                            밁
                                                                                        δÃ
                                                                                                                              ₿
                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
```

```
A;Cross-references: GB:S69336; NID:g545841; PIDN:AAB30165.1; A;Experimental source: early B-cell line Y16 A;Note: sequence extracted from NCBI backbone (NCBIN:145654, C;Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: A novel member of the interferon A;Reference number: A49947; MUID:94170381 A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A49947
R;Hemmi, S.; Bohni, R.; Stark, G.; Di
Cell 76, 803-810, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-349 <GIB>
A; Cross-references: GB: U53696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: JC6311
A; Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Gibbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A;Title: CRF2-4:isolation of cDNA clones encoding the human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-332 <HEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: JC631: R; Gibbs, V.C.; Peni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                  123 FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 YSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 VHLEAEDKAIVIHIS------PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENI 183
                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                        71 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I
                                                                                                                                                                                                                                                                   21 LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 -----CKRTASTQCDFS--HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 IKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 VGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MQIESLAESLELRFSAPQIENEPET-----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGFLLVPALG - -MIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDSEVLRNLEPWTTYCIQVQGFLLDQNRTGEWSEPICERT 212
                                                                                                     DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Similarity 62; Conserv
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.4%;
                                                                                                                                                                                                                                                                                                                                                  17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                                                                                                                                                                                                                                                                  Score 203; DB 2;
Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 220; DB 2;
Pred. No. 7.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor family complements functionality
-VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ቹ
:
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aguet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 349
                                                                                                                                                                                                                                                                                                                                                                         Length 332;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBIP:145656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:g545842
                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse proteins.
184
                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ø
```

```
interferon gamma receptor precursor - human C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 *sequence_revision 28-Feb-C:Accession: A31555
R:Aguet, M.; Dembic, Z.; Merlin, G.
Cell 55, 273-280, 1988
A:Title: Molecular cloning and expression of t A:Reference number: A31555; MUID:89003065
A;Accession: A31555
A;Accession: A31555
A;Residues: 1-489 <AGU>
A;Cross-references: GB:J03143; NID:g184650; PI
                                                                                                                                                                                                                                                                                                                                                                                                δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-63,'Q',65-337 <RE2>
A;Cross-references: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Identification and A;Reference number: A49946; A;Accession: I38500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
  C;Genetics:
A;Gene: GDB:IFNGR1;
A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: I38500; I38501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Homo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: clone pJS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I38501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-337 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      position: 21
                                                                                                                                                                                                                                                                                                                                                                  233
                                                                                                                                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 VLVAVGPWVLSAAAGG---KNLKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALHSAWVTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FC
                                                                                                                                                                                                                                                                                                                                                                SCYETMAD 240
                                                                                                                                                                                                                                                                                                                                                                                                    HCIKTTVE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                             YYVHYWE--KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLLLGVFAAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENT-SSWYEVDSFTPFRKAQIGPPEVHLE----AEDKAIVIHISPGTKDSVMWALDGLSFT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor accessory factor-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1994
    GDB:120688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of an accessory factor required for activation \ensuremath{\text{MUID:94170380}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          psk1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
    OMIM: 107470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 151.5; DB 2
Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                              28-Feb-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mariano, T.M.; Cook, J.R.; Wang, N.;
                                                                                                                                                    Of
                                                        PIDN: AAA52731.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor -
                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                    human
                                                                                                                                                    interferon-gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                      PID: g306915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                              23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emanuel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ö.
                                                                                        A;Molecule type: mRNA
A;Residues: 1-94,'E',96-477 <HEM>
A;Cross-references: GB:M28233; NID:g194131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
R;Munro, S.; Maniatis, T.

Proc. Natl. Acad. Sci. U.S.A. 86, 9248-9252, 1989
A;Title: Expression cloning of the murine interferon gamma
A;Reference number: A36224; MUID:90083245
A;Accession: A36224
                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-477 < COF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: A35468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-477 < KUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
```

```
A;Molecule type: mRNA
A;Residues: 1-94, E;96-477 <GRA>
A;Residues: 1-94, E;96-477 <GRA>
A;Residues: 1-94, E;96-477 <GRA>
A;Cross-references: GB:M26711; NID:g194126; PIDN:AAA37896.1; PID:g309330
A;Hemm1, S.; Peghini, P.; Metzler, M.; Merlin, G.; Dembic, Z.; Aguet, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 9901-9905, 1989
A;Title: Cloning of murine interferon gamma receptor cDNA: expression in A;Reference number: A34508; MUID:90099370
A;Accession: A34508
                                                                                                                                                                                                                                                                   A;Cross references: GB.J05265; NID:g197964; PIDN:AAA39178.1; PID:g309394 R;Gray, P.W.; Leong, S.; Fennie, E.H.; Farrar, M.A.; Pingel, J.T.; Fernar Proc. Natl. Acad. Sci. U.S.A. 86, 8497-8501, 1989 A;Title: Cloning and expression of the cDNA for the murine interferon gam A;Reference number: A34423; MUID:90046824 A;Accession: A34423 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change
C;Accession: A34368; A35468; A34508; A34508; A36224; I48941
R;Kumar, C.S.; Muthukumaran, G.; Frost, L.J.; Noe, M.; Ahn, Y.H.
J. Biol. Chem. 264, 17939-17946, 1989
A;Title: Molecular characterization of the murine interferon gam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 6q23-6q24
C; Superfamily: interferon
C; Keywords: cytokine recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M25764; NID:g197962; PIDN:AAA39177.1; R;Cofano, F.; Moore, S.K.; Tanaka, S.; Yuhki, N.; Landolfo, S.; Biol. Chem. 265, 4064-4071, 1990
A;Title: Affinity purification, peptide analysis, and cDNA sea;Reference number: A35468; MUID:90154099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A34368; MUID:90036866 A;Accession: A34368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon gamma receptor precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 ALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA---EKENTSSWYEV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MALLFLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYWEY--QIMPQVPV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VVLLGATTLYLVAVGPWVLSAA-AGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNV-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSFTPFRKAQIGPPEVHLEAEDKAIVIHI --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEFAVCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKE--SAYAKS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 22.
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EDDCDEIQCQLAIPVSSLNSQYCVSAEGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 117.5;
; Pred. No. 0.0:
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SPGTK----DSVMW 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                         interferon gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y.H.; Mariano, T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g309393
S.; Appella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           Fernandez-Luna, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

PIDN: AAA37898.1;

PID:g309331

human

cells

int

receptor cDNA

```
A; Map position: 4
A; Introns: 10/3; 61/3;
A; Introns: 6768/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB.M28995; NID:g194123; PIDN:AAA37895.1; PID:g309329 R;Raval, P.; Obici, S.; Russell, S.W.; Murphy, W.J. Gene 154, 219-223, 1995
A;Title: Characterization of the 5' flanking region and gene encoding the A;Reference number: I48941; MUID:95197006
A;Accession: I48941
                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A;Reference number: Z20442 A;Accession: T27934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U05960; NID:g454092; PIDN:AAA80980.1; C;Superfamily: interferon gamma receptor C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translation not shown; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-28 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-477 <MUN>
                                                                                                                                                                     A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                        A; Residues: 1-6831 <WI2>
                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, May 1996 A; Reference number: z20458
                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-6831 <WIL>
A;Cross-references: EMBL:273897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
A;Experimental source: clone ZK617
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZK617.1a - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
Accession: T27934; T28030
                                                                                                                                                                                                        Cross-references: EMBL:273899;
                                                                                                                                                                                                                                                               Status:
                                                                                                                                                                                                                                                                                Accession: T28030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
 Best Local Matches '
                                                                                                                                                                                                                                           Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                  CESP: 2K617.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
                                                                                                                                                                                                                                                           preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDG----LSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYC-LKVKAALLTS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE-KENTSSWYEVDSFTPFRKAQIGPP--EVHLEAEDKAIVIHISP-----GTKDSVMWA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YO-----KTGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIK-----LRIR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGRMILLVV--LMLSAKVGSGALTSTEDPEPPSVPVPTNVLIKSYNL-----NPVVCWE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTLVLVAVGPWVLSAAAGGKNLKS---PQKVEVDIIDDNFILRWNRSDESVGNVTFSFD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKVGQKESDYARSKEFLMCLKGKVGPPGLEIRRKKEEQLSVLVFHPEVVVNGESQGTMFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQNMSQTPIFTVQVKVYSGSW---DSCTNISDHCC-----NIYGQIMYPDVSAWARVK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DGSTCYTFDYTYYVEHNRSG-----EILHTKHTVEKEECNETLCELNISVSTLDS
 Similarity 22.
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                           135/2; 168/3;
6800/3
                                                                                                                                                                                       clone
               8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%;
22.9%;
                                                                                                                                                                                     999; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617 ZK829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
               Score 97.5;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102.5; D
Pred. No. 0.23;
B; Mismatches
                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       мау
                                                                                                             256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3;
 Mismatches
                                                                                                                                                                                                                                                             GB/EMBL/DDBJ
                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87;
                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change 29-Oct-1999
                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                     6831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding the mouse interfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:g454093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
 53;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
```

```
A;Map position: IV
A;Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/
152/3; 669/3; 6776/1; 6808/3
C;Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homol
C;Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; seri
F;806-898, 899-990, 991-1083,1084-1175,1178-1273,1474-1567,1770-1864,2066-2158,2358-2
96-5790,6263-6356,6386-6478,6541-6635,6649-6742,6745-6838/Region: motif 2
F;1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2
23,4215-4313,4314-4455,4415-4516,4612-4710,4711-4811,4908-5009,5010-5109,5110-5210,
F;5940-6197/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: myosin-regulating protein N;Contains: protein kinase (EC 2.7.1.-) C;Species: Caenorhabditis elegans C;Date: 28-oct-1995 *sequence_revision 24-oct-1997 C;Accession: S57242; S07571; S06797; S57218 C;Accession: S57242; S07571; S06797; S57218
                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
A;Experimental source: var. Bristol
C;Comment: Lack of unc-22 leads to a constant twitching of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics 134, 1097-1104, 1993
A;Tille: Additional sequence complexity in the muscle A;Reference number: $57218; MUID:93387664
A;Accession: $57218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: var. Bristol R;Benian, G.M.; L'Hernault, S.W.; M Genetics 134, 1097-1104, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence of an unusually large protein A; Reference number: S06797; MUID:90044042 A; Accession: S06797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: var. Bristol R; Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Nature 342, 45-50, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-6839 <BEN1>
A; Cross-references: EMBL:L10351
A; Experimental source: var. Bri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: Additional sequence complexity within twitching A;Reference number: S57242 A;Accession: S57242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Benian, G.M.; L'Hernault, S.W.; Morris, M.E. submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                         A; Gene: unc-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: X15423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 792-6839 <BEN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: S07571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data A; Reference number: S07571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    twitchin - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1856 LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP---CAKV 1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ဖွဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLKVKAALLTSWK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GTPDVVDWDADRVS----LEWEPPKSDGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVIHISPGTKDSVMWALDGLSFTYSLLIW----KNSSGVEERIENIYSRHKIYKLSPETTY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.W.; Morris, M.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       November
                                                                                                                                                                                                                                                                                                                                                                                 constant twitching of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moerman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene, unc-22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulation
                                                                                                                                                                                                                                                                                                                                                                                        body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -APITQY 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               얁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>e</u>1
```

```
밁
                                                                                                                                         ş
                                                                                                                                                                                                                                                                                                                                 A; Map position: 4
A; Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Harris, B.
submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: Fig. DNA
A;Molecule type: DNA
A;Molecule: 1-7160 <WIL>
A;Residues: 1-7160 <WIL>
A;Cross references: EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022;
A;Cross references: Clone ZK617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein ZK617.1b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T27935; T28031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
                                                                      ő
                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7160 <WIZ>
A;Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T28031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, May A; Reference number: 220442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;5948-5956/Region: F;5971/Active site:
   õ
                                    밁
                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T27935
                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: 2K617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: clone
                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1864
                                                                                                            2242
                                                                                                                                                                               2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002 VIEKKGKHGRDWQ 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1921 KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
       199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 22.8 tos 44; Conservative
                                                                                                                                                                                                        30 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 82
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV 1920
                                                                                                          KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                           TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 141
                                                                                                                                                                             LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP---CAKV 2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLKVKAALLTSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVIHISPGTKDSVMWALDGLSFTYSLLIW----KNSSGVEERIENIYSRHKIYKLSPETTY 198
     CLKVKAALLTSWK 211
                                                                        IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GTPDVVDWDADRVS----
                                       -GTPDVVDWDADRVS----LEWEPPKSDGG-
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase ATP-binding motif
Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.2%;
                                                                                                                                                                                                                                                                8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 97.5;
Pred. No. 21;
                                                                                                                                                                                                                                                                Score 97.5;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LEWEPPKSDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996
                                                                                                                                                                                                                                                                                                                                 379/3; 405/2;
7/1; 7129/3
                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6839;
                                                                                                                                                                                                                                                                              Length 7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                     463/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                53;
                                     APITOY 2322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-oct-1999
                                                                                                                                                                                                                                                                                                                                                     508/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CESP: 2K617.1b
                                                                                                                                                                                                                                              Gaps
                                                                          198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1971
                                                                                                          2292
                                                                                                                                                                                                                                                                                                                                                     542/3; 574/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                          R;Gattung, S.; Scheet, P.; Kemp, K.
submilted to the EMBL Data Library, November 1996
A;Bescription: The sequence of C. elegans cosmid i
A;Reference number: 220647
A;Accession: 729585
                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T29585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:HO, A.S.; L1u, Y.; Khan, T.A.; Hsu, D.H.; Bazan, Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 199 A;Ttle: A receptor for interleukin 10 is related A;Reference number: A49667; WUID:94068585 A;Accession: A49667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-10 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision
C:Accession: A49667
                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-925 <GAT>
                                                                                                                                                                                                                                                                                                               hypothetical protein F55F8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tcC;Accession: T29585
                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                        A; Introns:
                                                                                          A; Map position:
                                                                                                          A; Gene: CESP: F55F8.3
                                                                                                                                           A;Cross-references: EMBL:U80447; PIDN:AAB37807.1; GSPDB:GN00019; CESP:F55F8.3
A;Experimental source: strain Bristol N2; clone F55F8
                                                                                                                                                                                                            A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-575 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 51
   Query Match
Best Local Similarity
                                                                                                                          Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2323 VIEKKGKHGRDWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 EQCLLITTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 VHCIKTTVE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 VFKDLRVYKISIRKFSELKNATKRVKQETFTLTVPIGVRKFCVKVLPRLESRINKAEWSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 IYSRHKIYKLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 RKAQIGPPEVHLEAEDKAIVIHISPGTKDSV-MWALDGLSFTYSLLIWKNSSGVEERIEN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1110r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNSTWNDIHICRKAQALSCDLTTFTLDLYHRSYGYRARVRAVDNSQYSNWTTTETRFT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMDNWIKLSGCONITSTKCNFSSLKLNVYEE - - - IKLRIRA - EKENTSSWYEVDS - FTPF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRW----NRSDESVGNVTFSFDYQKT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVTISSLSLEFIAYGTELPSPSYVWFEARFFQHILHWKPIPNQSESTYYEVAL----KQY 64
                                                                          6/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
51; Conserv
                                                                        44/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:L12120;
                                                                        76/1; 109/2; 159/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%;
   8.0%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID: g437615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95.5; D
Pred. No. 1.2;
     Score
Pred.
                                                                                                                                                                                                               from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TVDSVTLKAMDGIIYGTIHPPRPTITPAGDEYEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                   15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-Jul-1995 #text_change 05-Nov-1999
   No .
                                                                          204/3;
       . 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bazan, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: AAA16156.1;
DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                          327/1;
                                                                                                                                                                                                                                                                  F55F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYCLKVKAALLTSWKIGVYSP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.F.; Moore,
                       Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                        469/3; 617/1; 775/1; 825/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g437616
                                                                                                                                                                                                                                                                                                                                   15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein protein search, using sw model

June 1, 2000, 04:38:52; Search time 34.71 Seconds (without alignments) 200.927 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-240-675-2\_COPY\_1\_229
1196
1 MMYVLLGATTLVLVAVGPMV......MKIGVYSPVHCIKTTVENEL 229

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

83857 segs, 30454973 residues

83857

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : SwissProt\_38:\*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution. printed,

#### SUMMARIES

3333322222222111111111098765432 4331098765432	Result No.
7 600.5 600.5 1522.5 117.5 117.5 117.5 95.5 90.5 90.5 90.5 80.	9 7
11566 1204 0 1304 0 130	- F4
560 560 590 332 337 489 489 477 578 578 880 5315 5315 5315 5315 5315 5315 5315 531	
	DB
INRI_BOVIN INRI_SHEEP INRI_MOUSE CORF4_HUMAN INGS_HUMAN INGS_HUMAN INGS_HUMAN INGS_HUMAN INGS_HOWAN INGS_MOUSE PWP2_CAREL I110R_HUMAN F_HUMAN CD45_HUMAN CD45_HUMAN CD45_HUMAN CD45_HUMAN INR2_BOVIN INR2_HUMAN INR2_HEEP INR2_YEAST INR2_YEAST HIR2_YEAST HI	ID INR1_HUMAN
Q04790 bos taurus Q04790 bos taurus Q28589 ovis aries P3886 mus musculu Q61334 homo sapien P15260 homo sapien P15261 mus musculu P91341 caenorhabdi Q13651 homo sapien P16575 aries P16242 saccharomyc Q9207 ovis aries P17404 bos taurus P16540 arabidopsis P17404 bos taurus P16540 arabidopsis P1221 marchantia P16504 saccharomyc P21183 mus musculu P40505 oryctolagus P1653 pinus thumb P1653 pinus thumb P1653 pinus thumb P1654 human rotav P32794 saccharomyc P26954 mus musculu	Description P17181 homo sapien

44	66666666666666666666666666666666666666
77 77	80 80 79.5 79.5 78.5 78.5 78.5 77.5
6.4	00000000 VV0000UU4
460 537	918 993 918 442 853 853 896 1124 377
μμ	
HEMO_RABIT IL2B_RAT	IL6B_HUMAN EPB3_MOUSE IL6B_RAT THDF_MYCGE TGR3_RAT CYRB_MOUSE TIE2_HUMAN VC06_SBVKA MTC3_CHYN1
	P40189 homo sapien P54754 mus musculu P40190 rattus norv P47254 mycoplasma P26342 rattus norv P26955 mus musculu Q02763 homo sapien P3226 swinnepox vi P10835 chlorella v

# ALIGNMENTS

7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	RRRRRR	2000 E E E E E E E E E E E E E E E E E E	RESULT INR1_H ID I AC P DT 0
YK2. Proudhon D., Vielh E., Uze Ge human interferon alpha/beta rece 802-2809(1992).  YK2.  YK2.  YK2.  YK2.  YK2.  YK2.  YK2.  Domanski P., Handa R., Smalley M., Krishnan K., Krolewski J.; Krolewski J.; And tyrosine phosphorylation of the eron receptor by p135tyk2 tyrosine 8133-8142(1994).  YROSSINE PHOSPHORYLATION OF A NUMB TYROSINE PHOSPHORYLATION OF A NUMB TYRE, STAT PROTEINS AND IFN-R ALPH AND BETA.  TY: IFN RECEPTORS ARE PROTEIN.  TY: IFN RECEPTORS ARE PRESENT IN A NACE OF MOST IFN-RESISTANT CELLS.  TED ON TYROSINE RESIDUES BY TYK2 TO THE CLASS II CYTOKINE FAMILINGS TO THE CLASS II CYTOKINE FAMILINGS.  TED ON TYROSINE RESIDUES BY TYK2 TO THE CLASS II CYTOKINE FAMILINGS.  TED ON TYROSINE RESIDUES BY TYK2 TO THE CLASS IN TYPE III-LIKE DINGS TO THE CLASS II CYTOKINE FAMILINGS.  TED ON TROSINE RESIDUES BY TYK2 TO THE CLASS II CYTOKINE FAMILINGS.  TED ON TROSINE RESIDUES BY TYK2 TO THE CLASS II CYTOKINE FAMILINGS.  THE CHARGE STATE TO THE STATE AND THE PARTITURE DINGS.  THE CHARGE STATE OF THE CLASS IN THE CASE AND T	NCE FROM N.A.  NE; 90124632.  3., Lutfalla G., Gresser I.;  tic transfer of a functional human int mouse cells: cloning and expression of	3-1990 (Rel. 15, Last se B-2000 (Rel. 39, Last an EERON-ALPHA/BETA RECEPTO 1 OR IFNAR. 1 OR IFNAR. 1 OR GROWN 1 OR GROWN	1 UMAN UMAN STANDARD; PRT; 1718]; 1-AUG-1990 (Rel. 15, Created)

```
RESULT
INR1_B
                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RREAR REAR RREAR R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                              INRI_BOVIN STANDARD: PRT; 560 AA. 004790; 001-0CT-1993 (Rel. 27, Created) 01-0CT-1994 (Rel. 28, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) INTERFERON-ALDHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                           LT 2
BOVIN
                                                                                                                                       Bovinae; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Transpression Phosphorylation SIGNAL 1
MEDLINE; 93076908.

Mouchel-Vielh E., Lutfaila G., Mogensen K.E., Uze G.;

"Specific antiviral activities of the human alpha interferons determined at the level of receptor (IFNAR) structure.";

FEBS Lett. 313:255-259(1992).
                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                     SEQUENCE FROM N.A.
TISSUE-LUNG;
                                                                                                                                                                                                                       IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                                                                                                        ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%;
Similarity 100.0%;
29; Conservative
                                                                                                                                                        Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
437
458
79
199
466
481
481
81
81
81
1100
1172
2254
433
314
433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436
457
557
2200
2466
4666
4666
58
81
1100
1100
1172
2544
4166
3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
63525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.

L -> V.
    /FTId-VAR_002717.

FTId-VAR_012717.

G -> A (IN REF. 2).

W: 0F6744CBALADBE73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (BY TYK2)
PHOSPHORYLATION (BY TYK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1196;
Pred. No. 1.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                      Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 1;
1.1e-98;
es 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY TYK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                       (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                           229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

```
RESULT 3
                                                                                                                                                                                                                                                                                                               밁
                                                                                         Š
                                                                                                                ઠ
                                                                                                                                    å
                                                                                                                                                             B
                                                                                                                                                                                  Š
                                                                                                                                                                                                           B
                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE; 93305725.

LIM J.-K., Langer J.A.;

"Cloning and characterization of a bovine alpha interferon receptor."

"Cloning and characterization of a bovine alpha interferon receptor."

Blochim. Blophys. Acta 1173:314-319(1993).

1 ITNS TRIGGERS FOR INTERFERONS ALPHA AND BETA. BINDING TO TYP.

1 ITNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

SUBGUNITS THEMSELVES.

1 SUBGUNITS THEMSELVES.

1 SUBGULULAR LOCATION: TYPE I MEMBRANE PROTEIN.

1 SUBGULULAR LOCATIONS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

1 SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                              CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Transmembrane; SIGNAL 1 24 CHAIN 25 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
INR1_SHEEP
Q28589; Q95206;
                                                                    179
                                                                                                                 119
                                                                                           179
                                                                                                                                      120
                                                                                                                                                             59
                                                                                                                                                                                   62
                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L; X68443; CAA48484.1;
L; L06320; AAA02571.1;
; S33770; S33770.
; S27387; S27387.
                                                                                                              MYVLLGATTLYLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
                                                                                RIENIYSRHKIYKLSPETTYCLKYKAALLISWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                          MLALLGATTLMLVA-GRWVLPAASGEANLK-PENVEIHIIDDNFFLKWNSSSESVKNVTF
                                                                    RTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPVYCINTTERHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00041; fn3;
                                                                                                                                                                                                                                                     Similarity 67.1
55; Conservative
                                                                                                                                                                                                                                                                                                               25
438
459
769
199
199
55
55
109
172
254
432
432
432
                                                                                                                                                                                                                                                                                                               ₽,
            STANDARD;
                                                                                                                                                                                                                                                                                                                          437
458
560
220
220
220
250
47
254
431
3313
377
                                                                                                                                                                                                                                                                                                               63818
                                                                                                                                                                                                                                                                 65.4%;
67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                 Score 782.5; DB 1
Pred. No. 5.4e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          ya
Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERFERON-ALPHA/BETA RECEPTOR
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY.
                                                                                                                                                                                                                                                         Mismatches
            560
            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A AND BETA. BINDING TO TYPE
N OF A NUMBER OF PROTEINS
IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                               560;
                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.";
                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outstation
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                    119
                                                                                                                                                             118
                                                                                                                                                                                                           58
                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  way
                                                                                                                                                                                                                                                        ر.
```

```
gerades es a constant de la constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, C)
01-NOV-1997 (Rel. 35, Le
15-FEB-2000 (Rel. 39, Le
INTERFERON-ALPHA/BETA RE
(INTERFERON ALPHA/BETA RE
                  CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                    CARBOHYD
CARBOHYD
                                                                                                                                DISULFID
DISULFID
  CONFLICT
                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                          pregnancy.";
endocrinology 138:4757-4767(1997).
erdocrinology 138:4757-4767(1997).
i. FUNCTION: RECEPTOR FOR INTERFERONS ALPHA
i. IFNS TRIGGERS TYROSINE PHOSPHORYLATION
INCLUDING JAKS, TYK2, STAT PROTEINS AND I
SUBUNITS THEMSELVES.
                                                                                                                                                                                                                                                                                                                                                                                                           Han C.-S., Mathalagan N., Klemann S.W., Roberts R.M.;
Han C.-S., Mathalagan P., Klemann S.W., Roberts R.M.;
"Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; |
                                                                                                                                                                                                           EMBL; X95939; CAA65183.1;
EMBL; U65978; AAB84231.1;
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaluz S., Fisher P.A., "Structure of an ovine endometrium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-ENDOMETRIUM;
MEDLINE; 97135690.
                                                                     CARBOHYD
                                                                             CARBOHYD
                                                                                      CARBOHYD
                                                                                              CARBOHYD
                                                                                                       CARBOHYD
                                                                                                                CARBOHYD
                                                                                                                       CARBOHYD
                                                                                                                                                  DOMAIN
                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                       entities
                                                                                                                                                                                                                                                              modified
                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                          ÷÷
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN TISSUES SECTIFICITY: EXPRESSED IN ALL TISSUES I CONCEPTUS AT DAY 15 OF PREGNANCY:
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-L:
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE I
                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                              an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinol.
                                                                                                                                                                                                                                            non-profit institutions as long and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               98006426
                                                                                                                                                                                                    Transmembrane;
 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
  ξ
                  17:207-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
A RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaluzova M.,
interferon re
                                                                                                                                                                              Glycoprotein; Signal.
BY SIMILARITY.
INTERFERON-ALPHA/BETA RECEPTOR
  ₹.
                                                                                                                      EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
S -> G (IN
A -> D (IN
A -> D (IN
                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                      POTENTIAL
                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
3 (IN REF. 2).
D (IN REF. 2).
98A1905D4805C (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheldrick E.L.,
                                                                                                                                                                                                                                                     (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                      as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and its expression
                                                                                                                                                                                                                                                                                                                                                                    A AND E
N OF A
IFN-R
                                                                                                                                                                                                                                                                                                                          III-LIKE
                                                                                                                                                                                                                                                             Usage
  CRC64;
                                                                                                                                                                                                                                                                                                                                                                   A NUMBER OF PROPRE A ALPHA-AND BETA
                                                                                                                                                                                                                                                                                                                 FAMILY OF
                                                                                                                                                                                                                                                                                                                                           EXAMINED
                                                                                                                                                                                                                                                              γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flint A.P
                                                                                                                                                                                                                                                                                                                           DOMAINS
                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                          1 for
                                                                                                                                                                                                                                                                                                                                           EXCEPT
                                                                                                                                                                                                                                                                                                                 RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                   PROTEINS
                                                                                                                                                                                  ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
...
                                                                                                                                                                                                                                                       .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                commercia.
                                                                                                                                                                                                                                                                        ņ
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
INR1_MOUSE
  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                             CHAIN
                                                                                                       MGD;
                                                                                                                       EMBL;
                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                      P33896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              μ
```

```
Query Match
Best Local S
Matches 153
DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                           This SWI
between
                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
use by non-profit institutions as lo
modified and this statement is not remo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sent
15-FEB-2000 (Rel. 39, Last anno
INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDCINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IFNAR1 OR IFNAR OR IFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR1_MOUSE
                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial field and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                    MGI:107658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPVYCINTTERHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIENIYSRHKIYKLSPETTYCLKVKAALLITSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMMALDGLSFTYSLLIWKNSSGVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SADYQILGTDNWKKLPGCQHITSSKCNFSSVELKDVFEKIELRIRAEEGNNTSTWYEVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFDYOKTGMDNWIKLSGCONITSTKCNFSSLKL-NVYEEIKLRIRAEK-ENTSSWYEVDS
                                                                                                                                                                                                                 M89641; AAA37890.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
92262522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
 27
430
450
78
199
199
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                    IFNAR.
 4429
590
86
220
109
                                                                                                                                     590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.0%;
                                                                                                                                                     Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
PTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                           INTERFERON-ALPHA/BETA RECEPTOR A CHAIN.
CHAIN.
EXPRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
 POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 765.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     590
                                                                                                                                                                                                                                                              moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
```

```
CRESULT STEEM AND ID CREAL HARD OF SEQUEN RC TISSUE RX MEDLIN RA LUTEAL RT SEQUEN RX MEDLIN CC -!- SU CC -!- SU CC -!- SU CC -!- SU CC This S CC betwee CC the ED CC use ED CC modifi CC or senitti CC or senitti CC or senitti CC or senitti CC sentiti C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 96054036. Lutfalla G., McInnis N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 3
01-FEB-1995 (Rel. 3
01-OCT-1996 (Rel. 3
CYTOKINE RECEPTOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lutfalla G., Gardiner K., Uze G.;
"A new member of the cytckine rec
21 at less than 35 kb from IFNAR.
Genomics 16:366-373(1993).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                               This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch). "
  EMBL; Z17227; CAA78933.1;
EMBL; U08988; AAA86872.1;
PIR; A47003; A47003.
HSSP; P13726; 1DAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRF4_HUMAN
Q08334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-FETAL BRAIN;
MEDLINE; 93300510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRFB4.
                                                                                                                                                                                                                                                                                                                                                             neighbor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match
Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                      MO1 Evol. 41:338-344(1995).
FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SY:
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DON
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSTYYVEKIPELLPETTYCLEVKAIHPSLKKHSNYSTVQCISTTVANKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLAVVGAAALVLVAGAPWVLPSAAGGENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESYGNVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPFYTAHMSPPEVRLEAEDKAILVHISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 52.0
119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
314
370
409
413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human).
etazoa; Chordata; Craniata;
etazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31, Created)31, Last sequence update)34, Last annotation update)CLASS-II CRF2-4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
314
370
409
413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65776
                                                                                                                                                                                                                                                                                                                                                                                                M.G.,
                                                                                                                                                                                                                                                                                                                                                                              3., Antonarakis S.E.,
CRFB4 gene: comparis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 600.5; |
Pred. No. 8.1e
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7EC6DFF370185D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; DB 1;
8.1e-46;
hes 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ното.
                                                                                                                                                                                                                                                                                                                                                                              Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                               DOMAINS
                                                                                                                                                                                                                                                                                                                    SYSTEM.
                                                                                                                                                                             restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                          OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                IFNAR
                                                                                                                                                                                                    a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
                                                                                                                                          for
                                                                                                                   .ch/announce/
                                                                                                                                                                                                  outstation
                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                             no
                                                                                                                                                                               8
                                                                                                                                                           way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
٠٠
```

```
RESULT 6
 멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 66
This SWISS-PR between the the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                 Soh J. Donnelly R.J., Kotenko S., Mariano T.M., Cool Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka "Identification and sequence of an accessory factor activation of the human interferon gamma receptor.";
                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERF
FROCEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA
IFNORT OR IFNGT1.
                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel.
01-OCT-1994 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                   INGS_HUI
P38484;
                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=LUNG FIBROBLAST;
MEDLINE; 94170380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 123889;
                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                               Eutheria;
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                      176
                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
                                  1 76:793-802(1994).

FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
SWISS-PROT entry is copyright.
sen the Swiss Institute of Bio.
European Bioinformatics Institu
                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                      EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD
                                                                                                                                                                                                                                                                                                                                                                                                                         HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRIFODKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                               Metazoa;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
20
221
250
66
188
102
102
161
124
124
269
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                   (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą.
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325
325
220
220
325
325
325
325
325
325
                                                                                                                                                                                                                              Chordata; C:
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.6%;
                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 222.5;
Pred. No. 1.3e
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A -> D (
FLGHP ->
MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (P
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                              Craniata; Ve
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A -> D (IN REF. 2).
FLGHP -> VGRME (IN
MISSING (IN REF. 2)
66706C79F8514B23
                                                                                                                                                                                                                                                                                                                                               PRT;
         ght. It is produced through a collaboration Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                               337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR CLASS-II
LULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                          Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 1;
.3e-12;
.es 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (12)
                                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                           224
                                                                                                                                                                                                                                                                                      (INTERFERON-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASS-II CRF2-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REF.
                                                                                                                                              Cook J.R.,
stka S.;
ctor required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                          TRANSDUCER-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
```

are

ö

restrictions

outstation -

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SO PETER TO THE PETER TO THE PETER TO THE PETER TO THE PETER THE P
                                                                                                                                                                                                                                                                                                                                                                                                   INGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                        INGR_HUMAN STANDARD,
P15260;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified
                                                                                                                  Aguet M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U05875; AAA16955.1; EMBL; U05877; AAA16956.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00041; fn3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                             Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
              SULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALHSAWVTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDENV----TLRLRAEL
                                                     55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCYETMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCIKTTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYVHYWE---KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLVAVGPWVLSAAAGG---KNLKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV
                                                                                                               E FROM N.A.
: 89003065.
., Dembic 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long and this statement is not removed
                                                                                                                                                                                            Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                PARTIAL
                                                                                           and expre
                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.7%;
                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal; Repeat
                SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                             G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 151.5; DB 1
Pred. No. 2.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R -> Q.
/FTId=VAR_002718.
18C61B10AD90E509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERFERON-GAMMA RECEPTOR EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                             얁
                AND
                                                                                             the
                                                                                                                                                                                                                                                                         update)
PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                MUTAGENESIS
                                                                                             human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its content
                                                                                                                                                                                                                                                                           (CDW119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is
ifor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              way
cial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
```

Ş 밁 Š

FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA---EKENTSSWYEV MALLFLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYWEY--QIMPQVPV VVLLGATTLVLVAVGPWVLSAA-AGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNV-T Query Match Best Local S Matches 52

Similarity

9.8%;

Score 117.5; DB 1; Pred. No. 0.0045; 4; Mismatches 99;

۲,

Length

35;

Gaps

8

58 60 Conservative

ω

```
CARBOHYD
CARBOHYD
SEQUENCE
                                                                              CHAIN
DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute. The European Bioinformatics Institute. The European Bioinformatics Institute on the European Bioinformatics Institutes on the European Bioinformatics Institutes as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Neutralizing epitopes on the extracellular interferon gan (IFNgammaR) alpha-chain characterized by homolog scanning and X-ray crystal structure of the A6 fab-IFNgammaR1-108 J. MOL. BIOL. 273:882-897(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Crystal structure of a complex between interferon-gamma and its soluble high-affinity receptor.";
Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95342235.
Walter M.R., Windsor W.T.,
Zauodny P.J., Narvala S.K.;
                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                PDB; 1JRH; 25-MAR-98
MIM; 107470; -.
                                                                                                                                                                                                                                                                                                                            EMBL; J03143; AAA52731.1; PIR; A31555; A31555.
                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sogabe S., Stuart F., Henke C., Winkler F.K., Robinson J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY. MEDLINE; 98035727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 32:2423-2430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Gan "Alignment of disulfide bonds of the extracellular domain interferon gamma receptor and investigation of their role biological activity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

PTM: PHOSPHORYLATED AT SER/THR RESIDUES.

SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERFERON-GAMMA DIMER.
                                                                                                                                                                                                                                                                               209950; -
                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                               domain;
   54404
                                                                                                                                                                                                                                               3D-structure
                                                                                                                                                                                                                                                            Glycoprotein;
   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagabhushan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGSTROMS) OF
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
CRESSESSADSF47400 CRC64;
                                                                                                                                                                              INTERFERON-GAMMA EXTRACELLULAR (POTENTIAL.
                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.L.,
                                                                                                                                                                                                                                                            Signal; Phosphorylation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A., Williams G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-248
                                                                                                                                                                                              MA RECEPTOR ALPHA CHAIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWO RECEPTORS BIND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lundell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garotta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birch A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lunn C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.;
```

```
I RESULT TO CONCRETE TRANSPORT OF THE SECRET TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
SEQUENCE OF 1-28 FROM N.A.

(MEDLINE; 95197006.

A RAVAL P., Oblci S., Russell S.W., Murphy W.J.;

"Characterization of the 5' flanking region and gene mouse interferon-gamma receptor.";

Gene 154:219-223(1995).

-1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECIONSTREED AT SER/THR RESIDUES.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- STMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gray P.W. Leong S., Fennie E.H., Fernandez-Luna J., Schreiber R.D.; "Cloning and expression of the CDN receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 90099370.

Hemmi S., Peghini P., Metzler M., Merlin G., Dembic Z., "cloning of murine interferon gamma receptor cDNA: exprehuman cells mediates high-affinity binding but is not suconfer sensitivity to murine interferon gamma."; Proc. Natl. Acad. Sci. U.S.A. 86:9901-9905(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGR_MOUSE STANDARD; PRT; 477 AA. P15261; 01-APR-1990 (Rel. 14, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 1NTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                               Appella E.;
"Affinity purification, peptide analysis,
mouse interferon gamma receptor.";
T. Biol. Chem. 265:4064-4071(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurharia: Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Munro S., Maniatis T., "Expression cloning of Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 90154099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 90036866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 90046824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 90083245.
                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                             Cofano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kumar C.S., Muthukumaran G.,
Mariano T.M., Pestka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFNGR1 OR IFNGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RMNGSEIQYKILTOK-----EDDCDEIQCQLAIPVSSLNSQYCVSAEGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEFAVCRDGKIGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCXIRVXNVXV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKE--SAYAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                   F., Moore S.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264:17939-17946(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
U.S
                                                                                                                                                                                                                                                                                                                                                                        Tanaka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine interferon gamma receptor. A. 86:9248-9252(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frost L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86:8497-8501(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Farrar M.A.,
                                                                                                                                                                                                                                                                                                                                                                        Yuhki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No
e
                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon
                                                                                                                                                                                                                                                                                                                                                                        Landolfo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                             cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pingel J.T.,
           C2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embic Z., Aguet M.;
DNA: expression in
is not sufficient
                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ahn
                                                                                                  RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                        s,
                                                                                                                                                                encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206
                                                                                                                                                                                                                                                                                                                             0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA.
                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ដូ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
```

```
RESULT
IIOR_MC
AC QI
DT 11
DT 11
DT 11
DT 11
DT 11
                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                         뮍
                                                                                                                                                                                             Ş
                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 54
                                                                          _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M28995; AAA37895.1; ALT_INIT.
EMBL; M26711; AAA37896.1; -.
EMBL; M2823; AAA37898.1; -.
EMBL; M25764; AAA39177.1; -.
EMBL; J05265; AAA39178.1; -.
EMBL; U05960; AAA80980.1; -.
TIOR_MOUSE STANDARD; PRT; 575 AA. 061727; 05-70L-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A35468;
PIR; A36224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [mmunoglobulin
                                                                                                                        170
                                                                                                                                               158
                                                                                                                                                                       110
                                                                                                                                                                                              106
                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A34368;
A34423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:107655; IFNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A34508;
                                                                                                                                      LDG---LSTTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYC-LKVKAALLTS
                                                                                                                                                                                                                                               YQ----
                                                                                                                                                                                                                                                                       AGRMILLVV--LMLSAKVGSGALTSTEDPEPPSVPVPTNVLIKSYNL-----
                                                                                                                                                                                                                                                                                         ATTLVLVAVGPWVLSAAAGGKNLKS---PQKVEVDIIDDNFILRWNRSDESVGNVTFSFD
                                                                                                                                                                         AKVGQKESDYARSKEFLMCLKGKVGPPGLEIRRKKEEQLSVLVFHPEVVVNGESQGTMFG
                                                                                                                                                                                             AE-KENTSSWYEVDSFTPFRKAQIGPP--EVHLEAEDKAIVIHISP----
                                                                                                                                                                                                                       YQNMSQTPIFTVQVKVYSGSW--TDSCTNISDHCC-----NIYGQIMYPDVSAWARVK
                                                                                                                        -DGSTCYTFDYTVYVEHNRSG-----EILHTKHTVEKEECNETLCELNISVSTLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P15260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement ( an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A34368.
A34423.
A34508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A35468.
A36224.
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                           n domain.
1 22
3 3 253
3 253
4 277
1 174
277
1 186
208
243
61
85
2104
221
95
52271 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1JRH
                                                                                                                                                                                                                                               -KTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIK-----LRIR
                                                                                                                                                                                                                                                                                                                                 8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                   ₹
:
                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
G -> E (IN REF. 2 );
AlfC66E9BAA0B20A
                                                                                                                                                                                                                                                                                                                     Score 102.5; DB
Pred. No. 0.094;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERFERON-GAMMA EXTRACELLULAR (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MA RECEPTOR ALPHA (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              DB. 1;
                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                  AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                -GTKDSVMWA
                                                                                                                                                                                                                                                                       NPVVCWE
                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                 157
                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                         169
                                                                                                                                                                                                                                                                                                                        14;
```

```
RESULT
PWP2_CA
ID PV
AC PS
DT 15
DT 15
DT 15
DT 15
DT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                          밁
                                                                                                                                                                                                Ş
                                                                                                                                                                                                                           유
                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 51
L_CAEEL
PMP2_CAEEL
P91341;
P91341;
15-JUL-1998
15-JUL-1998
15-JUL-1998
PERIODIC TRY
                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;
"A receptor for interleukin 10 is related to interferon receptors.";
Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
-I- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SUBCELLULAR LOCATION: TYPE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL10RA OR IL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L12120; AAA16156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                          223
                                                                                                                                                                           163
                                                                                                                                                                                                   183
                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                          EQCLLITTE
                                                                                                                                                   VHCIKTTVE 226
                                                                                                                                                                                                                                                 RKAQIGPPEVHLEAEDKAIVIHISPGTKDSV-MWALDGLSFTYSLLIWKNSSGVEERIEN
                                                                                                                                                                                                                                                                           GNSTWNDIHICRKAQALSCDLTTFTLDLYHRSYGYRARVRAVDNSQYSNWTTTETRFT--
                                                                                                                                                                                                                                                                                                                                                  LVAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRW----NRSDESVGNVTFSFDYQKT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:96538;
                                                                                                                                                                                                   IYSRHKIYKLS-----
                                                                                                                                                                                                                                                                                                  GMDNWIKLSGCQNITSTKCNFSSLKLNVYEE - - - IKLRIRA - EKENTSSWYEVDS - FTPF
                                                                                                                                                                                                                                                                                                                           LVTISSLSLEFIAYGTELPSPSYVWFEARFFQHILHWKPIPNQSESTYYEVAL----KQY 64
                                                                                                                                                                          VFKDLRVYKISIRKFSELKNATKRVKQETFTLTVPIGVRKFCVKVLPRLESRINKAEWSE
                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94068585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation updat
rPTOPHAN PROTEIN 2 HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
263
204
50
66
113
182
                                                                                                                                                                                                                         -----VDEVIL-----TVDSVTLKAMDGIIYGTIHPPRPTITPAGDEYEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X AJ F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 575
262
262
575
225
225
20
60
113
182
238
64248
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL10RA
                                                                                                                                                                                                                                                                                                                                                                                        8.0%;
20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HEMATOPOIETIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩;
                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
820B9CD576F686B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Score 95.5; D
Pred. No. 0.5;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERLEUKIN-10 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                   -PET----TYCLKVKAALLTSWKIGVYSP
                                                                                                                                                                                                                                                                                                                                                                                     95.5;
No. 0
                                                              925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.
            update)
                                                                                                                                                                                                                                                                                                                                                                                    DB
->.5;
                                                              ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL
                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                 217
                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ņ
                                                                                                                                                                                                                                                                                                                                                                            10;
```

```
STREET TO STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
       CCRRRRRRRCCOSCETTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
REPEAT 1
REPEAT 3
REPEAT 4
REPEAT 4
                                                                                                                                                                                                                                                                                                                                                                                                      I10R_HUMAN
Q13651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
MEDLINE; 94165477.

Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Expression cloning and characterization of a human: "Expression 152:1821-1829(1994).

J. Immunol. 152:1821-1829(1994).

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                     MYEARLE MY LIVA. LILIVA. LILIVA. HOMO Saplens (Human). Homo saplens (Human). """" Chordata; Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gattung S., Scheet P., Ke Submitted (NOV-1996) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F55F8.3.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U80447; AAB37807.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS006
PFAM; PF00400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WORMPEP; F55F8.3; CE11192.
PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence
15-DEC-1998 (Rel. 37, Last annotatic
                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                INTERLEUKIN-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                              ISSUE-LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 MDNWIKLSGCQNIT--STKCNFSSLKLNVYEEI--KLRIRAEKENTSSWYEVDSFTPFRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tung S., Scheet P., Kemp K.;
mitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: CONTAINS 6 MD REPEATS (TRP-ASP DOMAINS).
SIMILARITY: BELONGS TO THE PWP2 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHEFGKSIENKVYNPFSLSRTYKLSSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSISPSGYHLLASDERGVVHFVHLLSEFKIYTFRSNKPIGSLQWSPDATRVAICRENDLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQIGPPEVHLEAEDKAIVIHI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDTNFKLSNCIGTVYRDGQVAFSKDGYSVISPIGNKLSIFDLRNNTSKTLDIDCNYNIKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWKNSSGVEERIENIYSRHKIYKLSPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00678; WD_REPEATS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 protein;
188 218
358 388
400 430
486 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                    Z
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WD40;
                                                                                                                                                                                                                                                                                                             RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
388
430
514
554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103899 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                 ast sequence update)
ast annotation update)
PRECURSOR (IL-10R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 95.5; I
Pred. No. 0.91
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
B
B
B
B
B
                                                                                                                                                                                                              Craniata; Ve:
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439F35881B398CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPGTKDSVMWALDGLSFTY---
                                                                                                                                                                                                                                      Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .91;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                         Mammalia;
                        HIGH AFFINITY
                                                                         receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
```

```
Š
                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 51
                                                                                                                                                                           BOVIN
                                                                                                       TF_BOVIN STAN
P30931;
01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
01-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor;
SIGNAL
                           Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metaztiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U00672; AAA17896.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                           TISSUE FACTOR
                          Bovinae;
                                                                                                                                                                                                                                209
                                                                                                                                                                                                                                                                                                                                     116
                                                                                                                                                                                                                                                       206 LLTSWKIGVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                             u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PBMC. FAINT EXPRESSION IN PARCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA, LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS, LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL
                                                                                                                                                                                                                              VASRSNKGMWSKEECISLT
                                                                                                                                                                                                                                                                                                           NSSGVEERIENIYSRHKIYKLSPETT---
                                                                                                                                                                                                                                                                                                                                     TRESVDEVT - - - - LTVG - - SVNLEIHNGFILGKIQLPRPK - -
                                                                                                                                                                                                                                                                                                                                                               --YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMWALDGLSFTYSLLIWK
                                                                                                                                                                                                                                                                                                                                                                                                          SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEE--IKLRIRA-EKENTSSW----
                                                                                                                                                                                                                                                                                                                                                                                                                                             LVVLLAA--LLSLRLG-----SDAHGTELPSPPSVWFEAEFFHHILHWTPIPNQSESTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
                                                                                                                                                                                                                                                                                  -MAPANDTYESIFSHFREYEIAIRKVPGNFTFTHKKVKHENFSLLTSGEVGEFCVQVKPS
                                                                                                                                                                                                                                                                                                                                                                                         EVALLRYGIESWNSISNCSQTLS--YDLTAVTLDLYHSNGYRARVRAVDGSRHSNWTVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                          Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                          Rel. 35, Last annotation update)
PRECURSOR (TF) (COAGULATION FACTOR
                                                                                                                                                             STANDARD;
                                                                                                        26, Created)26, Last sequence update)35, Last annotation updat
 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.98;
19.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62903
 PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                                         224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 95; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERLEUKIN-10 RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EE1B29064338157C CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                            Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Length 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91;
                                                                                           III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                          ----YCLKVKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                        Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                     150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
```

```
RESULT 1
TF_HUMAN
ID TF_H
ID TF_H
AC P137
DT 01-J
DT 115-J
DT 115-J
DE TISSS
GN F3.
OS HOMOO
OC ENKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
DISULFID
DISULFID
LIPID
                                                  TF_HUMAN STANDARD; PRT; 295 AA. P13726; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR (THROMBOPLASTIN) (CD142 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takayenoki Y., Muta T., Miyata T., Iwanaga S.;

"CDNA and amino acid sequences of bovine tisue factor.";

Biochem. Biophys. Res. Commun. 181:1145-1150(1991).

-i- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND PROPAGATION OF THE COAGULATION PROTEASE CASCADE.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00346; TISSUEFACTOR, PROSITE; PS00621; TISSUE_FACTOR; PFAM; PF01108; Tissue_fac; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S74147; AAB20755.1; -. PIR; JQ1319; KFBO3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-ADRENAL GLAND;
               Homo sapiens (Human) 
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                               187
                                                                                                                                                                                                                                                             170
                                                                                                                                                                                                                                                                                        132
                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                              70
                                                                                                                                                                                 13
                                                                                                                                                                                                                                                       WK-NSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                      YLETNIGOPTIQSFEQVGTKLNVTVQDARTLVR----ANSAFLSLRDVFGKDLNYTLYY
                                                                                                                                                                                                                                                                                                                                                  LGNW--KNKCEYTTNTECDVTDEIVKNVRETYLARVLSYPADTSSSTVEPPFTNSPEFTP
                                                                                                                                                                                                                                                                                                                                                                              MDNWIKLSGCQNITSTKCNFS-SLKLNVYEEIKLRIRAEKENTSS-----WYEVDSFTP 122
                                                                                                                                                                                                                               WKASSTGKKKATTN--TNGFLIDVDKGENYCFHVQAVIL-SRRVNQKSPESPIKCT
                                                                                                                                                                                                                                                                                                                      FRKAQIGPP-----GLSFTYSLLI 169
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
 Primates;
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1A21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35
292
248
271
271
292
48
43
153
181
 Catarrhini;
                 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coagulation; Transmembrane; Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Œ,
                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PALMITATE (BY SIMILARITY).

PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5; DB
Pred. No. 0.39;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). WKS MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENT IAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
 Craniata; Ve
i; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR
                 Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                             292;
                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H
                                                                                                                                                                                                                                                                                                                                                                                                               9
```

```
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH FVIIA.

MEDLINE; 96175641.

A Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,

A Konigsberg W.H., Nemreson Y., Kirchhofer D.;

"The crystal structure of the complex of blood coagulation factor

"The crystal structure of the complex of blood coagulation factor

"The crystal structure of the complex of blood coagulation factor

"The crystal structure of the complex of blood coagulation factor

"The crystal structure of the complex of blood coagulation factor

"In crystal structure of the complex of blood coagulation for the complex with

"The crystal structure of the coagulation brother complex activates

"The crystal structure of the coagulation from the coagulation factor

"The crystal structure of the crystal structure of the coagulation factor

"The crystal structure of the crystal str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 89247359;
Mackman N., Morrissey J.H., Fowler
"Complete sequence of the human ti
"Complete Sequence of the human ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 88050796. Scarpati E.M., Wen I Flandermeyer R.R., S
                                                                                                                                                                                                                                               MEDIINE; 96190957.

Muller Y.A., Ultsch M.H., de Vos A.M.;

"The crystal structure of the extracellular factor refined to 1.7-A resolution.";

J. Mol. Biol. 256:144-159(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
Bach R.,
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94368785.
Muller YA., Ultsch M.H., Kelley R.F., de Vos A.M.;
"Structure of the extracellular domain of human tis
location of the factor VIIa binding site.";
Biochemistry 33:10864-10870(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morrissey J.H., Fakhrai H., Edgington T.S.; "Molecular cloning of the cDNA for tissue factor, the receptor for the initiation of the coagulation proteas (c) 50:129-135(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.; "Isolation of cDNA clones coding for human tissue factor: structure of the protein and cDNA."; Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 87260946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human tissue factor contains thioester-linked on the cytoplasmic half-cystine."; Biochemistry 27:4227-4231(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 28:1755-1762(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS, AND PALMITOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fisher K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 88100453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the gene."
                                                                                                                                                                                                                                                                                                                                                      (-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human tissue factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
87244317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .L., Gorman C.M., Vehar G.A., O' and expression of human tissue Res. 48:89-99(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26:5234-5238(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D., Broze G.J. Jr., Miletich J.P., Siegel N.R., Sadler J.E.; or: cDNA sequence and chromosome lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nemerson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 man tissue fact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fowler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and chromosome localization
                                                                                                                                                                                                                                                                                                                                                         ဝ္ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edgington factor gen lates the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33-243
                                                                                                                                                                                                                                                                                                                                                        33-243
                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene, a highl
e coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                palmitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease cascade.";
                                                                                                                                                                                                                                                                                                                                                                                                                           tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.S.;
                                                                                                                                                                                                                                                                                                   õŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellular
                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 highly
                                                                                                                                                                                                                                                                                                                                                                                                                           factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease
                                                                                                                                                                                                                                                                                                     tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stearate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ?
                                                                                                                                                                                                                                  FVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                        ä
 Š
                                    밁
                                                               δõ
                                                                                                       밁
                                                                                                                                      δÃ
                                                                                                                                                                            밁
                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SITE
SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                     LIPID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00621;
PFAM; PF01108; Tis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                      178
                                                                        160
                                                                                                         123
                                                                                                                                           114
                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J02931;
M16553;
M202846;
M27436;
A19048;
A28320; K
A43645; A
A47574; A
     SPVHCI
                                                                                                     EPLYENSPEFTPYLETNLGOPTIQSFEQVGTKVNVTVEDERTLVR--
                                                                                                                                                                                                          DYOKTGMDNWIKLSGCONITSTKCNFSSLKLNYYEEIKLRIRA-----EKENTSS--
                                                                                                                                                                                                                                                                               ATTLVLVAVGPWV---LSAAAGGKNLKSPQKVEVDIIDDNFILRWN-RSDESVGNVTFSF
                                      VFGKDLIYTLYYWKSSSS-GKKTAKTNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTD
                                                                      --GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL--LTSWKIGVY
                                                                                                                                                                            ----TKSGDW--KSKCFYTTDTECDLTD----EIVKDVKQTYLARVFSYPAGNVESTGSAG
                                                                                                                                                                                                                                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                         WYEVDSFTPFRKAQIGPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        β
                                                                                                                                                                                                                                                                                                                                                                                                        133
252
2752
2752
2757
777
190
1156
169
169
169
2188
2188
   221
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ξ
                                                                                                                                                                                                                                                GWVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQIS-
                                                                                                                                                                                                                                                                                                                                    7.78;
```

-EVHLEAEDKAIVIHISPGTKDSVMWALD-

RNNTFLSLRD

177 160 122 114 72 Score 92; DB Pred. No. 0.44 42; Mismatches

DB 1;

Length 295

Indels

52;

Gaps

13;

```
use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                           VASCULAR ENDOTHELIAL CELLS AS A CURRENT RESPONSE.

DATABASE: NAME-PROW; NOTE-CD guide CD142 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd142.htm".
                                                                                                                                                                                                                  A28320; KFHU3.

A43645; A43645.

A47574, A47574.

1BOY; 10-JUN-96.

2HFT; 29-JAN-96.

1DAN; 04-SEP-97.

1TFH; 25-FEB-98.

1AHW; 19-AUG-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
                                                                                                                                                                                               PR00346; TISSUEFACTOR
                                                                                                                                                                                                                                                                                                                                                                       equires a license agreement (See http://www.isb-sib.email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
                                                                                                                                                                                                                                                                                                          AAA61150.1;
AAA61151.1;
AAA61152.1;
AAA36734.1;
CAA01438.1;
                                                                                                                                                                  Blood coagulation;
                                                                                                                                                       structure.
                                                                                                                                                                          Tissue_fac;
48
79
192
156
159
169
241
277
260
33067
                                                                                                                                                                                     TISSUE_FACTOR;
   MW;
                                                                                                                                                                                                                                                                                                            . . . . .
                                                    WKS MOTIF.
WKS MOTIF.
POTENTIAL.
POTENTIAL.
   PALMITATE.
V -> A (IN REF. 4).
D3486C713ED8EAD0 CRC64;
                                                                                              WKS
                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                          TISSUE FACTOR.
EXTRACELLULAR
                                                                                                                                                                  Transmembrane;
                                                                                              MOTIF.
                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                  Signal; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                           ý
                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                           TEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                            commercial
                                                                                                                                                                                                                                                                                                                                                                                                      5
```

밁

237

SPVECM

242

```
EMBL; Y00638;
HSSP; P18052;
MIM; 151460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD45_HUMAN
P08575;
                                                 PRINTS; PR00700; PRTYPHPHTASE.

PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.

PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.

PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.

PFAM: PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-LYMPHOCYTES;

MEDLINE; 88061067.

Streuli M., Hall L.R., Saga Y., Schlossman S.F., Saito H.;

Tifferential usage of three exons generates at least five mRNAs encoding human leukocyte common antigens.";

J. Exp. Med. 166:1548-1566(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-197 (Rel. 35, Last annotation update)
LEUKOCYTE COMMON ANTIGEN PRECURSOR (EC 3.1.3.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charbonneau H., Tonks N.K., Walsh K.A., Fischer E "The leukocyte common antigen (CD45): a putative protein tyrosine phosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 85:7182-7186(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 89017162.
Charbonneau H., Tonks N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve:
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTPRC OR CD45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Distinct functional roles
                               PFAM; PF00041; fn3; 2.
PFAM; PF00102; Y_phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domains of the receptor-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION.
                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
ycoprotein; Transmembrane; Phosphorylation; ternative splicing; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THERE ARE 8 DIFFERENT VARIANTS OF L-CA,
WHICH ARISE BY ALTERNATIVE SPLICING.
SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
DATABASE: NAME-PROW; NOTE-CD guide CD45 entry;
WMW-"http://www.nobi.nlm.nih.gov/prow/cd4/cd45 htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) J. 9:2399-2407(1990).

FUNCTION: REQUIRED FOR T-CELLS ACTIVATION THROUGH THE ANTIGEN RECEPTOR. THE FIRST PYPASE DOMAIN HAS ENZYMATIC ACTIVITY, WHILE RECEPTOR. THE SEEMS TO AFFECT THE SUBSTRATE SPECIFICITY OF THE
                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE SECOND ONE SEEMS TO AFFECT THE SUBSTRATE SPEC
THE FIRST ONE.
CATALUTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE +
PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collab
meen the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its countries in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90316093.
                                                                                                                                                     CAA68669.1;
1YFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thai T., Tars of the two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang M., Saito H.;
two intracellular phosphatase like
tein tyrosine phosphatases LCA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fischer E.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                     B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (L-CA) (CD45 ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H(2)0
                     T-cell; Repeat;
                                                                                                                                                                                                                            is
for
                                                                                                                                                                                                                                                                                          a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    different
                                                                                                                                                                                                                                                                        9
```

```
Š
                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCETT RAX
                                                                                                                                                                                                                                                           RESULT 15
6DCS_SOYBN
                                                                                                                                                                                                                                                                                                        멂
                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN=CV. HAROSOY 63;

MEDLINE; 91177016.

Welle R., Schroeder G., Schiltz E., Grisebach H., Sci
"Induced plant responses to pathogen attack. Analysi
heterologous expression of the key enzyme in the bios
heterologous expression of the key enzyme in the bios
phytoalexins in soybean (Glycine max L. Merr. cv. Ha)
phytoalexins in Soybean (Glycine max L. Merr. cv. Ha)
EUT. J. Blochem. 196:423-430(1991).
-i- FUNCTION: CO-ACTS WITH CHALCONE SYNTHASE IN FORM
4,2',4'-TRIHYDROXYCHALCONE, INVOLVED IN THE BIOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                      Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                   P26690,
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
NAD(P)H DEPENDENT 6'-DEOXYCHALCONE SYNTHASE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                   Glycine.
                                                                                                                                                                                                                                                 edcs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                       324
                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                               227
                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                 SOYBN
                                                                                                                                                                                                                                                                                                       KNIETFTCDTQNITYRFQCGNMIFDNK---EIKLENLEPEHE-YKCDSEILY 371
                                                                                                                                                                                                                                                                                                                            KDSVMWALDGLSFTYSL----LIWKNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                   TNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKW
                                                                                                                                                                                                                                                                                                                                                                        SWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGT
                                                                                                                                                                                                                                                                                                                                                                                                DEKYANITVDYLYNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                    DESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147253
                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 90.5; DB
Pred. No. 3.9;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C->S: LOSS POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
FIBROMECTIN TYPE-III (POTENTIAL).
FIBRONECTIN TYPE-III (POTENTIAL).
PROTEIN-TYROSINE PHOSPHATASE.
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEUKOCYTE COMMON ANTIGEN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
W; 1F357BC5632618B2 CRC64;
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                 315
                                                                                                                                                                                                                                                                                                                                                                                               ETKLFTAKLNVNENVEC - - - - - GNNTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          얶
                                                                                                                                                                                                                                                 ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                       . Analysis and the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                           e
E
                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲
            BIOSYNTHESIS
                        FORMATION OF
                                                                                                                                                                                         1. -. -. -).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1304;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
            얽
                                             <u>`</u>=0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                              263
                                                                                                                                                                                                                                                                                                                                                                          151
```

```
Ş
                                                                                                                                                                           밁
                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                         Ş
Search completed: June
Job time: 14317 sec
                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X55730; CAA39261.1; --{
PIR; S14222; S14222.
HSSP; P14550; ZALR.
PRINTS; PRO0069; ALDKETRDTASE.
PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
PFAM; PF00248; aldo_ket_red; 1.
Flavonoid biosynthesis; Oxidoreductase; NADP.
SEQUENCE 315 AA; 35490 MW; C3A6BE07EF330F47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: MONOMER.
-1- INDUCTION: BY PATHOGEN ATTACK.
-1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
                                                                                                                                                                             218
                                                                                                  265
                                                                                                                    173 SSGVEERIENIY------SRHKIYKLSPETTYCLKVKAALLISW 210
                                                                                                                                                                                                                                                                                                                              105 KSLKTLQLEYLDL----YLIHWPLSSQP-GKFSFPIEVEDLLPFDVKGV--WESMEECQK 157
                                                                                                                                                                                                              123 FRK-AQIGPPEVH------LEAEDKAIVIHISPGTKDSVMWALD-GLSFTYSLLIWKN 172
                                                                                                                                                                                                                                                     158 LGLTKAIGVSNFSVKKLQNLLSVATIRPVVDQVEMNLAWQQKKLREFCKENGIIVTAFSP 217
                                                                                                                                                                                                                                                                                           28 KNIKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFD-----YQKTGMDNWIKLSGCQN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: THIS IS THE KEY ENZYME IN THE BIOSYNTHESIS OF PHYTOALEXINS IN SOYBEAN.
                                                                                           SYDKERMNQNLHIFDWALTEQDHHKISQISQSRLISGPTKPQLADLW 311
                                                                                                                                                                       LRKGASRGPNEVMENDVLKEIAEAHGKSI-----AQVSLRWLYEQGVTFV-----PK 264
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                1, 2000, 04:38:54
                                                                                                                                                                                                                                                                                                                                                                                                                                7.58;
                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 90; DB 1; Length 315;
Pred. No. 0.72;
BB; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              64:
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              13;
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 1000000
                                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_12: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-675-2_COPY_1_229
1196
1 MMYVLLGATTLVLVAVGPWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           June 1, 2000, 04:38:14; Search time 69.16 Seconds (without alignments) 229.577 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMVVLLGATTLVLVAVGPWV......WKIGVYSPVHCIKTTVENEL 229
                                                                                                                                                                                                                                                                                                                                        sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                            sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_human: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_archea: *
                                                                                                                                                                                                                                                                                                                                                                                                                     sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                          p_invertebrate:*
                                                                                                                                                                                                                                       Length DB
  1111144555564
                                                      095209
095209
088307
015467
                                                                                                             Q28733
Q16614
                                                                                                                                                         Q9YHW0
Q61190
Q63953
Q9YGC8
Q14936
Q23020
                                                                                                                                                                                                                                       Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       summaries
                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225878
                   09yhw0 gallus gall
06190 mus musculu
063953 mus musculu
09ygc8 gallus gall
014936 homo sapien
023020 caenorhabdi
023550 caenorhabdi
023551 caenorhabdi
028753 oryctolagus
016614 homo sapien
09yhv9 gallus gall
054711 mus musculu
095209 oryctolagus
088307 mus musculu
015467 homo sapien
012465 saccharomyc
099624 homo sapien
                                                                                                                                                                                                                                       Description
caenorhabdí
saccharomyc
```

0 w 4 r	0000	0 4 ti 0 C	80000	1664867
79 79 79	80 79.5 79.5	880 	82 81.5 81	8835 825
, , , , ,		თ თ თ თ ი 7 7 8 8 0	, a a a a a a	7.1 6.9 6.9
247 248 442 513	513 431 829 1074	1526 2340 334	817 1093 1040 1009 1375	26926 429 2214 430 406 746
1311	2 5 1 1 1			5110
035663 035983 006349 035238	035664 023861 09xWD9 09x257	Q94538 Q94538 Q60705 Q70367 Q94977	Q07784 070535 070535 Q9W675 Q58863 Q94537	Q10466 Q06103 Q0673 Q92673 Q23854 Q58459 Q58459 Q59754
O35663 mus musculu O35983 mus musculu Q06349 saccharomyc O35238 mus musculu	T ()	Q94538 drosophila Q94538 drosophila Q60705 mus musculu Q70367 rattus norv Q94977 homo sapien	- സസ	Q10466 homo sapien Q06103 saccharomyc Q92673 homo sapien Q23854 brassica ca Q58459 methanococc Q90754 foot-and-mo Q20930 caenorhabdi

## ALIGNMENTS

g Q	P 64	p 9	Фу	Qu Be Ma	SON	R R R R R R R R R R R R	88888	25555	RESULT Q9YHWO
179 RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTT 224 :: :	121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEE 178  -          -  -     -     -     -     -     -	67KTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSF 120	7 GATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ 66 	Query Match Best Local Similarity 43.8%; Score 430.5; DB 13; Length 569; Matches 99; Conservative 37; Mismatches 79; Indels 11; Gaps	EMBL; AF082664; AAD13669.1; Receptor. SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE-LIVER;  REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;  "Comparative genomic analysis of the interferon/interleukin-10  receptor gene cluster.";  Genome Res. 0:0-0(1999),	Ar Mari. Gallus gallus (Chicken). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	Ol-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) 1NTERFERON ALPHA/BETA RECEPTOR 1.	LT 1 WO OOXHWO PRELIMINARY; PRT; 569 AA.

```
RESULT OF STREET OF STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.";

Gene 186:97-101(1997).

EMBL; U53696; AAC53062.1;

MGD; MGI:109380; I110rb.

PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               061190:
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          063953 PRELIMINARY; PRT; 332 AA. 063953; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDILINE: 94170381.
HEMMI S., BOHNI R., STARK G., DI MARCO F.,
"A novel member of the interferon receptor
functionality of the murine interferon gamm
cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                     SEQUENCE FROM N.A.
STRAIN-129SV/J;
MEDLINE; 97128072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIBBS V.C., PENNICA "CRF2-4: Isolation c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 97199375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                061190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                   Cell 76:803-810(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFNGR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 VHLEAEDKAIVIHIS------PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 VGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDSEVLRNLEPWTTYCIQVQGFLLDQNRTGEWSEPICERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQIESLAESLHLRFSAPQIENEPET----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGGFLLVPALG--MIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR CRFB4 OR CRF2-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CKRTASTQCDFS--HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 AA;
   c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
   RHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.3%;
28.2%;
   s:
   MUTHUKUMARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 219; DB 11;
Pred. No. 4.5e-12;
7; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4AC1802A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
ດ.,
                                                                                                                                                                                                                                                  gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₿
   LEMBO
                                                                                                                                                                                                                                                                                           AGUET M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
.
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                        complements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
Mus.
   DONNELLY R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349;
                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
```

```
ONESCHE

ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                        밁
                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 69
                                                                                                                                                                                  Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U69599; AAC52938.1;
EMBL; U69594; AAC52938.1;
EMBL; U69595; AAC52938.1;
EMBL; U69596; AAC52938.1;
EMBL; U69597; AAC52938.1;
EMBL; U69598; AAC52938.1;
EMBL; U69598; AAC52938.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9YGC8 PRELIMINARY;
O9YGC8;
O1-MAY-1999 (TrEMBLrel. 10, C
O1-MAY-1999 (TREMBLrel. 10, I
O1-MAY-1999 (TREMBLrel. 10, I
INTERLEUKIN-10 RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wenomic organization encoding the second ch Scand. J. Immunol. 44:
                                                                                                                                                                                                                                                                                                        Receptor.
                                                                                                                                                                                                                                                                                                                                               "Comparative genomic analysis receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1; --
EMBL; AF082666; AAD13671.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL10R2.
Gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PESTKA S., DEMBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REBOUL J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                            89
                                                                                          24
                                                                                                                                      \omega_{\omega}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:107654; Ifngr2.
(; PF00041; fn3; 1.
ENCE 332 AA; 37471
                                    FSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YENVTVGPPKNISVTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRXAQIGPPE-VHLEAEDKAIVIHISPGTXDSVMWALDGLSFTYSLLIWKNSSGVEERIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH
VSS--LSVYGAYVLRVRTEWEDEHSDWAVVRFKPMADTVIGPPSVNVKSESGTLHVDFTG
                                                                                                                                      POKVEYDIIDDNFILRWNRSDESVGNVTFSFD----YOKTGMDNWIKLSGCONITSTKCN 88
                                                                                          PRNARISSVNFRSVLLWDPPGVRKGNLSYTVQAKSIFPKQNFNN----VTTNLNVTECD
                                                                                                                                                                                     l Similarity
53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARDINER K.,
                                                                                                                                                                                                                                                                                                        341 AA;
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ion and promoter analysis d chain of the mouse interest 44:599-606(1996).
                                                                                                                                                                                                                                                                                                        39062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%;
                                                                                                                                                                                                        15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MONNERON
alysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                     45;
                                                                                                                                                                                  Score 179; DB
Pred. No. 1.8e
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 203;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                        7433D364 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0BF24E9E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                               UZE G., LUTFALLA G.; interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ysis of the gene
interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC32;
                                                                                                                                                                                  DB 13;
.8e-08;
les 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                 Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 332;
                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                     22;
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                     9
```

in regulation WATERSON R.H.;

and

```
RESULT
Q23020
                                                                                                                õ
                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                   õ
                                                                                              밁
                                                                                                                                         뮍
                                                                                                                                                                                            용
                                                                                                                                                                                                                ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ő
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 47; Conser
                                                                                                                                                                                                                                                                                                        EMBL; U19247; AAC52064.1; JOINED. EMBL; U19241; AAC52064.1; JOINED. EMBL; U19242; AAC52064.1; JOINED. EMBL; U19243; AAC52064.1; JOINED. EMBL; U19244; AAC52064.1; JOINED. EMBL; U19245; AAC52064.1; JOINED. EMBL; U19245; AAC52064.1; JOINED. EMBL; U19246; AAC52064.1; JOINED. EMBL; U19246; AAC52064.1; JOINED. EMBL; U19246; AAC52064.1; JOINED. EMBL; U19246; AAC52064.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q14936 PRELIMINARY; PRT; 484 AA. Q14936; Q14936; O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89003065.
AGUET M., DEMBIC 2.,
"Molecular cloning a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The gene for receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BANNWARTH W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEMBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 45:413-421(1997).
                                                  157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137
                                                                       178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
                                                                                                                                               59
                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
              σ
                                                                                                                                                                                                          VQ-GVIPEWNKTGERSQELCEQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKAALLTSW-KIGVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55:273-280(1988).
                                                  QEVD--
                                                                       ERIENIYSRHKIYKLSPETTYCLKV
                                                                                                 EEFAVCRDGKIGPPKLDIRKEEKQIMIDI - - -
                                                                                                                     DSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                       FIVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKE--SAYAKS 116
                                                                                                                                                                     FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA---EKENTSSWYEV 117
                                                                                                                                                                                               MALLFLLPLVMQGVSRAEMGTADLGPSSVPTPTNVTIESYNMNPIVYWEY--QIMPQVPV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97246734.
.., VAN DER LEEDE B.-J.M., MCKUNE K., KI
H W., ROMQUIN N., VIEGAS-PEQUIGNOT E.,
                                                                                                                                                                                                                                             9.5%;
llarity 22.9%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the ligand binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g and eyr
                                                  YDPETTCYIRV
                                                                                                                                                                                                                                                                                                                                                                                                         to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ဂ
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                           Score 113.5; DB
Pred. No. 0.022;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217
                                                                       202
                                                  171
                                                                                                                                                                                                                                                                                                         EBC99D1F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the human
                                                                                                 -----FHPSVFV----NGDE
                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNEZEVIC
                                                                                                                                                                                                                                              77;
                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human interferon gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon-gamma
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΞZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGUET
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
                                                                                                 156
                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                             æ
RESULT
Q23550
ID Q2
AC Q2
DT Q1
DT 01
DT 01
DT 01
OS CG
                                                                                                                                               유
                                                                                                                                                                     Ş
                                                                                                                                                                                               밁
                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                             뫄
                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1996) to the EMBL/GenB
EMBL; X15423; CAA33463.1; --
EMBL; Z73899; CAA98081.1; ALT_INIT.
EMBL; Z73897; CAA98081.1; JOINED.
HSSP; Q63450; 1A06.
PFAM; PF00041; fn3; 31.
PFAM; PF00047; 1g; 13.
PFAM; PF00069; Pkinase; 1.
PFAM; PF00014; FNTYPEIII.
MyOSIN; KINASE.
SEQUENCE 6048 AA; 668449 MW; 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q23020
Q23020, Q27232;
Q13020, Q27232;
Q1-NOV-1996 (TIEMBLIEL, Q)
Q1-NOV-1996 (TIEMBLIEL, Q)
Q1-NOV-1999 (TIEMBLIEL, 1
                                   Q23550
Q23550;
Q1-NOV-1996
Q1-NOV-1998
Q1-NOV-1999
            UNC-22
UNC-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE; 90044042.
BENIAN G.M., KIFF J.E., NECKELMANN N., MOERMAN D.G.,
"Sequence of an unusually large protein implicated in
myosin activity in C. elegans.";
Nature 342:45-50(1989).
                                                                                                                                                                                                                                               1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "BENIAN G.M., L'HERNAULT S.W., MORRIS M.E.;
"Additional sequence complexity in the muscle
encoded protein, twitchin, of Caenorhabditis e
Genetics 134:1097-1104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNC-22 OR ZK617.1.
Caenorhabditis elegans
                                                                                                                                               1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
MEDLINE; 93387664.
                                                                                                                                                                       199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                       30
                     NV-1996 (TrEMBLrel. 01, (NV-1998 (TrEMBLrel. 08, 1NV-1999 (TrEMBLrel. 12, 1NV-1999 (TrEMBLrel. 12, 12)
                                                                                                                                               VIEKKGKHGRDWQ 1223
                                                                                                                                                                      CLKVKAALLTSWK 211
                                                                                                                                                                                                                                              KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                                                                                                                             TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA
                                                                                                                                                                                                                                                                                             LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV 1129
                                                                                                                                                                                                                                                                                                                     LKSPOK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI
                                                                                                                                                                                                                       IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 (TrEMBLrel. 01, 6 (TrEMBLrel. 01, 9 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                             8.2%;
ilarity 22.8%;
Conservative
                                                                                                                                                                                                -GTPDVVDWDADRVS----
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          ; Score 97.5; D
; Pred. No. 17;
22; Mismatches
                                   Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                -LEWEPPKSDGG
                                     sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                          1977C602 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6048
                                                                                    ጅ
                                                                                                                                                                                                                                                                                                                                                                       DB.
                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e gene, unc-22,
elegans.";
                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
```

Length 6048; Indels

53;

Gaps

10;

-APITQY

1210

198

5. 74;

Length 7160; Indels

Gaps

10;

2241 82

-APITQY

2322

198 2292

```
RESULT OF SET OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SO DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 273897; CAA98064.1; JOI EMBL; 273899; CAA98064.1; JOI HSSP; P02751; IFAA. PFAM; PF00041; fn3; 31. PFAM; PF00047; 1g; 17. PFAM; PF00069; pkinase; 1. PRINTS; PR00014; FNTYPEIII. PFANTS; PR00014; FNTYPEIII. SEQUENCE 6831 AA; 752579 M
                                                                                                                                                                                   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY J., COULSON A
GONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTEN N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAPERSTON R.,

"THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAPERSTON R.,
""THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAPERSTON R.,
""THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAPERSTON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1856
     WHITE S.;
Submitted
                                                                                                                        WATSON A., WEINSTOCK L., WILKINSO
"2.2 Mb of contiguous nucleotide
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q23551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                023551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1994 VIEKKGKHGRDWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1996)
EMBL; 273897; CAA980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZK617.1B PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
                                                                               Nature 368:32-38(1994).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HARRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLKVKAALLTSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVIHISPGTKDSVMWALDGLSFTYSLLIW----KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MAY-1996)
     (MAY-1996)
                                                                                                                                                                    WEINSTOCK L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTPDVVDWDADRVS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA98064.1; -.
CAA98064.1; JOINED
1FNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nematoda; Secernentea; Rhabditia; Rhabditida;
bidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            င်
     ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01,
08,
12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases.
     the
                                                                                                                                               WILKINSON-SPROAT J., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0A66C338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.5; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ģ
                                                                                                                                                                      WOHLDMAN, P.
     databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6831;
                                                                                                                                                  III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
     AT THE DOTART AND CONTRACT OF THE CONTRACT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q28733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                  Nature 345:273-276(1990).

EMBL; X64696; CAA45937.1; -

EMBL; X17329; CAA35207.1; -

HSSP; P56276; TILK.

PFAM; PF00041; fn3; 50.

PFAM; PF00047; 1g; 3.
                                                                                                                                                                                                                    MEDLINE; 90238553.

LABEIT S., BARLOW D.P., G
FRANCKE U., LEONARD K., W
"A regular pattern of two
of titin.";
Myosin;
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITIN (FRAGMENT).
OryCtolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92258380.
LABEIT S., GAUTEL M., LAKEY A., "Towards a molecular understand EMBO J. 11:1711-1716(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CE12;
LABEIT S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q28733 PRE
Q28733; Q28736;
                                                                                                                                                                                                                                                                                                                                          TISSUE-PSOAS MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 4305-5320 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CE12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-6805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 LKSPQK----VEV-DIIDDNFILRWNRSDESVGNVTFSFDYQK--TGMDNWIKLSGCQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Z73899; CAA98082.1; JOI

273897; CAA98065.1; JOI

273897; CAA98065.1; JOI

273899; CAA98065.1; JOI

273899; CAA98065.1; JOI

2751; IFNA.

2752; PF00047; fn3; 31.

2752; PR00047; pKinase; 1.

2752; PR00014; FNTYPEIII.

2752; PR00014; PNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIEKKGKHGRDWQ 2335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLKVKAALLTSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDTKAHIDGLKKG--QTYQFRVKAVNKEGASDALSTDKDTKAKNPYDEPGKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDRPSKPNGPLEVSDVFEDNLNLSWKPPDDDGGEPIEYYEVEKLDTATGRWVP----CAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVIHISPGTKDSVMWALDGLSFTYSLLIW---KNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 44; Conserv
                                                   Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GTPDVVDWDADRVS----LEWEPPKSDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         understanding
                                                                                                                                                                                                                                           two types
                                                                                                                                                                                                                                           GAUTEL M., GIBSON T., HOLT J., HSIEH C.L., WARDALE J., WHITING A., TRINICK J.; WO types of 100-residue motif in the sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Created)
, Last sequ
, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97.5;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRINICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDD567FE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                            e
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6875
                                                                                                                                                                                                                                                                                                                                                                                                                                            CK J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
```

update)

```
OR RESULT TO SEE TO SEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
   EMBL M23461; EMBL M23466; EMBL M23466; EMBL M23467; EMBL M23470; EMBL M23471; EMBL M23473; EMBL M23474; EMBL M23475; EMBL M23476; EMBL M23479; EMBL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q16614
Q16614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen).";
EMBO J. 6:1251-1257(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01.NOV-1996 (TIEMBLIEL 01, Created)
01.NOV-1996 (TIEMBLIEL 01, Last sequence update)
01.NOV-1999 (TIEMBLIEL 12, Last annotation update)
T200 LEUKOCYTE COMMON ANTIGEN (CD45, LC-A) PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M23492; AAD15273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete exon-intron organizati
antigen (CD45) gene.";
J. Immunol. 141:2781-2787(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE: 87275816.
RALPH S.J., THOMAS M.L., MORTON C.C
"Structural variants of human T200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HALL L.R., STREULI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PLACENTA;
MEDLINE; 89009812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENEIGVGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWKIGVYSP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEKHSVRW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIGTGPPTESKPVIAKTKYDRPGRPDPPEVTKVSKEEMTVVWSPPEYDGGKSITGYYLEK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E----NTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVI-------HISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GGCEIQNYILEKCESKRMVWSTYSATVLTPGTTVTRLIEGNEYIFRVRAEN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGMDNWIKLSGC -- QNITSTKCNFSSLKLNVY -------EEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATVNVLDKPGP------VRNLKIP-----DVSSDRCTIRWDPPEDD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 21.7
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 AAD15273.1;
AAD15273.1;
AAD15273.1;
AAD15273.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑĄ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VPVNKSAIPER-----RLKVQNLIPGHEYQFRVKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.78;
21.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  759127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHLOSSMAN S.E., SAITU n.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORTON C.C.,
   JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91.5; DI
Pred. No. 71;
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E5D3B61F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.5; 1
No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TROWBRIDGE I.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (leukocyte-common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1.3.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT.
Q9YHV9
                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
      밁
                                                                                                                                                                                                                                                                                                      SOURCE PROCESS OF THE PROCESS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 36
                                                                                                                                                               Query Match
Best Local
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                            Genome Res. 0:0-0(1999).
EMBL; AF082665; AAD13670.1;
HSSP; P13726; 1TFH.
Receptor.
SEQUENCE 508 AA; 57049 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M23480
EMBL; M23481
EMBL; M23483
EMBL; M23483
EMBL; M23485
EMBL; M23485
EMBL; M23486
EMBL; M23486
EMBL; M23486
EMBL; M23489
EMBL; M23489
EMBL; M23490
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of receptor gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6AHX60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00041; fn3; 2.
PFAM; PF00102; Y_phosphatase;
PRINTS; PR00700; PRTYPHPHTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEKYANITVDYLYNK----
                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6%;
Similarity 20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 11
1143 AA;
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD15273.
AAD15273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA68269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD15273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD15273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD15273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYR_PHOSPHATASE_1;
                                                                                                                                                                                                                                                                                                   57049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130897 MW;
                                                                                                                                                               7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 JOINED.
                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
```

```
Q9YHV9;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MOV-1999 (TrEMBLrel. 12, Last annotation update)
INTERFERON ALPHA/BETA RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archos
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 KNIETFTCDTQNITYRFQCGNMIFDNK---EIKLENLEPEHE-YKCDSEILY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 DESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTS 112
                                   2 MVVLLGAT----TLVLVAVGPWVLSAAAGGKNLKSPQKV--EVDIIDDNF--ILRWN-RS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDSVMWALDGLSFTYSL----LIWKNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKW 162
METLMGGPLRFYQLVFVSI----LCAACYSSLSEKIPREPPDNLQMTSNNFQHILSWRAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGT----------- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00700; PRTYPHPHTASE.
Alternative splicing; Hydrolase.
1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GNNTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          %; Score 90.5; D
%; Pred. No. 8.2;
23; Mismatches
                                                                            Score 89.5; DB Pred. No. 3.5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                        2DC4E498 CRC32;
                                                                                                                                                                                                                                                                                                                 D., UZE G., LUTFALLA G.;
the interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97A3A561 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                        13;
                                                                               96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1143;
                                                                                 Indels
                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria;
                                                                                                                           508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                               Gaps
  57
                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6,
```

```
RESULT OF APILITY OF A
    RESULT
Q95209
ID Q0
AC Q0
DT 00
DT 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 33
  Q95209;
Q95209;
O1-FEB-1997
O1-FEB-1997
O1-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         054711
054711;
                                                                                                                                                                                                                                                                                                                                                                                                        1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HERMANS-BORGMEYER I., HAMPE W., SUESENS U., FENGER U., HERBARTH Mech. Dev. 0:0-0(1997).
EMBL; AF031816; AAC16739.1; -.
HSSP, P01130; 1AJJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TIEMBLIEL. 06, Created)
01-JUN-1998 (TIEMBLIEL. 06, Last sequence update)
01-WOV-1999 (TIEMBLIEL. 12, Last annotation update)
SORTILIN-RELATED RECEPTOR, LDLR CLASS A REPEATS-CONTAINING
                                                                                                                                                                                                                  1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00041; fn3; 4.
PFAM; PF00057; ldl_recept_a;
PFAM; PF00058; ldl_recept_b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1202296; Sorl1.
PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GP250) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106
                                                                                                                                                                                                                                                            144
                                                                                                                                                                                                                                                                                                                                                         91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 NFILRWNRSDESV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNKHSIPSAWK-----CITT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- KAALLTSWKIGVYSPVHCIKT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGT---KDSVMWALDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPTVPTYYRVLYS-----SHSNWKIAKQCSRIVQPFCNLTDDFQVVSDEYSAFVQSFVG
                                                                                                                                                                                                                                                          --IHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                        NLLLNALYTVRV-AAVTSRGIGNWSDSKSITTIKGKVIQAPNIHIDSYDENSLSFTLTMD
                                                                                                                                                                                                                                                                                                                                                                                                     NLQLSLNREEEGVILGHWAPPVHTHGLIREYIVEYSRSGSKMWASQRAASNSTEIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LSLFDIYNKVNYEITLRTVGEEHKRSPEKVTEEPFSIVIEELYPNRNYCVSVMVTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFTYSLLIWKNSSGVEERIENIYSRHK------IYKLSPETTYCLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEVFNSSLLH----FSPLSETFLGPPEFNLSSCVHCINITIKLPPTHLRKNGKL-----
                                                                                                                                                                                                                GDIKVN-GYVVNLFWSFDAHKQEKKTLSFRGGSALSHKVSNL-TAHTSYEIS
                                                                                                                                                                                                                                                                                                                                                       SLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESVG---NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEE----IKLRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
2033
  7 (TrEMBLrel.
7 (TrEMBLrel.
9 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.5%;
19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
227305 MW;
    12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 89.5; DB Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               GNV-TFSFDYQKTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHINKE B., METHNER B., SCHALLER H.C.;
sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DC8108CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2033
                                                                                               2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                             ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYKJAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2033;
                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
```

```
RESULT
1D 88307
1D 908
AC 088
AC 080

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 32
                                                                                                                  KANAKI T., BUJO H., HIRAYAMA S., TANI
MORISAKI N., SCHNEIDER W.J., SAITO Y
"Developmental regulation of LR11 ext
DNA Cell Biol. 0:0-0(1998).
EMBL; ABO15790; BAA31219.1; -.
HSSP; P01130; 1AJJ.
PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sorting receptor are present in a novel mammalian lipoprotein receptor family member.";
J. Biol. Chem. 271:24761-24768(1996).
EMBL; D86350; BAA13075.1;
HSSP; P01130; 1AJJ.
PROSITE; PS01209; LDLRA_1; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              088307;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01209; LDLRA_1; 10.
PFAM; PF00057; ldl_recept_a; 11.
PFAM; PF00058; ldl_recept_b; 4.
PFAM; PF00041; fn3; 5.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96394640.
YAMAZAKI H., BUJO H., KUSUNOKI J., SEIN SCHMEIDER W.J., SAITO Y.;
"Elements of neural adhesion molecules
                      PFAM; PF00057; ldl_recept_a; PFAM; PF00058; ldl_recept_b; PFAM; PF00041; fn3; 4. PRINTS; PR00261; LDLRECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              088307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1652 APONLOLSLHGEEEGVIVGHWSPPTHTHGLIREYIVEYSRSGSKVWTSERAASNFTEIK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 LSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 SPOKVEVDIIDDN---FILRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKC : | : : | : : | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTAQTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NSLSFTLTVDGNIKVNGYVVNLFWAFDTHKQEKKTMNFQGSSVSHKVGN 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGTKDSVMWALDGLSFTYSL------LIWKNSSGVEER----IENIYSRHKIYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NLLVNTLYTVRV-AAVTSRGIGNWSDSKSITTVKGKAIPPPNIHIDNYDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
     LDLRECEPTOR FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 89.5;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                TANAKA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B35F3995 CRC32;
                                                                                                                                                                                                                       expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEIMIYA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a yeast
                                                                                                                                                                                                                                                                     YAMAZAKI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                updațe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                    in murine brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KANAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥0¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vacuolar protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                       SEIMIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORISAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    z
```

7;

Job time: 14311 sec

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SO THE TAKE THE PROPERTY OF TH
                                                                                                                                      밁
                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                             몽
                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
Q15467
                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.5%; Score 89.5; DB 11; Length 2215; Best Local Similarity 19.2%; Pred. No. 24; Matches 33; Conservative 33; Mismatches 77; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.4%; Score 89; DB 4; Length 239; Best Local Similarity 22.7%; Pred. No. 1.4; Matches 46; Conservative 26; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q15467 PRELIMINARY: PRT; 239 AA. Q15467; Q1-467; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) SOLUBLE IFN ALPHA/BETA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
SEQUENCE 2215 AA; 247021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1771 GDIKVN-GYVVNLFWSFDAHKQEKKTLSFRGGSALSHKVSNL-TAHTSYEIS 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1656 NIQLSLNREEEGVILGHWAPPVHTHGLIREYIVEYSRSGSKMWASQRAASNSTEIK---- 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1712 NLLLNALYTVRV-AAVTSRGIGNWSDSKSITTIKGKVIQAPNIHIDSYDENSLSFTLTMD 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.";
J. Leukoc. Biol. 57:712-718(1995).
-i- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
EMBL; X89814; CAA61940.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 95279874.
NOVICK D., COHEN B., TAL N., RUBINSTEIN SOLUBLE and membrane-anchored forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFNABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 -- IHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                       198
                                                                                                                                                                                                                                                                                                                                                101 KLRIRAEKENT-----SSWYEVD-SFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 NFILRWNRSDESV-------GNV-TFSEDYQKTGMDNWIKLSGCQNITSTKCNFS 90
206 YCVSVYLEHSDEQAV-IKSPLKC 227
                                                                                                                                                                                                                                                                                 107 VTVLEGFSGNTTLFSCSHNFWLAIDMSFE-----PPEFEIVGFTNHINVMVKFPSIV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 SLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 NF--ILRWNRSDESVGNVTFSFDYQKTGMDNWIK-LSGCQNITSTKCNFSSLKLNVYEEI 100
                                                                   YCLKVKAALLTSWKIGVYSPVHC 220
                                                                                                                                                                                   DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHK------IYKLSPETT 197
                                                                                                                                                                                                                                                                                                                                                                                                                               NFRSILSWELKNHSIVPTHYTLLYTIMSKPEDLKVVKNCANTTRSFCDLTDEWRSTHEAY 106
                                                                                                                                      E-----EELQFDLSLVI------EEQSEGIVKKHKPEIKGNMSGNFTYIIDKLIPNTN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 239 SOLUBLE IFN ALPHA/BETA RECEPTOR BETA CHAIN.
239 AA; 27336 MW; 9DA1F03E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFEBECF8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.;
the human IFN-alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
```

Search completed: June

1, 2000, 04:38:19

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0% Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                13:12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       June 1, 2000, 05:53:09; Search time 903.62 Seconds (without alignments)
-1445.806 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-240-675-1
1343
1 CTGCAGGGATCTGCGGCGGC.....ATACCTCTAAATGAGGTACC 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882769 seqs, -486395729 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                         gb_p12: *
gb_pr1: *
gb_pr2: *
gb_pr3: *
gb_ro: *
gb_sts: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9b_ba1:

9b_om:**

9b_ov:**

9b_ov:**

9b_pat:**

9b_ph:**
                                                                                                  em_un: *
em_vi: *
gb_htg1: *
gb_htg2: *
gb_in1: *
gb_in2: *
                                                                                                                                                                                                                                                      em_or: *
em_ov: *
em_pat: *
em_hum3:*
em_hum4:*
gb_pr4:*
gb_htg3:*
gb_htg4:*
gb_htg5:*
gb_htg6:*
                                                                                                                                                                                                                              em_ph:*
em_pl:*
                                                                                                                                                                                                                                                                                                         em_hum2:*
em_in:*
                                                                                                                                                                                                      em_ro:*
em_sts:*
                                                                                     em_ba2:*
                                                                                                                                                                                            em_sy:*
                                                                                                                                                                                                                                                                                                                                                                       3b_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1765538
```

```
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_htg3:*
50: gb_p13:*
51: gb_p2:*
52: gb_htg1:*
53: gb_htg11:*
55: gb_htg11:*
57: gb_htg11:*
58: gb_htg14:*
58: gb_htg14:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

																																													***
4.5	4	C 43	42	4.	c 40	39	c 38	37	ω	c 35	w	33	w	c 31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	= ;	10	، ب	<b>20</b> ·	7 (	ייכ	رب ر	4	ω	N	щ.	Result No.
43.2	43.2	، ت	43.4	ũ	ū	4		44.2	4		44.8	45		5.		4		ω.	9	ω.		12	55.	90.	51.	51.	51.	51.	251.8	6	<u>1</u> 9	82	4	824	330	30.	330	330.		ω ω	ω w	34	1343	3	Score
3.2	3.2		υ 		ω . ω	3.3	3.3	3.3	•	3.3	ω .ω	3.4	3.4	٠	ა . 5	•	3.7	•	•		9.0	•	11.6	٠.	18.7	8	œ •	œ	18.7		_'	- !	- !	_ :	9	9	9		0		99.		8	100.0	10 C
8071	6291	83//	181949	107/	6747	358	8892	3404	3572	176109	4557	175815	3559	7430	10176	168	41667	46304	907	18188	1311	360	25560	2425	100000	100000	100000	9	293	8	55	91	28	23	78	78	75	75	75	1755	u	4	1343	1343	Length
U <sup>1</sup>	55	10	4.0	. u	4.5	44	33	34	œ	. 51	44	45	7	34	35	ഗ	7	4	12	9	12	v	9	4	9	9	φ	9	ø	12	ω	ω	ω	w	U)	ر ا	س	9	J.	υ	υ	σ	տ	u	BG
AC020/12	022	2 5	AC006196	١N	AC019247	AC011041	AL138927	CEF45E6 .	CHCRRPS18	AC003992	AC016875	AC009621	CPU30821	SFENDOFUR	AE00	50850	SPBC365	S.	238	AP000296	MMIF	I50846	9	AF082664	AP000188	AP000112	AP000044	HSIFNAR	AP000297	MUSIFNAR	OAOIFNARE	OAU65978	BOVIENRA	H	2	AR030347		MIT	612	w	659	12	A32389		
ACUZU/12 Homo Sapi	022/58 Homo sap	000000	196 HOMO Sap	Drosophi	247 Hom	1 Home	8927 Homo	117 Caenorhab	6473 Chl	03992 Human	16875 Homo	009621 Homo s	821 Cyanophora	888 S.frugipe	AE001370 Plasmo	50 Sequ	Φ,	2667 Gal	<b>06238 Mus muscu</b>	0296 Homo sap	40 Mus musc	Se	298 ното ѕар	664 Gallus g	Homo sap	sap	Home	9 Hu	00297 Homo sap	9641 N	39 O.aries	978 Ovis arie	320 Bos tauru	443	602 Sequence	030347 Sequence	8571 human STS	3171 Human int	76129 Sequence	32391 Interf	95 H	6127	89	6593 Human int	Description

ALIGNMENTS

9 9 9 9 9 9

```
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                    õ
                       Ş
                                                        밁
                                                                                S
                                                                                                                밁
                                                                                                                                     ð
                                                                                                                                                                 В
                                                                                                                                                                                               Š
                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1343; DB 5; Best Local Similarity 100.0%; Pred. No. 2.8e-296; Matches 1343; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
    421
                                                                                                                                                                                                                                                                                        121
                                                                                                                 301
                                                                                                                                            301
                                                                                                                                                                         241
                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                    ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                          CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                             TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                               TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                       CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                TGCTCGTCGCCGTGGGCCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human inte
A26593
A26593.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WATER-SOLUBLE POLYPEPTIDES HAVING HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon alpha receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /TIANSLATION "MOVULGATTLVLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDN
/TIANSLATION "MOVULGATTLVLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDN
FILRWARSDESVGNVFTSFEDYQKTGMDNWIKLSGCQNITSTKONFSSLKLNVYEEIKL
RIRAEKENTSSWYEVDSFTPFRKAQIGPPEVYLLEAEDKAIVIISPGTKDSVMWALDG
LSFTYSLLIWKNSSGVEERIBHIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPV
HCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYK
WKQIPDCENVKTTQCVFFQNVFQKGIYLLRVQASDGNNTSFWSEIKFDTEIQAFLLP
PVFNIRSLSDSFHIYIGAPKQSAGTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVT
VPNLKPLTYYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGNTSK"

254 c 264 g 376 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) 9218626-A 17 29-OCT-1992;
cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFFINITY FOR INTERFERONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                             480
                                                                                   420
                                                                                                                                                                                                  300
                                                       420
                                                                                                                                            360
                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
```

A32389
LOCUS
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Interferon A32389 A32389.1 G

1343 bp Dreceptor gene.

PAT

Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.

Mammalia;

Eutheria;

8 8	8 8	8 3	8 8	8 %	8 5	8 %	8 %	8 8	8 8	₽ ¾	8 5	8 8	8 8	გ <del>ჯ</del>
1321 1321	. 1261 1261	1201	1141 1141	1081	1021	961 961	901	841	781 781	721 721	661	601	541 541	481 481
GAAATACCTCTAAATGAGGTACC 1343 	ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG 1320 	CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACCACCACCATGG 1260 	TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAACTGATGTTA 1200 	CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140 	TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTC	GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 1020 	TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960 	ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG 900	ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA 840 	CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780 	TIGGIGICIATAGICCAGIACATIGIATAAAGACCACAGITGAAAAIGAACTACCICCAC 720 	TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 660 	ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC 600 	ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTA

```
REFERENCE
AUTHORS
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE CO
                  ð
                                                             Š
                                                                                        밁
                                                                                                          Š
                                                                                                                                    밁
                                                                                                                                                       Š
                                                                                                                                                                               В
                                                                                                                                                                                                  Š
                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
  밁
                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                      당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 1343; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                             541
                                                                                                                                                           421
   601
                        601
                                                                  541
                                                                                           481
                                                                                                               481
                                                                                                                                     421
                                                                                                                                                                                 361
                                                                                                                                                                                                      361
                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                    ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                         TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                                                                    CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                   CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                            CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                             ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                        CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                          CTGCAGGGATCTGCGGCGCGCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FR 2657881-A 18 09-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYK WKQIPDENVKTTQCVFPQNVFQKGIYLLRVQASGANNTSFYSEZIKFDTEIQAFLLP PVFUNIASLSSFHIYIGAPKQASGANDTSFYSEZIKFOTEIQAFLLF PVFUNIASLSSFHIYIGAPKQASGANTSFYSEZIKFWENTSNAERKIIEKKTDVT VPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGNTSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA02097.1"
/db_xref="GI:1567383"
/translation="mmythcattlylaygpwylsaaaggknlkspokyevdiiddn
/translation="mmythcattlylaygpwylsaaaggknlkspokyevdiiddn
filrwarsdesvgnytesfdyoktgynnwiklsgconitstkchryseiikl
riraekentsswyevdsftpfrkaqigppeyhleaedkaivihlspgtkdsymmaldg
LSFTYSLLIWKNSSGYEERIENIYSRHKIYKLSPETTYCLKYKAALLTSWKIGVYSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
27. .1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="chimeric IFN-receptor"
27. .1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="chimeric IFN-receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ៥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1343; DB 5;
Pred. No. 2.8e-296;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                               180
 660
                      660
                                            600
                                                                  600
                                                                                        540
                                                                                                             540
                                                                                                                                     480
                                                                                                                                                           480
                                                                                                                                                                                420
                                                                                                                                                                                                     420
                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                  RESULT 3
A76127
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                      뮍
                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γQ
                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멂
                                                                  FEATURES
                                                                                                                                                         ORGANISM
                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                1321
                                                                                                                                                                                                                                                                                                     1321
                                                                                                                                                                                                                                                                                                                            1261
                                                                                                                                                                                                                                                                                                                                                 1261
                                                                                                                                                                                                                                                                                                                                                                       1201
                                                                                                                                                                                                                                                                                                                                                                                             1201
                                                                                                                                                                                                                                                                                                                                                                                                                  1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021
                       SgS
                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                       1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  721
                                                                                                                                                                                    1343 b

8 Sequence 1 from Pat

A76127

A76127.1 GT.600000
                                                                                                                                                                                                                                                                                GAAATACCTCTAAATGAGGTACC
                                                                                                                                                                                                                                                                                             GAAATACCTCTAAATGAGGTACC 1343
                                                                                                                                                                                                                                                                                                                                                                                CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACCACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG 1320
                                                                                                                                                                                                                                                                                                                                                                       CAGTTCCTAATTTGAAAACCACTGACTGTATATTGTGTGTAAAGCCAGAGCACACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                            ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                     1 (bases 1 to 1343)
Benoit, P. and Meyer, F.
MONOCLONAL ANTIBODIES AGAINST THE INTERFERON RECEPTOR,
NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON
PATENT: WO 9320187-A 14-OCT-1993;
EUROP BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)
1. 1343
                                                                                                                                             unidentified unclassified.
                                                                                                                                                                   unidentified.
                   /organism="unidentified"
/db_xref="taxon:32644"
27. .1337
/note="unnamed
/codon_start=1
                                                                                                                                                                                          GI:6088263
                                                                                                                                                                                                              43 bp
Patent
                                                                                                                                                                                                               DNA
W09320187
           protein
          product"
                                                                                                                                                                                                                          PAT
                                                                                                                                                                                                                          19-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                       1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  780
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1343; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                             721
                                                                                                                            661
                                                                                                                                                                                       109
                                                                                                                                                                                                                     601
                                                                                                                                                                                                                                                    541
                                                                                                                                                                                                                                                                                                                  481
                                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                781
                                                               721
                                                                                                                                                                                                                                                                                   541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 660
                                                                                                                                                                                                                                                                                                               AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                               CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                             CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                 ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                            AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1343; DB 5; Length ilarity 100.0%; Pred. No. 2.8e-296; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="Cab58590.1"
//db_xref="G1:6088264"
//tanslation="mdvvllgartivlvavgpmvlsaaaggknlkspokvevdiiddn
/translation="mdvvllgartivlvavgpmvlsaaaggknlkspokvevdiiddn
filemursdesvgnvtfssdygktgmdnniklsgcqniistkcnesslklnvveeikl
riaekentsswevdstpfpfrkaoloppevhleaedkaivhispotkdsvekaldd
Lsftysllimknusgveerieniysrkiyklspettyckvkaalltsmkigvyspv
hcikttvenellppenievsvononvvlkmdytyanmtgovgmhafikrrigovspv
hcikttvenellppenievsvononvvlkmdytyanmtsvasekirdvtspv
kkolpdenvkttocvpponvfoxgivllrvoasdgnntsfnasekiletktdvt
vpnlkslsdsfhiyigabpkosgntpvlodypliyeiffmentsnaekkilekktdvt
vpnlkpltyvcvkarahtmdeklmkssvesdavcektkpgntsk"
a 254 c 264 g 376 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                                 600
                                                                                                                                                                                                                                                                                                                                             540
                                                                                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                               780
                                                                                             780
                                                                                                                           720
                                                                                                                                                        720
                                                                                                                                                                                                                                                    600
                                                                                                                                                                                                                                                                                                                                                                            480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
```

Qy

밁 δõ 밁 Ş В δ В

781

Š

В

δ

밁

Š

В

Š 밁 δÃ 밁 õ 밁

밁

Š

밁 δ 망양 멍 δ

	CDS	JOURNAL FEATURES SOUTC	TITLE	REFERENCE	SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION	RESULT 4 A26595	Db 1321 (	ОУ 1321 (	1261	1261	. Qy 1201 (	1141	Oy 1141 :	Oy 1081 (	ОУ 1021:	961	Оу 961 (	Db 901:	ОУ 901	Db 841 /	ОУ 841 /	
/ COUNTY CALL' I / product = "Interferon beta receptor" / protein_id="CAA01831.1" / protein_id="CAA01831.1" / protein_id="CAA01831.1" / protein_id="CAA01831.1" / protein_id="CAA01831.1" / translation="MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDN / translation="MMYVLLGATTLVLVAVGPWVLSAAATVIHISPGTKOSYMWALDG / transkentsswyeudsftpprkaQlGppepvHLsAEDKATVIHISPGTKOSYMWALDG LSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPV HCIKTTVENELPPPRNIEVSYONQNYVLKWDYTYAANTEQVOWLLAFLKRNPGHHLYK WKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLP PVFNIRASLSDSFHIYIGAPKOSGNTPVIQDYPLTKEIIFWRNTSNAERKIIEKKTDVT VPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGNTSKHLIVGICIALFAL PFVIYAAKLFLRCINVYFFPSLKPSSSIDEYFSEDPLKNLLSTSEEQIEKCFIIENI STIATVEETNQTDEDHKKYSSOTSQDSGNYSNEDESESKTSEELQQDFV"	/db_xref="taxon:9606" 271700	:: WO 9218626-A 19 29 Location/Qualific 11755 /organism="Homo:	SOLUBLE POLYPEPTIDES HAVI AND beta	πюн	human. Homo saplens	A26595 1755 bp DNA PAT 02-OCT-1995 Human interferon beta receptor gene. A26595 A26595.1 GI:1247460		GAAATACCTCTAAATGAGGTACC 1343	GAAATACCTCTAAATGAGGTACC: 1343	N	ТСЕ І ЭРАСІЛАВАН ВАБЛЕВІДІВ В ПОВІЛЬНІ В В В В В В В В В В В В В В В В В В В	CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG 1260  -   -		TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAAA	CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTATGAAATTA 1140	TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTTCCATATCTATATCGGTG 1080		SAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 1020	TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960	TOTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG 960	ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG 900	ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG 900	

```
BASE COUNT
ORIGIN
                                                                               S
                                                                                              밁
                                                                                                            Q
                                                                                                                            В
                                                                                                                                       õ
                                                                                                                                                         밁
                                                                                                                                                                    Ş
                                                                                                                                                                                     ġ
                                                                                                                                                                                                 Š
                                                                                                                                                                                                                밁
                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                           νŞ
                        Ş
                                       g
                                                     Ő
                                                                     밁
õ
              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.3%;
Best Local Similarity 100.0%;
Matches 1334; Conservative
                                                                                                                              661
                                                                                                                                                                                                   541
                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                          121
                           901
                                          841
                                                        841
                                                                      781
                                                                                                                                           661
                                                                                                                                                         601
                                                                                                                                                                       601
                                                                                                                                                                                     541
                                                                                                                                                                                                                  481
                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                       121
961
               106
                                                                                    781
                                                                                                  721
                                                                                                               721
                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...
                                                                                                                                                                                                                                                                                                                                                                                                CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                    CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                            CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCAGGGATCTGCGGGGGGCGCCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                         ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                            TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                         ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                 CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                     TCTTTCCTCAAAAGCTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                      TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
               TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1334; DB 5; Length Pred. No. 3.1e-294; O; Mismatches O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                        660
                                                                                                                                                                                                   600
                                                                                                                                                                                                                               540
                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                      840
                                                                                   840
                                                                                                 780
                                                                                                               780
                                                                                                                              720
                                                                                                                                          720
                                                                                                                                                         660
                                                                                                                                                                                     600
                                                                                                                                                                                                                  540
                                                                                                                                                                                                                                             480
                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                                       420
                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                            960
                                          900
                                                        900
               960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

Ş

1 CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG

Query Match Best Local Sim: Matches 1334;

h 99.3%; Score 1334; DB 5; Similarity 100.0%; Pred. No. 3.1e-294; 34; Conservative 0; Mismatches 0;

Length

Indels

0

Gaps

0

```
A32391
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
JOURNAL
FEATURES
BASE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021
                     COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAATACCTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Ver
Primates; Catarrhini; Hominidae;
1 (bases 1 to 1755)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A32391 1755 bp DN Interferon alpha and beta A32391 A32391.1 GI:1567384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                     ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FR 2657881-A 20 09-AUG-1991;
Location/Qualifiers
              /translation="mmvvligattlvlvavgpwvlsaaaggknlkspokvevdiiddn triansdesvgnvtpspdyoktgmdwiklsgognvitstkorsslklnvvæeikl riraerbatssyvevdsetpravagloppevilleaedbatuvhitspotrosvemalde istryvenelpppenitsvyokgvlgherikleaedbatvuhitswkigvspv hgirtyvenelpppenitsvyokgnvylkaddyryanarfovophaflkrnpochtly wkqipdcenvkttgcvpponvpokjivltukvdyryanarfovopheliketopptly pvinirsuspfhiyigapkosgntpviddypliyeiifwentsnaerkiiekktdvt vnlkplivycvkarhitmdkklnkssyfsdavcektrpgnyskimllvgicialeat ppviraakvelkcinvefpslkksssiderfbedhkkrssotsdegekknullstseedekcfiieni stianvefingtdedhkkrssotsgosnysnedesekstseeloodfy" and statveethotoppenskinssyfsdavckrknullstseedekcfiieni stianvefingtdedhkkrssotsgosnysnedesekstseeloodfy" and statveethotoppenskinssyfsdavckrknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstseedekknullstse
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
27...1700
                                                                                                                                                                                                                                                                         /codon_start=1
/protein_id="CAA02098.1"
/db_xref="GI:1567385"
                                                                                                                                                                                                                                                                                                                                                                     /gene="chimeric IFNalpha/beta-receptor" 27. .1700
                                                                                                                                                                                                                                                                                                                                               /gene="chimeric IFNalpha/beta-receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Нолю
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1080
```

B

```
721
                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                    961
                                                                                   901
                                                                                                 901
                                                                                                              841
                                                                                                                            841
                                                                                                                                          781
                                                                                                                                                       781
                                                                                                                                                                                   721
                                                                                                                                                                                                  661
                                                                                                                                                                                                               661
                                                                                                                                                                                                                              601
                                                                                                                                                                                                                                           601
                                                                                                                                                                                                                                                         541
                                                                                                                                                                                                                                                                      541
                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCATGGTATGAGGTTGACTCATITACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                    ATTGGATAAAATTGTCTGGGTGTGAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                  TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                             ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                        CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                 TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA
                                                                                                                                                                                                                                    TCTCACCAGAGACTACTTATTGTCTAAAAGGTAAAGCAGCACCTACTTACGTCATGGAAAA
                                                                                                                                                                                                                                                        ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                    CTGCAGGGATCTGCGGCGCCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                      CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                           1080
                                                       1020
                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                           1080
                                                                    1020
                                                                                                                                          840
                                                                                                                                                       840
                                                                                                                                                                                                                              660
                                                                                                                                                                                                                                           660
                                                                                                                                                                                                                                                         600
                                                                                                                                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                   540
                                                                                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                                                             420
                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                   960
                                                                                                 960
                                                                                                              900
                                                                                                                            900
                                                                                                                                                                      780
                                                                                                                                                                                   780
                                                                                                                                                                                                  720
                                                                                                                                                                                                               720
                                                                                                                                                                                                                                                                      600
```

õ

밁

참 청

δõ 밁 õ 밁 õ 밁 δÃ 밁 Š 밁 Š 밁 S ₽ õ В Š 밁 Š

멂

8 8

В

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
A76129
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                          δÃ
                                                                                    Š
                                                                                                                         Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
 밁
                                                          B
                                                                                                                                                  δ
                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1334; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                               121
 121
                                                               61
                                                                                           61
                                                                                                                         CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACCACCACCATGG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A76129
Sequence 3 f
A76129
A76129.1 G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1755)
Benoit, P. and Meyer, F.
MONOCLOAIN ANTIBODIES AGAINST THE INTERFERON RECEPTOR,
NEUTRALIZING ACTIVITY AGAINST TYPE I INTERFERON
Patent: WO 9320187-A 14-CCT-1993;
EUROP BIOTECHNOLOGIE (FR); BENOIT PATRICK (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unclassified
                                                                                                                                                                                                                                                                                      593
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                              /protei_id="Cab58591.1"
//protei_id="Cab58591.1"
//db_xref="01:6088266"
//transflaton="mmvvLlgattlvlvavgpwvLsaaaggknlkspqkvevDIIDDN
/firansflaton="mmvvLlgattlvlvavgpwvLsaaaggknlkspqkvevDIIDDN
/firansflaton="mmvvLlgattlvlvavgpwvLsacbkaIvIHISPGTKDSVMMALDG
/firanskdbsvgnvrysfbykoktghnwikLsgctykaIvIHISPGTKDSVMMALDG
RIFAREKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMMALDG
LSFTYSLLIWRNSSGVESERIENIYSREKIIXKLSBCTTYCLKVKAALLTSWKIGVVSPV
HCIKTTVENELPPPENIEVSVQNQNYVLMDYTYAMWIFOVQWLHAFLKRNFGNHLYK
WKQIPDCENVKTTQCVEFQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDDTEIQAFLLP
PVFNIRSLSDSFHIYIGAPKQGSNTPVIQDYPLIYEIIFWHT9NAERKIIEKKTDVT
VPNIKKLTIVVCYKARAHTMDEKLNKSSVFSDAVCEKTKPGNTSKIWLIVGICIALFAL
PFVIYAAKVFLRCINYVFFPSLKKPSSSIDEYFSGDFLKNLLLSTSEEQIEKCFIIENI
STIATVEETNOTDEDHKKYSSQTSQDSGNYSNEDESESKTSEELQQDFV"
93 a 324 c 334 g 504 t
                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unidentified"
/db_xref="taxon:32644"
27. .1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"unnamed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:6088265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1755 bp
from Patent
                                                                                                                                                                                 99.3%; 5cc
100.0%; Pr
                                                                                                                                                                                      Score 1334; DB 5; Pred. No. 3.1e-294; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9320187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product'
                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-OCT-1999
                                                                                                                                                                                         0
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1200
                                                                                                                              60
                                                               120
                                                                                                                                                                                           0
```

ő

```
밁
                                                      밁
                                                                                            B
                                                                                                                                밁
                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                              Š
 1261
                                                                           1141
                                                                                                                                   1021
                                                                                                                                                      1021
                                                                                                                1081
                                                                                                                                                                         961
                                                                                                                                                                                          961
                                                                                                                                                                                                             106
                                                                                                                                                                                                                                                   841
                                                                                                                                                                                                                                                                     841
                                                                                                                                                                                                                                                                                                                                                                                                        601
                                                                                                                                                                                                                                                                                                                                                                                                                                              541
                                                                                                                                                                                                                                                                                                                                                                                                                                                               541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                901
                                                                                                                                                                                                                                                                                        781
                                                                                                                                                                                                                                                                                                                             721
                                                                                                                                                                                                                                                                                                                                                721
                                                                                                                                                                                                                                                                                                                                                                  661
                                                                                                                                                                                                                                                                                                                                                                                     661
                                                                                                                                                                                                                                                                                                                                                                                                                           601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                           781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAG
                                                      CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGTTCCTAATTTGÄAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                                                                                  TCTTTCCTCAAAACGTTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                            ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACTT
ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGAGCGCTGTATGTGAGAAAACCAAAACCAG
                                                                                                                                                    TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                  ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                        ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                 ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                       TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                    1080
                                                                                                                                                                                         1020
                  1260
                                    1260
                                                                                                                                  1080
                                                                                                                                                                        1020
                                                                                                                                                                                                                                960
                                                                                                                                                                                                                                                                     900
                                                                                                                                                                                                                                                                                        840
                                                                                                                                                                                                                                                                                                           840
                                                                                                                                                                                                                                                                                                                                               780
                                                                                                                                                                                                                                                                                                                                                                  720
                                                                                                                                                                                                                                                                                                                                                                                    720
                                                                                                                                                                                                                                                                                                                                                                                                        660
                                                                                                                                                                                                                                                                                                                                                                                                                          660
                                                                                                                                                                                                                                                                                                                                                                                                                                                               600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                             960
                                                                                                                                                                                                                                                 900
                                                                                                                                                                                                                                                                                                                            780
                                                                                                                                                                                                                                                                                                                                                                                                                                             600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
```

Ş 멿 Qy 밁 ð 밁 Qy В δÃ 밁 õ В ð 밁

Š

Ś

S

Ş

Š 밁 Š ş

Ş

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
δÃ
                                                                                                                 ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
HUMIFNRA
                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                Query Match
Best Local s
Matches 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
   61
                                                                    53
                                                                                                                               ب
                                                                 GAAATACCTCTAAA 1334
                                                                                                                                  CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                                                                                                                                                                   1332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2755)

2 (bases 1 to 2755)

2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Draft entry and computer-readable sequence for [1] kindly submitted by G.Uze, 29-NOV-1989, for release after publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon-alpha receptor. Human cell line DAUDI, cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human interferon-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J03171.1 GI:184645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMIFNRA
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       867
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:G00-120-078"

/protein_id="AAA52730.1"

/db_xref="GIB:G00-120-078"

/db_xref="GIB:G00-120-078"

/db_xref="GIB:G00-120-078"

/db_xref="GI:306914"

/translation="MAVVILGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDN

filrwnrsdesvgnvtfsfdyQktgmdnwiklsGCQNITSTKCNFSSLKLNVYEEIKL

RIRAEKENTSSWYEVDSFTPFKKAGIGPEVHLEAEDKAIVIHISPGTKOSVMWALDG

LSTTYSLLIWKNSSGVEERIENIYSHRIYKLSPETTYCLKVRAALTSWKIGVYSPV

HCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYK

WKQIFDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSWSEEIKFDTEIQAFILP

PVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVT

VPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTRFGNTSKULIVGICIALFAL

PFYIYAAKVFLRCINYVFFPSLKPSSSIDEYFSEQPLKNLLLSTSEEQIEKCFIIENI
                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                /gene="IFNAR"
/note="interferon-alpha
553 c 578 g 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STIATVEETNOTDEDHKKYSSQTSQDSGNYSNEDESESKTSEELQQDFV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="interferon-alpha receptor signal peptide (put.);
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21922.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IFNAR"
/note="interferon-alpha receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2755 bp
                                                                                                                                                                                                                               99.1%;
                                                                                                                                                                                                Score 1330.8; DB 9
Pred. No. 1.7e-293;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor (HulfN-alpha-Rec) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                    na receptor"
757 t
                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor'
                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-1994
                                                                                                                                                                                                                                                                    2755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                   0
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                       0
```

```
멍
                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                         뭥
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                           S
                                                             밁
                                                                          δ
                                                                                                        Š
                                                                                                                         밁
                                                                                                                                     Ş
                                                                                                                                                     B
                                                                                                                                                                    Š
                                                                                                                                                                                                  Š
                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
 밁
             Š
                              В
                                                                                                                                                                                     뮍
  1193
                                                                             1021
                                                                                             1013
                                                                                                            961
                                                                                                                                         901
                                                                                                                                                         893
                                                                                                                                                                        841
                                                                                                                                                                                       833
                                                                                                                                                                                                      781
                                                                                                                                                                                                                     773
                                                                                                                                                                                                                                                   713
                                                                                                                                                                                                                                                                   199
                                                                                                                                                                                                                                                                                   653
                                                                                                                                                                                                                                                                                                 601
                                                                                                                                                                                                                                                                                                                593
                                                                                                                                                                                                                                                                                                                                541
                                                                                                                                                                                                                                                                                                                                                533
                                                                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                             473
                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                             413
                                                                                                                                                                                                                                                                                                                                                                                                                   361 CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           353
                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
                                                                                                                                                                                                                                     721
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                     TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                      ACCATTIGTATAAATGGAAACAAATACCIGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                             ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                    CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                            TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                                                                                                ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                              AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                           CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                                             TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                                                                                                                                               AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAAT
                               CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                      ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                             1140
                                                             1132
                                                                            1080
                                                                                                          1020
                                                                                                                                                                                                                                                                                                                                                            540
                                                                                          1072
                                                                                                                         1012
                                                                                                                                                                                                     840
                                                                                                                                                                                                                                                                                  712
                                                                                                                                                                                                                                                                                                 660
                                                                                                                                                                                                                                                                                                                                600
                                                                                                                                                                                                                                                                                                                                                                             532
                                                                                                                                                                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                                                                                                                                                           472
                                                                                                                                                                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                                                                                                                                                          412
                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232
                                                                                                                                         960
                                                                                                                                                        952
                                                                                                                                                                       900
                                                                                                                                                                                      892
                                                                                                                                                                                                                    832
                                                                                                                                                                                                                                    780
                                                                                                                                                                                                                                                   772
                                                                                                                                                                                                                                                                 720
                                                                                                                                                                                                                                                                                                                652
                                                                                                                                                                                                                                                                                                                                              592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292
```

BASE CO

STS
primer\_bind
primer\_bind
ccount 8

/organism="Homo sapiens" /db\_xref="taxon:9606" /map="21" 1750..1924 1750..1771

867

complement(1901. .1 1 553 c 578 g

.1924) 757

FEATURES

```
RESULT 8
G28571
LOCUSTION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1321 GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATACCTCTAAA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G28571 2755 bp DNA STS human STS SHGC-35315, sequence tagged site. G28571 G1:1408386 STS; STS sequence; primer; sequence tagged
                                                                                                                                                                                                                                                                                                                                                                         Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2755)
Myers,R.M.
Unpublished (1996)
                                                                                                                                                                                                                                                                                                 Primer A: TGACCAGAAATGAACTGTGTCA
Primer B: TTTAAATAGTTAAGAGCTTGCCCG
STS size: 175
PCR Profile:
Prepared with primer pairs provided by Sandoz,
-- Washington University/Merck EST sequence.
Location/Qualifiers
1. 2755
                                                                                                              Buffer:
                                                                                                                                                                                                   Protocol
                                                                                                                                                                                                                                                                                                                                                               Email: myers@shgc.stanford.edu
                                                                       MgCl2:
KC1:
Tr1s-HC1:
                                                                                                                                      Taq Polymerase:
Total Vol:
                                                                                                                                                               dNTPs:
                                                                                                                                                                         Primer:
                                                                                                                                                                                      Template:
                                                                                                                                                                                                              Thermal Cycler:
                                                                                                                                                                                                                           PCR Cycles:
                                                                                                                                                                                                                                     Polymerization:
                                                                                                                                                                                                                                                    Annealing:
                                                                                                                                                                                                                                                              Denaturation:
                                                                                                                                                                                                                                                                                       [nitial incubation:
                                                                                                                                     25 ng
each 1 uM
each 200 uM
each 200 uM
c 0.05 units/ul
10 ul
                                                               50
50
8.3
                                                                                                                                                                                                             94 degrees C:
62 degrees C:
72 degrees C:
30
Perkin Elmer '
                                                                          222
                                                                                                                                                                                                                                                                                      94 degrees
                                                                                                                                                                                                                                                                                       ဂ
                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                     CA
                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                      94305,
                                                                                                                                                                                                                                       15
30
                                                                                                                                                                                                                                                                                       90
                                       derived
                                                                                                                                                                                                                                        seconds
                                                                                                                                                                                                                                                    seconds
                                                                                                                                                                                                                                                              seconds
                                                                                                                                                                                                                                                                                       seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-1996
                                       from J03171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1312
```

```
Query Match
Best Local S
Matches 1332
  1013
                                                                                                                                                                                593
                                                                                                                                                                                                                                                                          361
                          953
                                      901
                                                   893
                                                               841
                                                                            833
                                                                                         781
                                                                                                      773
                                                                                                                  721
                                                                                                                              713
                                                                                                                                           199
                                                                                                                                                        653
                                                                                                                                                                     601
                                                                                                                                                                                              541
                                                                                                                                                                                                           533
                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                    473
                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                              413
                                                                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCAGGGATCTGCGGCGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                             CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                         CTCCTCAAAAAGTAGAGGTCGAÇATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                  ACCATITGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                            ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                     CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                              TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                        ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                             TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                   TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                1332;
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.1%;
99.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1330.8;
Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8; DB 1
1.7e-293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                          292
                                                                                                                                                        712
                                                                                                                                                                     660
                                                                                                                                                                                                                      540
                                                                                                                                                                                                                                                                                       412
                                                                                                                                                                                                                                                                                                                                                                   232
                                                                                                                                                                                                                                                                                                                                                                                                                      112
                                                                                                                                                                                                                                                                                                                                                                                                                                   60
  1072
                          1012
                                                   952
                                                               900
                                                                            892
                                                                                        840
                                                                                                     832
                                                                                                                               772
                                                                                                                                           720
                                                                                                                                                                                 652
                                                                                                                                                                                              600
                                                                                                                                                                                                                                    532
                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                              472
                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                352
                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                              Q
Š
           g
                       οy
                                      멎
                                                Ş
                                                               밁
                                                                                        В
                                                                                                 δõ
                                                                                                                  8 8
                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                           멎
                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
```

õ 밁 δ

밁

B 5

밁 S B S 밁 S 밁 S 밁 S 닭 ő 밁 δ B Ş 밁 Ş 밁 Ş 밁 Q 밁 Š 밁 Q 及 ő

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
AR030347
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 1332; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1081
                                                                                                                                                                                                                                                           121
301
                                         293
                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                           113
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCAGGGATCTGCGGCGCGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG
TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 2784)

2 (bases 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AR030347
Sequence 1 1
AR030347
AR030347.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.1%;
99.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1330.8; DB 5; pred. No. 1.7e-293; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5861258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 1140
                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                              172
                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1132
  360
                                           352
                                                                                     300
                                                                                                                                 292
                                                                                                                                                                             240
                                                                                                                                                                                                                        232
                                                                                                                                                                                                                                                                                                                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
```

		GAAATACCTCTAAA 1334                 GAAATACCTCTAAA 1386	1321 1373	р <sub>у</sub>
νο	132 137	LATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAAAAA	1261 1313	g 8
ν ο	126 131	CAGTICCIAATITGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG 	1201 1253	β δ δ
N O	120	TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTA 	1141 1193	B 8
νо	114	CTCCAAAACAGTCTGGAAACAGGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA	1081	g Q
2 0	108	TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTC	1021	g g
2 0	102	GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 	961	g Q
N	960	TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG	901 953	B 8
	900	L ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG 	841	B 64
	840	ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTI	781 833	D Q
	780 832	CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACA? 	721 773	p 8
	720	TIGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC	661 713	8 & 8
	1 660 1 712	TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGGAGCACTACTTACGTCATGGAAAA	653	유 양
	652	ACTCTTCAGGTGTAGAAGAAAGG	541 593	g S
	540	. ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTA	481 533	B 8
	3 480 3 532	L AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAG 	421 473	D Oy
	3 420 3 472	CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG 	361 413	D Q
	1 412		353	₽ .

RESULT 10

Oy 66 Db 71	Оу 60 ОБ 65	Оу 54 Db 59	Qy 48 Db 53	Qy 42 Db 47	Оу 36 Db 41	Qy 30 Db 35	Qy 24 Db 29	Qy 18 Db 23	Qy 121 Db 173	Qy 6 Db 11	Qy 5	Query   Best L Matche	LOCUS LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE TITLE TEATURES SOURCE GOURCE OURNAL FEATURES SOURCE OURNAL FEATURES OURCE BASE COUNT ORIGIN
1 TIGGIGICTATAGICCAGIACATIGIATAAAGACCACAGIIGAAAAIGAACIACCICCAC 7	1 TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 6	1. ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATTAAAC 6	1 ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTA	1 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG 4	1 CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG	1 TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACTT	1 ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC 3	1 GCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAACTGGGATGGAT	CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA	1 TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT	1 CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGCACCCTAG	y Match 99.1%; Score 1330.8; DB 5; Length 2784; Local Similarity 99.9%; Pred. No. 1.7e-293; hes 1332; Conservative 0; Mismatches 2; Indels 0; Gap	I93602 2784 bp 'DNA PAT 01-DEC-1998 ON 193602.1 GI:3938072 IS Unknown. USM Unknown. Unclassified. UCE 1 (bases 1 to 2784) CE Mogensen, K.Erik, Uze,G., Lutfalla,G. and Gresser,I. CDNA fragment coding the alpha interferon receptor gene and p for the preparation of a corresponding protein AL patent: US 5731169-A 1 24-MAR-1998; Increase 12784 UNT 896 a 553 c 578 g 757 t
72	112	600 652	540 592	80	420 472	360 412	100	240	180 232	120 172	60 112	0;	process

```
망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                 DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                     RESULT
BTIFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                FEATURES
                                                                                                                                                                                                                                                                                                                          rocus
                                                                            JOURNAL
MEDLINE
                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATTIGTATAAATGGAAACAAATACCIGACIGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                                                                                                        GAAATACCTCTAAA 1334
||||||||||||||
GAAATACCTCTAAA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACCACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                BTIFNAR 3230 bp
B.taurus IFNAR mRNA
X68443
                                                                                      Submitted (14-SEP-1992) G. Lutfalla, CNRS Lab of Viral Oncology-IRSC, 7 Rue Guy Moquet BP 8, 94801 Villejuif Cedex, 2 (bases 1 to 3230)

Mouchel-Vielh,E., Lutfalla,G., Mogensen,K.E. and Uze,G. Specific antiviral activities of the human alpha interferons determined at the level of receptor (IFNAR) structure FEBS Lett. 313 (3), 255-259 (1992)
                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                      cytokine receptor; interferon
                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae;
                                                                                                                                                                                                                                                          Bos taurus.
                                                                                                                                                                                                                                                                                     X68443.1
                                                                                                                                                                                                          (bases
                                                              Location/Qualifiers
                                                                                                                                                                                                        1
to
/germline
/tissue_type="kidney"
                         /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                        3230 bp ...
                                                                                                                                                                                                                                                                                                     Interferon receptor
                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                            type
                                                                                                                                                                                                                                                                                                            20-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840
                                                                                                                                                                                                                                                                                                                                                                                                                                          1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960
                                                                                                                                                        FRANCE
                                                                                                                                                                                                                      Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                 뮍
                                                                                                                                                                                                                                                                                                                                                                      Ş
             Ş
                                        밁
                                                          Ş
                                                                                        멂
                                                                                                          δÕ
                                                                                                                                         밁
                                                                                                                                                                                            밁
                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1057; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                  169
                                                                                                                                                                                                                                                                                                                                                                                                     109
                                                                                                                                            403
                                                                                                                                                                    311
                                                                                                                                                                                                                      254
                                                                                                                                                                                                                                                283
                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                                                                                              GTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCT---GAA
                                                                                                                                                                                                                                                              GAG---ATGGGTGCTGCCGCCGCCTCAGGGGAAGCAAATCTGAA---GCCTGAAAATGT
                                                                                                                                                        TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAA ---CACTTCTTCATG
             GTCTGGATGTCAACATATTACTAGTACCAAATGCAACTTTTCTTCAGTCGAGCTTGAAAA
                                                                                                                                                                                                                                                CAAGAATGTGACTTTTTCAGCAGATTATCAAATACTAGGAACGGATAACTGGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                          GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGT
                                     TTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT----CCTGGAACAAAAGATAG
                                                                                                                                          TGTTTTTGAAAAATTGAATTGCGCATAAGAGCAGAAGAAGAAACAACACTTCCACATG
951
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="IFNAR"
197. .1804
/gene="IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xfef="SWISS-PROT:Q04790"
/translation="MLALLGATTLMLVAGRWVLPAASGEANLKPENVEIHIIDDNFFL
KWNSSESVKNUTFSADYOLLGT DWKKLSGCOHITSTKCNTSSVELENVFEKIELRI
RAEEGNNTSTWYEVEPFVPFLEAQIGPVDVHLEAEDKAIILSISPPGTKDSIMWAMDR
SSFRYSVVIWKNSSSLEERTETYYPEDRIYKLSPEITYCLKVKAELRLOSRVGCYSPV
YCINTIERHKVPSPENIQINADNGIYVLKWDYPYENATFDAQWLRAFFKKIPGNHSDR
WKQIPNCENYTSTHCVFPREVSSRGIYYVRVRASNGNGTSFWSEKEEWTEMKTIIFP
PVISVKSVTDDSLHVSYGASEESENMSVNOLYPLIYEVIFWENTSVAERKVLEKRTNF
IFPDLKPLITYYCVKARALIENDRRNKGSSFSDTVCEKKTPGNTSKTWLIVGTCTALFS
IPVIYVSVFLACVKYVFFPSSKPPSSVDEYTSDQPLRNLLLSTSEEDGTECTIIEN
ASIITELEETDEIDEVHKKYSSGTSQDSGNYSNEDENGGSKISEEFPQQDSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="interferon
2171. .3230
/note="clone MDd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="interferon reco
/protein_id="CAA48484.1"
/db_xref="GI:432"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
643 c 751 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="MDBK"
/clone="MD5, MDd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="IFNAR"
125. .1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.48;
79.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone MD5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ore 824.2; DB 3;
ed. No. 5.9e-178;
Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor
```

type

Indels Length

Gaps

6,

133

222

168

193

282

402

310 342 253

367

462

427

484 522

544 582

3230 18;

```
RESULT 1
BOVIFNRA
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                           KEYWORDS
SOURCE
ORGANISM
                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
 REFERENCE
AUTHORS
                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                            멍
                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                            뭥
                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멍
                                                                                                                                                                                              융
                                                                                                VERSION
                                                                                                                                                                                              1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      763
                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTACCTCTTTTTGGTCTGAAGAGAAGGAATTTAATACTGAAATGAAAACTATCATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACGCAACTTTTCAAGCTCAGTGGCTCCGTGCCTTTTTTAAAAAGATTCCTGGGAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCAAGTCTAGAAGAAGAACGGAAACTGTTTATCCCGAAGATAAAATTTATAAACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCATGTGGGCTATGGATCGTTCAAGCTTTAGGTATAGCGTCGTTATCTGGAAAAACTC
                                                                                                                                                                                              AAATACTTCCAAA 1435
                                                                                                                                                                                                           AAATACCTCTAAA 1334
                                                                                                                                                                                                                                            CTTTCCTGACTTGAAAACCGCTGACTGTGTATTGTGTCAAAGCCAGAGCACTCATTGAAAA
                                                                                                                                                                                                                                                                                                         TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAGTTCTAGAGAAAAGAACCAATTTTAT
                                                                                                                                                                                                                                                                                                                                                        TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTAC
                                                                                                                                                                                                                                                                                                                                                                                            TTCAGAAGAGTCTGAAAACATGTCTGTGAATCAGCTCTACCCGCTAATTTATGAAGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                          TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTCGAGAGGTTTCCTCAAGGGGAATTTACTATGTCCGTGTACGAGCATCTAATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAGACAAATGGAAACAAATACCGAACTGTGAAAATGTCACAAGTACCCACTGTGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGA
                   L06320.1 GI:163187
L06320.1 GI:163187
alpha-interferon receptor.
alpha-interferon receptor.
Bos taurus lung cDNA to mRNA.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Ruminantia; Pecora; Bovoidea; Bovi
 1 (bases 1 to 3284)
Lim, J.K. and Langer,
                                                                                                                        Bos
                                                                                                                                   BOVIENRA
                                                                                                                       taurus alpha-interferon
and Langer, J.A.
                                                                                                                                   3284 bp
                                                                                                                                    mRNA
                                                                                                                       receptor
                                                                                                                      (IFNAR) mRNA,
                                                                                                                                   11-AUG-1993
                                                                                                                      complete
                                    Bovidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604
                                                                                                                                                                                                                                                                                                                                                                                             1242
                                                                                                                                                                                                                                                                                                                                                                                                                    1141
                                                                                                                                                                                                                                                                                                                                                                                                                                            1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      762
                                                                                                                       cds.
```

```
TITLE
JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                           Š
                   밁
                                     δÃ
                                                             밁
                                                                                Š
                                                                                                     밁
                                                                                                                      δÃ
                                                                                                                                              밁
                                                                                                                                                                δÃ
                                                                                                                                                                                      밁
                                                                                                                                                                                                                                먕
                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                     Š
Š
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1057; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                             allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
485
                    582
                                        428
                                                              522
                                                                                  368
                                                                                                       462
                                                                                                                         311
                                                                                                                                              402
                                                                                                                                                                   254
                                                                                                                                                                                        342
                                                                                                                                                                                                            194
                                                                                                                                                                                                                                 282
                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                         228
                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                       14 CGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGT
                                                            GTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCT---GAA
                                                                                                                                                                                                      AGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGT
                                                                                                                                                                                                                                                                        TTTAGAAGCTGAAGATAAGGCAATAATACTGAGTATCTCTCCCCCTGGAACAAAGATAG
                                TTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT---CCTGGAACAAAAGATAG
                                                                                                                 TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAA---CACTTCTTCATG
                                                                                                                                                                                        CAAGAATGTGACTTTTTCAGCAGATTATCAAATACTAGGAACGGATAACTGGAAGAAATT
                                                                                                                                                                                                                                 CGAGATCCACATCATTGATGACAATTTTTTCCTGAAGTGGAACAGCAGCAGTGAGTCTGT
TGTTTTTGAAAAATTGAATTGCGCATAAGAGCAGAAGAAGAACAACACTTCCACATG
                                                                                                                                              GTCTGGGTGTCAACATATTACTAGTACCAAATGCAACTTTTCTTCAGTCGAGCTTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning and characterization of a bovine alpha interferon receptor Biochim. Biophys. Acta 1173 (3), 314-319 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                        954
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="alpha-interferon 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="alpha-interferon receptor"
/protein_id="AAA02571.1"
/db_xref="GI:163188"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="IFNAR"
651 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASIITEIEETDEIDEVHKKYSSQTSQDSGNYSNEDENSGSKISEEFPQQDSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene-"IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84. .1866
                                                                                                                                                                                                                                                                                                                                                                      61.4%;
79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFNAR"
                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                           Score 824.2; DB 3;
Pred. No. 5.9e-178;
0; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                        793
                                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor"
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                   310
                                                                                   427
                                                                                                                                                 461
                                                                                                                                                                                        401
                                                                                                                                                                                                                                  341
                                                                                                                                                                                                                                                       193
                                                                                                                                                                                                                                                                          281
   544
                       641
                                          484
                                                               581
                                                                                                        521
                                                                                                                           367
                                                                                                                                                                                                                                                                                                                                                             ŝ
```

of Missouri, 1, USA

cycle and

```
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                              LOCUS
DEFINITION
ACCESSION
                                                                                                                                                     RESULT 1
OAU65978
                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                               용
                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                          밁
                                                                                                                                                                                                          1482
                                                                                                                                                                                                                                     1322
                                                                                                                                                                                                                                                              1422
                                                                                                                                                                                                                                                                                                                                                                                                                           1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  702
                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                               TGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGA
                                                                                                                                                                                                         AAATACTTCCAAA
                                                                                                                                                                                                                        AAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                    TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTCCAGTCTTTAACATTAGATCCCTTA---GTGATTCATTCCATATCTATATCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTTCCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                           TTCAGAAGAGTCTGAAAACATGTCTGTGAATCAGCTCTACCCGCTAATTTATGAAGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTCCAGTCATCAGCGTGAAATCCGTTACTGATGATTCACTGCATGTCAGTGTTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTACCTCTTTTTGGTCTGAAGAGAAGGAATTTAATACTGAAATGAAAACTATCATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGCTATAGTCCAGTGTATTGTATAAATACCACAGAGAGACATAAAGTACCTTCACCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCAAGTCTAGAAGAAGAACGGAAACTGTTTATCCCGAAGATAAAATTTATAAACTGTC
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
Caprinae; Ovis.
1 (bases 1 to 2914)
                                                                                                   U65978.1
                                                                                                               OAU65978 2914 bp
Ovis aries interferon
U65978
                                                                                                                                                                                                          1494
                                                                                                                            alpha/beta
                                                                                                                             mRNA,
                                                                                                                            complete
                                                                                                                                         12-NOV-1997
                                  Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       941
                                                                                                                                                                                                                                                                                       1321
                                                                                                                                                                                                                                                                                                                                                                                               1201
                                                                                                                                                                                                                                                                                                                                                                                                                           1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1001
                                                                                                                             cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
FEATURES
                       밁
                                           δÃ
                                                                 뮍
                                                                                            Š
                                                                                                                            밁
                                                                                                                                              Qy
                                                                                                                                                                              밁
                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.:
Best Local Similarity 79.:
Matches 1055; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                            169
                       523
                                                                          463
                                                                                                                             403
                                                                                                                                                       311
                                                                                                                                                                                   343
                                                                                                                                                                                                            254
                                                                                                                                                                                                                                     283
                                                                                                                                                                                                                                                               194
                                                                                                                                                                                                                                                                                         223
                                                                                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                               AGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGT
                                                                        TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAA----CACTTCTTCATG
                                                                                                                                                                                                                                                                                                                                            GAGG---TGGGTGCTGCCCGCCGCCTCAGGGGAAGCAAATCTGAAGT---CTGAAAATGT
                                                                                                                                                                                                                                                                                                                                                          GGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTAAAATCTCCAAAAAGT
                                                                                                                                                                                                                                     CAGGAATGTGACTTTTTCAGCAGATTATCAAATACTAGGGACGGATAACTGGAAAAAATT
                                                                                                                                                                                                                                                                                         TGAGATCCACATCATTGATGACAATTTCTTCCTGAAGTGGAACAGCAGCAGTGAGTCTGT
                       TTTAGAAGCTGAAGATAAGGCGATAATACTGAGCATCTCTCCCCCTGGAACAGAAGATAG
                                               TTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT----CCTGGAACAAAAGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Han,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AUG-1996) Animal Sciences, University of Mi:
158 ASRC, East Campus Drive, Columbia, MO 65211-0001, USA
On Nov 12, 1997 this sequence version replaced gi:1553001
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pregnancy
Endocrinology 138 (11), 4757-4767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Han, C.S., Mathialagan, N., Klemann, S.W. and Roberts, R.M. Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 2914)
n,C.S., Mathialagan,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLSLLGATTLMLVAGRWVLPAASGEANLKSENVEIHIIDDNFFL KWNSSSESYRNVTFSADYOLLGTDNWKKLPGCOHITSSKCNFSSVELKDVFEKIELLR RAEEGINNTSTWYEVEFPYPFLKAOLGPDVHLEAEDKAILSTSPECTESIMMALDR SSFRYSVVIWKNSSSLEERTETVYPEDKIYKLSPEITYCLKVKAELRLOSRVGCYSPV YCINTTERHKYPSPENVOINUDNOAYVLKWDYPYESTTFOAGHLAFLKKIPGKHSNK WKOIPNCENVTTHCVFFRDIFSMGIYYVRVRASGNGNGTSFWSEEKEFNTEVKPIIFFPVISMKSITDDSLHVSVGASESSENNSVNQLYPLVYEVIFWENTSNAEKVLEKRTDFTFPNLKPLTVYCVKARALIENDRWNKGSYSDTVCEKTKPGNTSNAEKVLEKRTDFTFPNLKPLTVYCVKARALIENDRWNKGSYSDTVCEKTKPGNTSEEQTERCFIIEN ILVVIYVVRVFLRCVKYYFFPSSKPPSSVDQYFSDDENSGKISEEFLOODSV" ASIITELEETNEVDEVHEENSNSONSGNYSNEDENSGSKISEEFLOODSV" ASIITELEETNEVDEVHEENSNSONSGNYSNEDENSGSKISEEFLOODSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="interferon alpha/beta receptor-1"
/protein_id="AAB84231.1"
/db_xref="GI:2612835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Ovis aries"
/db_xref-"taxon:9940"
/tissue_type-"endometrial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 821; DB 3; 1
Pred. No. 3.2e-177;
0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klemann,S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roberts, R.M
```

484

522

582

427

462

402

310 342 253

193

222

282

168 73

```
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                        RESULT 14
OAOIFNARE
LOCUS
                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                      Ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                     밁
                                                                                                                                                                                        õ
                                               SOURCE
                                    ORGANISM
                                                                                                                                                                                                                                                                                                                    1243
                                                                                                                                                                                                                                                                                                                                                                   1183
                                                                                                                                                                                                                                                                                                                                                                                          1082
                                                                                                                                                                     1423
                                                                                                                                                                                                                                                                                            1202
                                                                                                                                                                                                                                                                                                                                                                                                                                            1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - ANGCACAACTTTTCAAGCTCAGTGGCTCCGTGCCTTTTTAAAAAAGATTCCTGGGAAACA
                                                                                                                                                                                                                                                                 CTTTCCTAACTTGAAACCGCTGACTGTGTATTGTGTCAAAGCCAGAGCACTCATTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                 AAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCA
                                                                                                                                                                                                                  AGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACCACCATGGA
                                                                                                                                                                                                                                                                                                                                                                                TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAGAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACCACTACGTCATGGAAAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCAGGTGTAGAAGGAATGGAAAATATTTATTCCAGACATAAAATTTATAAACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACCTTATCTGGAAAAACTC
                                                                                                                                                                     AAACACTTCCAAA 1435
                                                                                                                                                                                   AAATACCTCTAAA 1334
                                                                                                                                                                                                                                          TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAATTATCGAGAAAAAAACTGATGTTAC
                                                                                                                                                                                                                                                                                                                                                                  TTCAGAAGAGTCTGAAAATATGTCTGTGAATCAGCTCTACCCACTAGTTTATGAAGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTACCTCTTTTTGGTCTGAAGAGAAGGAATTTAATACGGAAGTGAAACCTATCATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTCGAGATATTTTCTCAATGGGAATTTACTATGTCCGTGTACGAGCATCTAATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATGTACAAATCAATGTTGACAACCAGGCCTATGTTCTTAAGTGGGATTACCCATATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGCTATAGTCCAGTGTATTGCATAAATACCACAGAGAGACATAAAGTGCCTTCACCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAGAGATTACTTATTGTTTGAAAGTTAAAGCAGAACTGCGTTTACAAAGTAGAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAAGTCTAGAAGAACTGAAACTGTTTATCCCGAAGATAAAATTTATAAACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCATGTGGGCTTTGGATCGTTCAAGCTTTAGGTATAGCGTCGTTATCTGGAAAAACTC
Ovis aries
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae
Ovis
                                             X95939.1 GI:1213626 IFNAR gene; interferon sheep.
                                                                                 O.aries mRNA
X95939
                                                                                                         OAOIFNARE
                                                                                         2559 bp r
                                                          receptor
                                                                                             mRNA
interferon
                                                                                                         17-JAN-1997
                                                                                                                                                                                                                   1422
                                                                                                                                                                                                                                                                    1362
                                                                                                                                                                                                                                                                                                                                          1201
                                                                                                                                                                                                                                                                                                                                                                                         1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1062
                                                                                                                                                                                                                                                                                         1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        964
                                                                                                                                                                                                                                           1321
                                                                                                                                                                                                                                                                                                                   1302
                                                                                                                                                                                                                                                                                                                                                                                                                   1182
                                                                                                                                                                                                                                                                                                                                                                                                                                          1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      604
                                                                                                                                                                                                                                                                                                                                                                   1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642
```

```
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                               BASE CO
                                                                                                                  Š
                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
Ş
                   밁
                                   δÃ
                                                         밁
                                                                             Ş
                                                                                                밁
                                                                                                                                                          Ş
                                                                                                                                                                              밁
                                                                                                                                                                                                Ş
                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                            Query Match
Best Local Sim
Matches 1054;
                                                                                                                                                                                                                                                                                                                         polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                   349
                                      311
                                                           289
                                                                             254
                                                                                                 229
                                                                                                                    194
                                                                                                                                        169
                                                                                                                                                           134
                                                                                                                                                                               115
                                                                                                                                                                                                  74
                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                 14 CGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGT 73
                                                         GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACA
                            TGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGGAAAA ---CACTTCTTCATG
                                                                                                 CAGGAATGTGACTTTTTCAGCAGATTATCAAATACTAGGGACGGATAACTGGAAAAAAATT 288
                                                                                                           CGGCGGCCCGCGGACGATGCTCTCCCTCCTTGGCGCGACGACCCTGATGCTGGTCGCTGG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Mol. E
97135690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 2559)
Kaluz,S., Fisher,P.A.,
Structure of an ovine:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-FEB-1996) S. Kaluz, University of Nottingham, Deptartment of Physiology and Environmental Sciences (PES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaluz, S.
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 2559)
                                                                                                                                                                                                                                                                                                                          778
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonington, Loughborough, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrinol.
                                                                                                                                                                                                                                                                                                                         /gene="IFNAR"
2519. .2524
a 501 c 5
                                                                                                                                                                                                                                                                                                                                                                                  /gene-"IFN
143. .1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"type I interferon receptor"
/protein_id="cAA65183.1"
/db_xref="EGI:121367"
/db_xref="SWISS-PROT:Q28589"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="IFNAR"
71. .1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="IFNAR"
                                                                                                                                                                                                                                                                      61.0%;
                                                                                                                                                                                                                                                                                                                                                                 IFNAR"
                                                                                                                                                                                                                                                              Score 819.4; DB 3;
Pred. No. 7.3e-177;
0; Mismatches 261;
                                                                                                                                                                                                                                                                                                                          572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon receptor and its
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LE12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5RD, UK
                                                                                                                                                                                                                                                                                 Length 2559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciences (PES-A),

    and Flint,
expression

                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                              Gaps
                                       367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n.P
                                                                                                                                                                                                                                                               6.
```

```
RESULT 1
                                                                       밁
                                                                                     δÃ
                                                                                                              밁
                                                                                                                              Ş
                                                                                                                                                      밁
                                                                                                                                                                         S
                                                                                                                                                                                              밁
                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      吊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
           DEFINITION
                     Focus
                                                                       1369
                                                                                                                                                                                                                                                                                1069
                                                                                                                                                                                                                                                                                                    1025
                                                                                                                                                                                                                                                                                                                        1009
                                                                                                                                                                                                                                                                                                                                            965
                                                                                                                                                                                                                                                                                                                                                                949
                                                                                                                                                                                                                                                                                                                                                                                     905
                                                                                                                                                                                                                                                                                                                                                                                                        688
                                                                                                                                                                                                                                                                                                                                                                                                                            845
                                                                                                                                                                                                                                                                                                                                                                                                                                                 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428
                                                                                                                         TGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAAACCAGG
                                                                                                                                                                AGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGGCACACACCATGGA
                                                                                                                                                                                                          TITTIGGGAAAACACTICAAAIGCIGAGAGAAAAATITATCGAGAAAAAAACTGATGTTAC
                                                                                                                                                                                                                                                 TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                     AAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACCTACTTACGTCATGGAAAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACACTTCCAAA 1381
                                                                                          AAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                         TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTTGATACCTGAAATACAAGCTTTCCTACT 1024
                                                                                                                                                                                                                                                                                                                                                              TCCTCGAGATATTTTCTCAATGGGAATTTACTATGTCCGTGTACGAGCATCTAATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTAGAAGCTGAAGATAAGGCGATAATACTGAGCATCTCTCCCCCTGGAACAGAAGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTTCCTAACTTGAAACCGCTGACTGTGTATTGTGTCAAAGCCAGAGCACTCATTGAAAA
                                                                                                                                                                                                                                     TTCAGAAGAGTCTGAAAATATGTCTGTGAATCAGCTCTACCCACTAGTTTATGAAGTAAT
                                                                                                                                                                                                                                                                              TCCTCCAGTCATCAGCATGAAATCCATTACTGATGATTCACTGCATGTCAGTGTCAGTGC
                                                                                                                                                                                                                                                                                                                      TGGTACCTCTTTTGGTCTGAAGAGAAGGAATTTAATACGGAAGTGAAACCTATCATATT
                                                                                                                                                                                                                                                                                                                                                                                  TCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCACAACTTTTCAAGCTCAGTGGCTCCGTGCCTTTTTAAAAAAAGATTCCTGGGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANATGTACANATCANTGTTGACAACCAGGCCTATGTTCTTAAGTGGGATTACCCATATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGCTATAGTCCAGTGTATTGCATAAATACCACAGAGAGACATAAAGTGCCTTCACCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCAGAGATTACTTATTGTTTGAAAGTTAAAGCAGAACTGCGTTTACAAAGTAGAGTTGG
                                                                                                                                                                                              TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAGTTCTAGAGAAAAGAACCGATTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT - - - CCTGGAACAAAAGATAG
MUSIFNAR
Mus musculus
cds.
         3894 bp
interferon
          alpha/beta
          receptor (IFNAR) mRNA, complete
                    ROD
                    27-APR-1993
                                                                                                                                                                           1261
                                                                                                                                                                                                                  1201
                                                                                                                                                                                                                                                         1141
                                                                                                                                                                                                                                                                                                  1081
                                                                                                                                                                                                                                                                                                                      1068
                                                                                                                                                      1308
                                                                                                                                                                                                                                      1188
                                                                                                                                                                                                                                                                              1128
                                                                                                                                                                                                                                                                                                                                                               1008
                                                                                                                                                                                                                                                                                                                                                                                  964
                                                                                                                                                                                                                                                                                                                                                                                                                           904
                                                                                                                                                                                                                                                                                                                                                                                                                                               888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484
                                                                                                                                                                                              1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544
                                                                                                                                                                                                                                                                                                                                                                                                       948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
        Ş
                            밁
                                               Ş
                                                                    B
                                                                                       ğ
                                                                                                            В
                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                      유
                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                             Matches
                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sdo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                           polyA_site
                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                              267
                                                                     207
                                                                                                             147
                                                                                                                                 82
                                                                                                                                                      87
                                                                                                                                                                                             864;
                                                                                                                                                                                                                                                         1005
```

```
262 GTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAG
                                                                                                                                                                                                                                                                                                                                                               22 CCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGTCGCCGTGGGCCCAT
                                                                                        TGACTTTTTCATTCGATTATCAAAAAACTGGGATGGATAAATTGGATAAAATTGTCTGGGT
                                                                                                                                                                              ACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATG
                                                                                                                                                                                                                                                                           GGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCCTCAAAAAAGTAGAGGTCG 141
                                                                   TGACCTTTTCAGCAGAATATCGAACAAAAGACGAGGCGAAGTGGTTAAAAGTGCCTGAAT
                                                                                                                                                                                                                                               GGGTGCTACCCTCAGCTGCAGGTGGAGAAAATCTGAAACCTCCTGAGAATATAGACGTCT
                                                                                                                                                                                                                                                                                                                                        ACATTATAGATGACAACTACACCCTAAAGTGGAGCCACCGAGAGTCAATGGGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 3894)
Uze,G., Lutfalla,G., Bandu,M.-T.T., Proudhon,D. and Mov
Uze,G., Lutfalla,G., Bandu,M.-T.T., Proudhon,D. and Mov
Behavior of a cloned murine interferon alpha/Deta recei
expressed in homospecific or heterospecific background
proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M89641
M89641.1 GI:194111
B2 repeat; interferon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="B2" 3894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene-":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTVYCVQARVLFRALLNKTSNFSEKLCEKTRPGSFSTIWIITGLGVVFFSVMVLYALR
SVWKYLCHVCFPPLKPPRSIDEFFSEPPSKNLVLLTAEEHTERCFIIENTDTVAVEVK
HAPEEDLRKYSSQTSQDSGNYSNEEEESVGTESGQAVLSKAPCGGPCSVPSPPGTLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Translation="MLAVGAAALVLVAGAPWVLPSAAGGENLKPPENIDVYIIDDNY
/TLKWSSHGESMGSVTFSAEYERKDEAKWLKVPECQHTTTTKCEFSLLDTNVYIKTQFR
VRAEEGNSTSSWNEVDPFIPFYTAHMSPEVRLEAEDKAILVISPPGQDGNMWALEK
PSFSYTIRIWQKSSSDKKTINSTYVEKIPELLPETTYCLEVKAIHPSLKKHSNYSTV
QCISTTVANKMPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPGYSKSSGSHSD
KMKPIPTCANVQTTHCVFSQDTVYTGTFFLHVQASEGNHTSFWSEKFIDSQKHILPP
PPVITVTAMSDTLLVVVNCQDSTCDGLNYEIIFWENTSNTKISMEKOGPEFTLKNLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="
95. .17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map-"
95. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="IFNAR"
973 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCFLGNEKYLQSPALRTEPALLC"
173. .1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="IFNAR"
95. .1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="interferon alpha/beta receptor"
/protein_id="AAA37890.1"
/db_xref="GI:194112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="L1210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 540.2; 1
Pred. No. 3.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                942
                                                                                                                                                                                                                                                                                                                                                                                                                            2; DB 12;
3.5e-113;
hes 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interferon-alpha/beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Mogensen, K.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Māmmalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                         321
                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                     326
                                                                                                                                                         266
                                                                                                                                                                                                   201
                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                                                4
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                              Ş
                                                                                                                                                                                  Š
                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                         Ş
                                                   밁
                                                                           Š
                                                                                                       멼
                                                                                                                                                           밁
                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
 밁
                                                                                                        1206
                                                                                                                                                         1096 GAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACA 1155
                                                                                                                                                                                                                                        1036
                                                                                                                                 1156
                                                                                                                                                                                                               1107
                                                                                                                                                                                                                                                                  1047
1323 AGACCAGCAACTTCAGTGAAAAAGCTGTGTGAGAAAACACGTCCAGGAAGTTTTTCCA 1379
                                                                  1216 AACCACTGACTGTATATTGTGTGAAAAGCCAGAGCACCACCATGGATGAAAAGCTGAATA 1275
                                                                                                                                                                                                                                                                                             976
                                                                                                                                                                                                                                                                                                                      987
                                                                                                                                                                                                                                                                                                                                                                           927
                                                                                                                                                                                                                                                                                                                                                                                                   856
                                                                                                                                                                                                                                                                                                                                                                                                                             867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507 AAGATAAAGCCATACTAGTCCACATCTCCTCCCGGACAAGACGGGAACATGTGGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387
                                                                                                                                                                                                                                                                                                                                                916
                                                                                                                                                                                                                                                                                                                                                                                                                                                       796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                       GGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACG 915
                                                                                                                                                                                                                                                                                                                                                                                                                         TTAACATTAGATCCCTTAGTGATTCCATTCCATATCTATATCGGTGCTCCAAAACAGTCTG 1095
                                                                                                                                                                                                                                                                                                                   CTGTCTACACAGGAACGTTCTTCTCCATGTACAAGCCTCAGAGGGAAATCACACATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTA---TACATATGCAAACATGACCT 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAGAAACCTTCCTTCAGTTACACCATACGAATCTGGCAGAAGTCTTCCAGTGACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCGTTTATTCCATTCTACACAGCTCACATGAGCCCCCCAGAAGTACGTTTAGAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTG
                         AAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATACCTCTA 1332
                                                                                                    CTTCCAATACTAAGATAAGCATGGAGAAGGATGGCCCAGAGTTCACCCTCAAGAACCTGC 1265
                                                                                                                                                                                                  TTACTGTCACCGCCATGAGTGACACCTTGCTTTATGTC------
                                                                                                                                                                                                                                                                                          TTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCT 1035
                                                                                                                                                                                                                                                                                                                                    TTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGTTTAGAAGTTAAAGCAATACATCCGTCACTTAAGAAACACAGCAATTACAGCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATGGTTTAAGCTTTACATATÆGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGATAAGGCAATAGTGATACACATCTCCTCGGAACAAAAGATAGTGTTATGTGGGCTT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCAACATACTACAACGACCAAGTGTGAATTCTCTTTACTGGACACAAATGTGTATATCA
                                                                                                                                CTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGA 1215
                                                                                                                                                                                                                                                                 ATGCCCAAGGCAAGAGCTATGTCCTGAAATGGGACTACATTGCGTCTGCAGACGTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAGTGTATAAGCACCACAGTGGCAAATAAAATGCCTGTGCCAGGAAATCTCCAAGTGG
                                                   AGCCGCTGACTGTGTGTGTCCAGGCCAGAGTGCTCTTCAGG---GCCCTGCTGAATA 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626
                                                                                                                                                                                                              1148
                                                                                                                                                                                                                                                                                                                                               975
                                                                                                                                                                                                                                                                                                                                                                                                                             926
                                                                                                                                                                                                                                                                                                                                                                                                                                                     855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386
                                                                                                                                                                                                                                                                                                                      1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446
```

Job time: 17841 sec

```
Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match
Listing first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                           and is derived
Score
                                                                                                                                                                                                                                                                                                                           1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length:
seq length:
                                                                                                                                                                                                                                                                                                                                                                                                   No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed.
                                                                                                                                                                                                                                                                                                                                                                                             derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                           Query
Match
                             N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-1
1343
1 CTGCAGGGATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311585 segs, 125096042 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCAGGGATCTGCGGCGGC.....ATACCTCTAAATGAGGTACC 1343
                                                                                                                                                                                                                                                                                                                                                                                           by analysis of the total
 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000, 05:54:19; Search time 64.86 Seconds (without alignments) 5180.511 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
                 Q28302
Q66798
Q14508
X30838
X52139
Q94449
Q94449
T49507
V21443
X20273
V01871
                                                                                                                          Q86458
Q11701
T73519
T73521
T73521
Q11377
Q11377
Q11377
Q138654
N91495
Q27945
X13068
X13068
X13068
X20277
                                                                                                                                                                                                                                                               Q86457
Q14240
Q30533
Q49624
                                                                                                                                                                                                                                                                                                      Q14239
Q30532
Q49625
                                                                                                                                                                                                                                                                                                                                                                                                                                                    summaries
                   02
                                                                                                                                     09
                                                                                                                                                                                                                                                                                                                                                                                            score distribution
                                                                 AmEPV entomopoxvir
Streptococcus pneu
Streptococcus pneu
Bacterial transfer
                                                                                                                                                                                   Interferon alphar Genes encoding T. Antiscarab pest to btpGS1208 gene. Ne Bt isolate 43F cod
                  Human brain s
Continuation
                                                                                                                 Borrelia burgdorfe
Amepy tk DNA. New
                                                                                                                                  Staphylococcus aur
Continuation (10 o
                                                                                                                                                      Bacillus thuringie
Sequence of CryIII
Enterococcus faeca
                                                                                                                                                                                                                                   Human IFN receptor
Human alpha-interf
Transmembranal int
                                                                                                                                                                                                                                                                                            Human interferon r IFN-R extracellula
                            Borrelia burgdorfe
Human brain specif
                                               H. influenzae stra
                                                         Transferrin recept
                                                                                                        Amepy thymidine-ki
                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                          Sequence encoding
                                                                                                                                                                                                                                                                                    Encodes complete
                                                                                                                                                                                                                                                                                                               Sequence encoding
                                                                                                                                                                                                                                                                                                                       Encodes soluble
                                                                                                                                                                                                                                                                                                                                            Description
         of btI260
                                                                                                                                                                                                                                                                 interferon
                   3
                                                                                                                                                                                                                                            Õ
                                     В
                                                      80
                                                                            멍
                                                                                             Ş
                                                                                                                 밁
                                                                                                                                δÃ
                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဂ ဂ
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 1343; Conserv
                                                                                                                                                                                                                                                                                                                                                   09-AUG-1991.

05-FEB-1990; 001298.

05-FEB-1990; FR-001298.

(EUBI-) LAB EURO BIOTECHNO.

Eld P. Gresser I. Lutfalla G

Tovey MG, UZe G;

WPI; 91-319778/44.

P-PSDB; R14487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q14239 standard; DNA; 1343 BP.
Q14239;
16-JAN-1992 (first entry)
Encodes soluble interferon-alpha/beta receptor.
IFN; autoimmune disease; graft rejection; histocompatibility; ss.
Homo sapiens.
Location/Qualifiers
Key
Cds 27, 1337
                                                                                                                                                                                                                                                                      New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus; Behoet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 10; Page 45; 52pp; French.

The protein encoded by this sequence corresponds to the soluble, extracellular portion of the interferon-alpha and/or beta receptor. The transmembrane and cytoplasmic domains of the native receptor. The transmembrane and cytoplasmic domains of the native receptor. The transmembrane and cytoplasmic domains of the native receptor. The transmembrane and cytoplasmic domains of the native receptor.
                                                                                                                                                                                                                                           receptor. Potentially immunogenic epitopes have thus been eliminated See also Q14240. Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;
                                      181
                                                        181
                                                                             121
                                                                                               121
                                                                                                                  61
                                                                                                                                     61
                                                                                                                                                                          \vdash
                                                                                                                                                                  CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGCCTAG
                                    CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                                                                                           TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                             CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                                                                                                                        CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                  TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= soluble receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3543
3543
3940
4571
4934
5391
5407
11466
28994
11271
                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                 ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q14669
Q81178
Q81178
N93054
N93059
N81490
V71729
V71738
V48228
V15826
Q46869
N91695
                                                                                                                                                                                               0
                                                                                                                                                                                                      Score 1343;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                Meyer F, Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                  멂
                                                                                                                                                                                                                 ۲,
                                                                                                                                                                                               0
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                Length 1343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.t. toxin PS7IM3
Delta-endotoxin cr
Delta-endotoxin cr
Insecticidal (Dipt
Upstream sequence
Upstream sequence
Interleukin 18 con
Genomic DNA for in
Growth factor gene
Sequence of fowlpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B.t. toxin PS71M3
                                                                                                                                                                                               0
                                                                                                                                                                                              Gaps
```

Minimum DB Maximum DB

Sequence:

OM nucleic -

8

Database

õ

0 000 000

180 180

240

300

60 60

0

```
Ş
                                                                                                                                                                                                                                                                                                                      ğ
                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                          ρy
                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                               οy
           Š
                       유양
                                                  밁
                                                             δ
                                                                          용
                                                                                       ð
                                                                                                        밁
                                                                                                                 Š
                                                                                                                                밁
                                                                                                                                          Š
                                                                                                                                                           밁
                                                                                                                                                                     δ
                                                                                                                                                                                     B
                                                                                                                                                                                               δ
                                                                                                                                                                                                               В
                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                   8 8
                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
밁
                                                                                                                     1081
                                                                                                                                  1021
                                                                                                                                                            961
                                                                                                                                                                                                                841
                                                                                                                                                                                                                             841
                                                                                                                                                                                                                                                                                                                       601
                                                                                                                                                                                                                                                                                                                                    601
                                                                                                                                                                                                                                                                                                                                                 541
                                                                                                                                                                                                                                                                                                                                                              541
                                                                                                                                                                                                                                                                                                                                                                           481
                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                   901
                                                                                                                                                                                                                                          781
                                                                                                                                                                                                                                                      781
                                                                                                                                                                                                                                                                   721
                                                                                                                                                                                                                                                                                721
                                                                                                                                                                                                                                                                                              661
                                                                                                                                                                                                                                                                                                          661
                                                                                                                                                                                                                                                                                                                                                                                        481
                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                  CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                                                                                                                                                                                        CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAATACCTCTAAATGAGGTACC
                                 ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                             CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                 GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                   GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                     TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                       ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                  CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                            ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                        ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                          ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG
1343
             1343
                                       1320
                                                                              1200
                                                                                           1200
                                                                                                                     1140
                                                                                                                                              1080
                                                                                                                                                                        1020
                           1320
                                                                 1260
                                                                                                                                  1080
                                                                                                                                                            1020
                                                                                                                                                                                      960
                                                                                                                                                                                                                900
                                                                                                                                                                                                                                         840
                                                                                                                                                                                                                                                      840
                                                                                                                                                                                                                                                                                780
                                                                                                                                                                                                                                                                                                          720
                                                                                                                                                                                                                                                                                                                       660
                                                                                                                                                                                                                                                                                                                                    660
                                                                                                                                                                                                                                                                                                                                                 600
                                                                                                                                                                                                                                                                                                                                                              909
                                                                                                                                                                                                                                                                                                                                                                           540
                                                                                                                                                                                                                                                                                                                                                                                                    480
                                                                                                                                                                                                                                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                                                                                                                                                                                               420
                                                                                                                                                                                                                                                                                                                                                                                                                                            42C
                                                                                                                                                                                                                                                                   780
                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
```

```
RESULT
Q30532 standa
AC Q30532;
DD Q30532;
AC MINTERFERYON TE
Synthetic.
FH Key
FT cds
FT APR-1991;
PA 17-APR-1991;
PA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                            Qγ
                                                                                                                                                                         밁
                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                            吊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mater soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune of diseases and transplant rejection

In diseases and transplant rejection

Claim 10; Fig 1; 58pp; English.

DAR encoding the water-soluble polypeptide with a high affinity for DIR encoding the water-soluble polypeptide with a high affinity for coligonization of the inverse and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFW-alpha and -beta receptor (Q3053), was incubated with oligos colors, and polosis. R28496 represents the complete receptor. R28495 clacks the transmembrane and cytoplasmic domains. Both forms bind lacks the transmembrane and cytoplasmic domains. Both forms bind if in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.

Sequence 1343 BP; 449 A; 254 C; 264 G; 376 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sin
Matches 1343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1993 (first entry)
Sequence encoding a soluble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P. Gresser I, Lutfalla G, Meyer
Tovey N, Uze G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; R28495
                             421
                                                                            361
                                                                                                                            361
                                                                                                                                                                               301
                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                          CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                            CTGCAGGGATCTGCGGCGGCGCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92-382110/46.
AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAG
                                                                                                                                                                                                                                                                                                           ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                    ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; score 1343; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
27. .1337
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                             480
                                                                               420
                                                                                                                            420
                                                                                                                                                                                 360
                                                                                                                                                                                                                                 360
                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

Ş 뮍 Š

5 B

δõ 밁 B 8

Ş

융 ő 밁

B

```
Q49625 standard; DNA; 1343 BP.
Q49625;
Q49625;
Q20-APR-1994 (first entry)
Phyman interferon receptor extracellular domain coding sequence.
Human interferon domain; monoclonal antibody; viral infection;
IFN-R; extracellular domain; monoclonal antibody; viral infection;
cell proliferation; allograft rejection; systemic lupus erythematosus;
psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;
immunodeficiency; measles virus; interferon-alpha-beta; ss.
                                                                                                        1321
                                                                                                                                                                                         1201
                                                                                                                                                                                                                         1141
                                                                                                                                                                                                                                           1081
                                                                                                                                                                                                                                                                            1021
                                                                                                                                                                                                                                                                                           1021
                                                                                                                                                                                                                                                                                                           961
                                                                                                                                                                                                                                                                                                                                                                                             841
                                                                                                                                                                                                                                                                                                                                                                                                                             781
                                                                                                                                                                                                                                                                                                                                                                                                                                               721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                            961
                                                                                                                                                                                                                                                                                                                                             901
                                                                                                                                                                                                                                                                                                                                                             901
                                                                                                                                                                                                                                                                                                                                                                              841
                                                                                                                                                                                                                                                                                                                                                                                                              781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721
                                                                                                       CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAAAGCTGAATAAAAGCAGTGTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                                                                                       CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                                                                                                                                                        CTCCAAAACAGTCTĠGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                          TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                             ACCATITGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                              ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                       1260
                                                                                                                                                                                                                         1200
                                                                                                                                                                                                                                          1140
                                                                                                                                                                                                                                                          1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540
                                                                                                                                                                                                                                                                           1080
                                                                                                                                                                                                                                                                                                            1020
                                                                                                                                                                                                                                                                                                                            1020
                                                                                                                                                                                                                                                                                                                                                                                                              840
                                                                                                                                                                                                                                                                                                                                                                                                                               840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480
                                                                                                                                                                                                                                                                                                                                                              960
                                                                                                                                                                                                                                                                                                                                                                                              900
                                                                                                                                                                                                                                                                                                                                                                                                                                                780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600
                                                                                                                                                                                                                                                                                                                                             960
                                                                                                                                                                                                                                                                                                                                                                              900
                                                                                                                                                                                                                                                                                                                                                                                                                       å å
                                당
                                                 δÃ
                                                                      D O
                                                                                                밁
                                                                                                                   Ş
                                                                                                                                  밁
                                                                                                                                                  Qy
                                                                                                                                                                       g g
                                                                                                                                                                                                   당 성
                                                                                                                                                                                                                                      B 6
                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                           B 8
                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                       Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                   PP 16-563487-A.

PP 10-6-CCT-1993.

PF 31-MAR-1992; EP-400902.

PR -PSDB; R42635 (part).

PR -PSDB; R42635 (part).

PR -PSDB; R42635 (part).

PR -PSDB; R42635 (part).

PT Concolonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis

PT Therapy and diagnosis

PS Disclosure; Fig 2; 21pp; English.

CC Interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. (See 049624 for sequence coding for full-length IFN-R). The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1343; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
cds
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                              infection.
      601
                                                                      481
                                                                                      481
                                                                                                                       421
                                                                                                                                        361
                                                                                                                                                        361
                                                                                                                                                                        301
                                                                                                                                                                                         301
                                                                                                                                                                                                         241
                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                           121
                                                                                                       421
                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                             <u>بــ</u>
     CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                       CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       1343
                                                                                                                                                                                                                                                                                                                                                                                                                       ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "encodes extra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
27. .1337
                                                                                                                                                                                                                                                                                                                                                                                                                       449
                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                             Score 1343;
Pred. No. 0;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       254
                                                                                                                                                                                                                                                                                                                                                                                                                       Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular
                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                       264
                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                       င့
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ဝှု
                                                                                                                                                                                                                                                                                                                                                                                                                       н
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                             Gaps
```

120

60 60

0

Š 밁 Ş g Ş

660 660

600

540 540 480 480 420 360 360 300 300 240 240 180

유

밁 ΩÝ В Š g Q В δÃ 밁

```
RESULTATION OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    å Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
WO9507716-A.

23 MAR-1995.

23 MAR-1995.

3 17-SEP-1993; EP-402279.

(EUBI-) LAB EURO BIOTECHNOLOGIE SA.

BENIZII EJ. Tovey MG;

WPI; 95-131187/17.

7 P-PSDB; R71723.

Compsn. of monoclonal antibodies against interferon recuseful as immuno:modulator, eg. for treating AIDS

Disclosure; Fig.2A-2B; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Q86457 standard; DNA; 1343 BP. Q86457; Q86457; Q66457; Q6657; Q6657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321
                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
27. .1337
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1343
                                                                                                                                                                                                                                                                                                                                                                                                         interferon-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           780
                                                                              밁
                                                                                                                     Š
                                                                                                                                                                           밁
                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÔ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
```

```
გვვვ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.6%;
Best Local Similarity 99.8%;
Matches 1340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding the extracellular domain of receptor is given in Q86457. Monoclonal against the recombinant soluble form of texpressed in either E. coli or COS cell? Seguence 1343 BP; 449 A; 257 C;
        901
                         841
                                          841
                                                           781
                                                                           781
                                                                                           721
                                                                                                            721
                                                                                                                              661
                                                                                                                                              661
                                                                                                                                                               601
                                                                                                                                                                               601
                                                                                                                                                                                                541
                                                                                                                                                                                                                 541
                                                                                                                                                                                                                                  481
                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                          CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                            TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                             ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                   CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                       CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                         ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1338.2; pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the human IFN class I al antibodies were raise if the encoded protein (Fil hosts: 261 G; 376 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s I
ised
(R71723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                          840
                                                                                                                                                                              660
                                                                                                                                                                                                600
                                                                                                                                                                                                                 600
                                                                                                                                                                                                                                 540
                                                                                                                                                                                                                                                 540
                                                                                                                                                                                                                                                                                   480
                                                                                            780
                                                                                                            780
                                                                                                                              720
                                                                                                                                             720
                                                                                                                                                              660
                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                   420
                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                        240
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
           Ş
                              g
                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   β Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                  Query Match 99.3%; S
Best Local Similarity 100.0%;
Matches 1334; Conservative 0;
                                                                                                                                                                                                               FR2657881-A.
09-AUG-1991.
05-FEB-1990; 001298.
05-FEB-1990; FR-001298.
05-FEB-1990; FR-001298.
(EUBI-) LAB EURO BIOTECHNO.
E1d P, Gresser I, Lutfalla G
TOVEY MG, UZE G;
WPI: 91-319778/44.
P-PSDB; R14488.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1321
                                                                                                                 New water-soluble polypeptide(s) with affinity for IFN-alpha and beta used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52p; French.

The protein encoded by this sequence corresponds to the complete interferon-alpha and/or beta receptor. The invention covers derivatives of the receptor obtained by deleting the transmembrar and cytoplasmic domains of the native receptor or by substitution see also 014239.

Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T;
                                                                                                                                                                                                                                                                                                                                  Encodes complete IFN; autoimmune of Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                               Q14240;
16-JAN-1992 (first
                                                                                                                                                                                                                                                                                                                                                                                  Q14240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901
            61
                            CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATACCTCTAAATGAGGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAACTGATGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
27. .1700
/*tag= a
                                                                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                       interferon-alpha/beta receptor.
lisease; graft rejection; histocompatibility;
                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                  1755
                                                                                                                                                                                                                                         ဂ
                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                  Score 1334; D; Pred. No. 0; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1343
                                                                                                                                                                                                                                            Meyer
                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                            Mogensen
                                                                                      DB
                                                                  0;
                                                                                                                                     transmembrane substitution.
                                                                   0
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1080
                              60
                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960
                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
   유
양
                                      밁
                                                     δ
                                                                           밁
                                                                                             οy
                                                                                                                  밁
                                                                                                                                  οy
                                                                                                                                                      밁
                                                                                                                                                                      δ
                                                                                                                                                                                            밁
                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                δõ
                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                              밁
                                       1081
                                                        1081
                                                                            1021
                                                                                               1021
                                                                                                                                     961
                                                                                                                   961
                                                                                                                                                                          901
                                                                                                                                                                                                                                   781
                                                                                                                                                                                                                                                                         721
                                                                                                                                                                                                                                                                                                               661
                                                                                                                                                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                                                                                                                     601
                                                                                                                                                                                                                                                                                                                                                                       601
                                                                                                                                                                                                                                                                                                                                                                                         541
                                                                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                     781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAACTGATGTTA 1200
                                                                           CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                               CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                             GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTTGATACTGAAATACAAGCTTTTCC
                                                                                                                                                     TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                            ACCATITGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                  ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                        AGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCCTCGCTGGAACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                        TIGGIGICIATAGICCAGIACATIGIATAAAGACCACAGIIGAAAAIGAACTACCICCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                       CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                               TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACTT
                                                                            1080
                                                                                               1080
                                                                                                                  1020
                                                                                                                                                       960
                                                                                                                                                                                             900
                                                                                                                                                                                                                900
                                                                                                                                                                                                                                   840
                                                                                                                                                                                                                                                     840
                                                                                                                                                                                                                                                                          780
                                                                                                                                                                                                                                                                                           780
                                                                                                                                                                                                                                                                                                                                 720
                                                                                                                                                                                                                                                                                                                                                     660
                                                                                                                                                                                                                                                                                                                                                                       660
                                                                                                                                                                                                                                                                                                                                                                                          600
                                                                                                                                                                                                                                                                                                                                                                                                            600
                                                                                                                                                                                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
```

300

```
RESULT OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
õ
                     밁
                                      Š
                                                                 밁
                                                                                   Š
                                                                                                               밁
                                                                                                                               Ş
                                                                                                                                                          B 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                           water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as immunosuppressants, for treating auto:immune diseases and transplant rejection

In diseases and transplant rejection

Claim 10; Fig 2; S8pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oilgonuclectides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q3053), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.

Sequence 1755 BP; 593 A; 325 C; 333 G; 504 T;
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 1334; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             W09218626-A.
29-OCT-1992; F00318.
17-APR-1991; W0-F00318.
17-APR-1991; W0-F00318.
(EUBI') LAB EURO BIOTECHNOLOGIE.
Eld P. Gresser I. Lutfalla G. Meyer F.
Tovey M. Uze G;
WPI; 92-383110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         030533; standard; DNA; 1755 BP.
030533;
31-MAR-1993 (first entry)
Sequence encoding a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; R28496
                       181
                                                                    121
                                                                                        121
                                                                                                               61
                                                                                                                                   61
                                                                                                                                                                                 ...
                                                                                                                                                          CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATACCTCTAAA 1334
||||||||||||||
|GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                          TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                       99.3%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
27. .1700
/*tag= a
                                                                                                                                                                                                        0;
                                                                                                                                                                                                                 Score 1334;
Pred. No. 0;
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F, Mogensen
                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                            1;
                                                                                                                                                                                                       0,
                                                                                                                                                                                                                            Length 1755;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                        0
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1320
                                                                 180
                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1260
                                                                                        180
                     240
                                         240
                                                                                                                                                          60
                                                                                                                                                                                 60
                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
         Ş
                                                  δÃ
                                                                           В
                                                                                               Ş
                                                                                                                         В
                                                                                                                                             Ş
                                                                                                                                                                     밁
                                                                                                                                                                                         Š
                                                                                                                                                                                                                В
                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                               P.
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                δã
                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                         1141
                                                                                                                                                                                                                   1021
                                                                                                                                                                                                                                        1021
                                                                                                                                                                                            1081
                                                                                                                                                                                                                                                               961
                                                                                                                                                                                                                                                                                                           901
                                                                                                                                                                                                                                                                                                                                                                             841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                   961
                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                                       841
                                                                                                                                                                                                                                                                                                                                                                                                    781
                                                                                                                                                                                                                                                                                                                                                                                                                          781
                                                                                                                                                                                                                                                                                                                                                                                                                                                 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                     CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                        CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                                                                                     TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                    ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                  ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATTTATTACCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAATTATCGAGAAAAAAACTGATGTTA
                                                                                                                                                                                                                                                                                                           TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                        ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
```

780

720

720

660

660

540

600

360 360 420 420 480

540

1080

1080

1020

780 840 840 900 900 960

1320

```
B 8
                                                       유 성 유
                                                                                                Ş
                                                                                                                   B 5
                                                                                                                                           B 8
B &
                                                                                                                                                                       Å å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                         Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                     EP-563487-A.
06-CCT-1993:
31-MAR-1992: 400902.
31-MAR-1992: EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SI
BENO1L P, Maguire D, Meyer F, 1
WPI, 93-312951/40.
                                                                                                                                                                                                                                            Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis

Disclosure; Fig 3; 21pp; English.

Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-sequence are claimed. (See 049625 for sequence coding for soluble IFN-R, i.e. just the extracellular domain). The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral infection.

Sequence 1755 BP; 593 A; 324 C; 334 G; 504 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human interferon receptor coding sequence. IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psorlasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measies virus; interferon-alpha-beta; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q49624 standard;
Q49624;
20-APR-1994 (f1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1321
                                                                                                                                                                                                                                                                                                                               P-PSDB; R42635
            361
361
                             301
                                          301
                                                         241
                                                                       241
                                                                                      181
                                                                                                                   121
                                                                                                    181
                                                                                                                                 121
                                                                                                                                                                                                         y Match
Local Similarity 100
hes 1334; Conservative
                                                                                                                                                52
                                                                                                                                                             61
                                                                                                                                                                                            ,_
                                                                                     CTGCAGGGATCTGCGGCGCGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                           ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAATACCTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product hIFN-R
/product antibodies are p
/notes of the receptor, i
extracellular domain"
                                                                                                                                                                                                                 99.3%;
                                                                                                                                                                                                          Score 1334; D; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                          <u>..</u>
                                                                                                                                                                                                                                                                                                                                            SA.
Plavec
                                                                                                                                                                                                                                                                                                                                                                                                pref.
                                                                                                                                                                                                                                                                                                                                             Ή
                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                               to the
                                                                                                                                                                                                                                                                                                                                            Tovey
                                                                                                                                                                                                          0
                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                             នី
                                                                                                                                                                                                                                                                                                                                                                                                       ៥
                                                                                                                                                                                                          0
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                    눇
              420
                                           360
                                                          300
                                                                        300
                                                                                      240
                                                                                                     240
                                                                                                                   180
                                                                                                                                 180
                                                                                                                                                120
                                                                                                                                                                              60
                                                                                                                                                                                            60
                             360
                                                                                                                                                                                                          0
RESULT
Q86458
ID Q
AC Q
DT 1
DE H
KW II
                                                                          Ş
                                                                                          밁
                                                                                                        õ
                                                                                                                        밁
                                                                                                                                    δ
                                                                                                                                                      В
                                                                                                                                                                  Š
                                                                                                                                                                                   밁
                                                                                                                                                                                               Š
                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                          ρy
                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
      Q86458 standa
Q86458;
16-OCT-1995
Human IFN rec
                                                                                              1261
                                                                                                            1261
                                                                                                                           1201
                                                                                                                                        1201
                                                                                                                                                       1141
                                                                                                                                                                                     1081
                                                                                                                                                                                                   1081
                                                                                                                                                                                                                  1021
                                                                                                                                                                                                                               1021
Human IFN receptor
Interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                              961
                                                                                                                                                                                                                                                                                                         841
                                                                                                                                                                                                                                                                                                                       841
                                                                                                                                                                                                                                                                                                                                                                                                661
                                                                                                                                                                                                                                                                                                                                                                                                              661
                                                                                                                                                                                                                                                                                                                                                                                                                            601
                                                                                                                                                                                                                                                                                                                                                                                                                                           601
                                                                                                                                                                                                                                                                                                                                                                                                                                                         541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                               961
                                                                                                                                                                                                                                                                             901
                                                                                                                                                                                                                                                                                          901
                                                                                                                                                                                                                                                                                                                                      781
                                                                                                                                                                                                                                                                                                                                                    781
                                                                                                                                                                                                                                                                                                                                                                   721
                                                                standard;
                             DNA;
      gene.
              entry)
 interferon-alpha;
                              ВP
```

```
CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                 AAGTACATTTAGAAGCTGAAGATAAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                             GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                            TCTTTCCTCAAAAGGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                  ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                         ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                        TIGGIGICIATAGICCAGIACATIGIAIAAAGACCACAGIIGAAAAIGAACIACCICCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1020
                                                                                                                                                                                                                                               960
                                                                                                                                                                                                                                                                                     900
                                                                                                                                                                                                                                                                                                                                                                                                                                                 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540
                                                                                                                                                                                                                                                                  960
                                                                                                                                                                                                                                                                                                        900
                                                                                                                                                                                                                                                                                                                            840
                                                                                                                                                                                                                                                                                                                                                                  780
                                                                                                                                                                                                                                                                                                                                                                                      780
                                                                                                                                                                                                                                                                                                                                                                                                          720
                                                                                                                                                                                                                                                                                                                                                                                                                            720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600
```

```
SOCCCCPPT RAPPRITES X
                             B
                                                                                         ğ
                                                                                                                     Š
                                                                                                                                                       밁
                                                                                                                                                                              δõ
                                                                                                                                                                                                                   뮍
                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
õ
                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 1333; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09507716-A.
23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE S.
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; R75356.

Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, &g. for treating AIDS Disclosure; Fig. 38-2B: 105pp; English.

DNA encoding the extracellular domain of the human IFN class I receptor is given in Q86457; the full IFN receptor gene is given in Q86458. Immunomodulator monoclonal antibodies were raised against the recombinant soluble form of the extracellular domain (R71723) expressed in E. coli or COS cell hosts.

Sequence 1755 BP; 592 A; 324 C; 334 G; 505 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody; immunomodulator; AIDS;
                                                                                                                                                                                    481
                                                                                                                                                         481
                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             بر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                       AAGTACATTTAGAAGCTGAAGATAAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                 CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                  CTTCATGGTATGAGGTTGACTCAGTTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                            ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                         AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTCGTCGCCGTGGGCCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
 TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 27. 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1332.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                             660
                                                                                                                           600
                                                                                                                                                                                      540
                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                    48C
                                                                                                                                                                                                                                                                                   42C
                                                                                                                                                                                                                                                                                                               420
                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                                         30C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                            600
                                                                                                                                                       540
                                                                                                                                                                                                                                                                                                                                                                           36C
                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
PARSULT PARSUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                 drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1081
                           misc_rna
                                                                            misc_rna
                                                                                                                           misc_rna
                                                                                                                                                                      signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661
```

```
Ol1701 standard; DNA; 2784 BP. 011701; 18-JUL-1991 (first entry) Human alpha-interferon receptor protein encoding sequence. Human alpha IFN; IFN agonists; antiviral; anti tumour agen drug targetting; ss.
                                                                                                                                                                                                                                                                                                                          GAAATACCTCTAAA 1334
|||||||||||||
GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                        CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCATITGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                           ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                             /product= h
79. 159
/*tag= b
                                                          /label-
250. .25
                                                                                              /*tag= b
/product=
226. .234
                     /label- glycosylation 319. .327
                                                                               /*tag=
                                                                                                                                                                              Location/Qualifiers
/label=
glycosylation
                                                                     glycosylation
                                                                                                                                            human alpha
                                                                                                          signal
                                                                      site
                                                                                                                                                                                                                                                                                                                                                                                                  1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780
                                                                                                                                                                                                                                                                                                                                                                                                                           1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 780
```

```
밁
            õ
                               gg
VQ
                                                            B 5
                                                                                               Query Match 99.1
Best Local Similarity 99.9
Matches 1332; Conservative
                                                                                                                                                                                                                                           W09105862-A.
02-MAY-1991.
19-OCT-1999; F00758.
20-OCT-1989; FR-013770.
4 (CNRS ) CNRS CENT NAT RECH SCI.
4 (CNRS ) CNRS Uze G, Lutfalla G, GY
                                                                                                                                    New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis bisclosure; fig 4; 30pp; French.

This sequence encodes a recombinant human alpha interferon (IFN) receptor protein useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, e.g. where overexpression of alpha-IFN is harmful. The Abs are also useful for e.g. drug-targetting. Variants of the protein, having residue 164 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.
                                                                                                                                                                                                                                       Mogensen KE, Uze G
WPI; 91-148740/20.
P-PSDB; R11958.
                                                                                                                                                                                                                                                                                                                      misc_rna
                                                                                                                                                                                                                                                                                                                                               misc_rna
                                                                                                                                                                                                                                                                                                                                                                      misc_rna
                                                                                                                                                                                                                                                                                                                                                                                              misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                     misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_rna
173
                121
                                113
                                               61
                                                                53
                                                                               ۲
                                                               CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                               CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                   /iabel= glycosylation 1324. .1332
                                                                                                                                                                                                                                                                                                                  /*tag= p
/label= glycosylation
1687. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-glycosylation 1015. .1023
                                                                                                                                                                                                                                                                                                       /*tag-
/label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                      /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                              label glycosylation 204. .1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    habel-glycosylation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tag= g
bel= glycosylation:
                                                                                                                                                                                                                                                                                                                                                                     ig= n
el= glycosylation :
    1605
                                                                                                       99.1%;
                                                                                                                                                                                                                                                                                                                                                                                             y= m
el= glycosylation
.1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1- glycosylation
1026
                                                                                                                                                                                                                                                                                                                                               l= glycosylation
.1638
                                                                                                                                                                                                                                                                                                      q
glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosylation
                                                                                               0
                                                                                                       Score 1330.8;
Pred. No. 0;
                                                                                                                                                                                                                                                        Gresser
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                              site
                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                      site
                                                                                                                                                                                                                                                                                                                                                                              site
                                                                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                                                                                               site
                                                                                                                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site
                                                                                                                                                                                                                                                        H
                                                                                                                DB
                                                                                               2
                                                                                                               1;
                                                                                               Indels
                                                                                                               Length 2784;
                                                                                               0,
                                                                                               Gaps
               180
                                               120
                                172
                                                                112
                                                                               60
232
                                                                                               0
                    Qy
                                                    δô
                                                                       밁
                                                                                   δõ
                                                                                                      밁
                                                                                                                    δÃ
                                                                                                                                       용
                                                                                                                                                   δõ
                                                                                                                                                                      밁
                                                                                                                                                                                  γQ
                                                                                                                                                                                                      8
                                                                                                                                                                                                                  VQ.
                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                   δô
                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                    VQ
                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                     묫
                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
       밁
                                      В
       1253
                       1201
                                        1193
                                                      1141
                                                                       1133
                                                                                        1081
                                                                                                       1073
                                                                                                                                        1013
                                                                                                                       1021
                                                                                                                                                       961
                                                                                                                                                                       953
                                                                                                                                                                                        901
                                                                                                                                                                                                        893
                                                                                                                                                                                                                      841
                                                                                                                                                                                                                                       833
                                                                                                                                                                                                                                                                                                                       661
                                                                                                                                                                                                                                                                                                                                       653
                                                                                                                                                                                                                                                                                                                                                      601
                                                                                                                                                                                                                                                                                                                                                                      593
                                                                                                                                                                                                                                                                                                                                                                                      541
                                                                                                                                                                                                                                                                                                                                                                                                       533
                                                                                                                                                                                                                                                                                                                                                                                                                       481
                                                                                                                                                                                                                                                                                                                                                                                                                                       473
                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                       781
                                                                                                                                                                                                                                                                       773
                                                                                                                                                                                                                                                                                       721
                                                                                                                                                                                                                                                                                                       713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
      CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                      TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                      ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                               CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                      AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCCTCGTGGAACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTA
                                                                                                                                                                                                                                              ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                      CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                       ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                       CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                        TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTA
                                                                                                                       1080
        1312
                                        1252
                                                        1200
                                                                        1192
                                                                                        1140
                                                                                                       1132
                                                                                                                                       1072
                                                                                                                                                       1020
                                                                                                                                                                       1012
                                                                                                                                                                                        960
                                                                                                                                                                                                                                                                                                                                      712
                                                                                                                                                                                                                                                                                                                                                                                                                       540
                                                                                                                                                                                                        952
                                                                                                                                                                                                                       900
                                                                                                                                                                                                                                        892
                                                                                                                                                                                                                                                        840
                                                                                                                                                                                                                                                                        832
                                                                                                                                                                                                                                                                                       780
                                                                                                                                                                                                                                                                                                        772
                                                                                                                                                                                                                                                                                                                       720
                                                                                                                                                                                                                                                                                                                                                      660
                                                                                                                                                                                                                                                                                                                                                                      652
                                                                                                                                                                                                                                                                                                                                                                                       600
                                                                                                                                                                                                                                                                                                                                                                                                       592
                                                                                                                                                                                                                                                                                                                                                                                                                                       532
                                                                                                                                                                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
```

```
S
                                                             밁
                                                                                           Š
                                                                                                                                                                                                            몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
   밁
                                                                                                                                Matches
                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                  New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Disclosure; Fig 6; 46pp; English.

A cDNA sequence (T73519) corresponds to nucleotides 1260-1620 of a cDNA clone for human interferon alpha receptor (IFNAR, see also W21804), covering the region that codes for the transmembrane region of IFNAR. Differential splicing of INFAR gene transcripts (see also T73520 and T73521) produces novel soluble, non-membrane bound forms of IFNAR (see also W21805 and W21805) that can be used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                  1269 CTGAATAAAAGCAGTGTTTTTAGTGAGCGCTGTATGTGAGAAAACAAAACAAAACCAGGAAATACC 1328
                                                                               1209 AATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAAG 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1997 (first entry)
Transmembranal interferon albha-receptor cDNA fragment.
Interferon alpha-receptor; IFNAR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1373 GAAATACCTCTAAA 1386
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Abramovich C, Ratovitski E, WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-1994; 075977
24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LTD
(ABRA/) ABRAMOVICH C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T73519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU9475977-A.
    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                μ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GANATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG 1320
                                                               CTGAATAAAAGCAGTGTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; cDNA; 360
                                                                                                                                                                                                            360 BP;
                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "primer l
71. .82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "p
262. .282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= f
/note= "primer:
341. .360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "exon
10. .30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "primer
238. .255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "exon IX-exon X junction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "primer 1601. .1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '*tag=
                                                                                                                                             9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 282
                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer
                                                                                                                                                                                                         A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                              0;
                                                                                                                                             Score 126; DB 1;
Pred. No. 1.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-exon XI junction"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1270-1290"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1498.
                                                                                                                                                                                                         64 C;
                                                                                                                                Mismatches
                                                                                                                                                                                                         62 G;
                                                                                                                                                            Length 360
                                                                                                                              Indels
                                                                                                                                                                                                         117 T;
                                                                                                                            0;
                                                                                                                            Gaps
                                                                                                                                0
RESULT ID 1377 ID 1377 ID 1377 ID 1377 ID 1377 ID 1577 ID 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.6%;
Best Local Similarity 100.0%;
Matches 49; Conservative
                                                                                                                                                                                                                   02-JUL-1991 (first entry)
02-JUL-1991 (first entry)
Genes encoding T. hyo 39 kD family 1 an Swine dysentery; vaccine; ss.
Treponema hyodysenteriae serotype B204.
Location/Qualifiers
                  cds
                                                                               cds
                                                                                                                                             cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1329
                                                                                                                                                                                                                                                                                                        Q11377 standard; DNA; 6119
Q11377;
                                                                                                                                                                                                                                                                                                                                                                                                                                 nomo sapiens.
AU9475977-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interferon alpha-receptor splice-deleted form 2 cDNA interferon alpha-receptor; IFNAR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1995.
20-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TCTAAA 126
                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                /label= gene 3
/note= "39 kD a
4707. .5859
                                                                                                                                          /note= "39 kn
2067
                                                                                              label gene inote 39 kD
                                                                               .4550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                                                                                                                      kD family 1 antigens
                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB; Pred. No. 0.(
                                 antigen
                                                                                              antigen
                                                                                                                                                            antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
3. 0.0004;
0;
                                                                                                Ŋ
                                                                                                                                                              ۳,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>;</u>
```

```
W09104036-A.

W09104036-A.

D04-APR-1991.

D04-APR-1990; U05129.

PF 11-SEP-1990; U5-406535.

PR (MITE-) ML Technology Ventures.

PI Gabe J, Dragon E, McCaman M;

PR PFSDB; R11484, R11485, R11486, R11487.

PT Treponema hyodysenteriae antigens - having molecular wt. of ?

PT and their DNA codes, and use for preparing vaccine.

PS Claim 18; Page 49; 84pp; English.

PS Claim 18; Page 49; 84pp; English.

CC The DNA includes family 1 contg. genes 1-4 encoding 39 kD an CC of T. hyo. The sequence was obtd. from clones isolated from CC hyo genomic library in lambda gtil. The antigens can be exical used to prepare vaccines to protect against swine dysen:

CC see also 011378-011409.

2111 A; 683 C; 990 G; 2323
TA 32217 TA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                             US5544534-A.
10-SEP-1994; 315468.
30-SEP-1994; 315468.
16-DEC-1991; US-828430.
01-FEB-1992; US-914941.
30-SEP-1994; US-315468.
(MYCO ) MYCOGEN CORP.
Foncerrada L, Michaels T)
WPI; 96-424659/42.
               New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult pests and their larvae against adult pests and their larvae Example 3; Column 37-42; 24pp; English.

T43221-T43223 represent the coding sequences for toxins that are active against scarab pests. This sequence was isolated from the Bacillus thuringiensis strain toluvorthi. Insects in the family Scarabaddae constitute a serious pest control problem, especially when destructive larval stage insects infest high value turf found in golf courses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-1997 (first entry)
Antiscarab pest toxin 43F coding sequence.
Toxin 50C(b); scarab pest; toxin; insect; scarabaeidae;
larval stage insect; grain; tuberous crop; white grub; c
cyclocephala; popillia; 43F gene; ds.
Bacillus thuringiensis strain tolworthi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATCCTTTTATTAAAGTAG 5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACCAGAAAATATAGAAG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGGATATAAAAATGCTCCGTATGTTGGTAAAAATTATGAAGAAGAACTTTTTTCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATTTGGTTTTGAAACAAGATTCTATTTTTTGAATACTACTGTTGGAAATGTAACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                           W06419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= gene 4
/note= "39 kD antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.0%;
                                                                                                                                                                                                                                                                                                                                                    ŦE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.6; DB Pred. No. 0.33; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                    Narva
   of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be expressed dysentery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       grub;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656
grains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÔ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 147
                                                                                                                                                                                    22-AUG-1990.
15-FEB-1989; 400428.
15-FEB-1989; EP-400428.
(PLAN-) PLANT GENETIC SI
                                                                                                                                                                                                                                                                                                                                                                                                                          Q05679 stand
Q05679;
Q3-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chafer grubs, and can be found in decaying organic matter, or in the so where they consume plant roots. In Europe and the U.S. populations of these larvae and adults have developed resistance to chemical insecticides such as the organochlorines and DDT. The toxins encoded because sequences, and intact cells that are capable of expressing the proteins, can be used to control many pests of the family scarabaeidee, such as species of Cyclocephala, and Popillia. The toxins are active against larvae (present in soil) and against adults.

Sequence 1953 BP; 679 A; 323 C; 344 G; 607 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1089
              against Coleoptera claim 3; Fig 1; 30pp; English.
Claim 3; Fig 1; 30pp; English.
The BtPGS1208 strain was isolated from grain dust and was deposited at the DSM (19/1/1989) under Acc. No. 5131. The protoxin crystals produced on expression of the gene can be digested with trypsin to produce the mature protein. Plants contg. the gene are resistant to Coleoptera pests while the crystals are useful as insecticides.
                                                                                                                                                                                                                                                                                                                                                           btPGS1208 gene.
Toxin; crystal; insecticide;
Bacillus thuringiensis strai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberous crops, and ornamentals. chafer grubs, and can be found in
                                                                                                                                                          Peferoen M, Lambert WPI, 90-255362/34.
                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1209
                                                                                                                           New Bacillus thuringiensis strains -
                                                                                                                                           P-PSDB; R06460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTATGAAGAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACAGATGAACCACTTGAAAAAGCA 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACTTATTGTCTAAAAGTTAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATAAATCTATTGAACCTATACAAAAGCTAAGCTTTGATGGACAAAAAGTTTATCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATGTAGAAACTAGACCTAGTATAGGATCTAATGATACAATCACTTCCCCATTTTATGG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAAACTCTTCAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATAGCTAATACAGACATAGCGGCTTTTCCGGATGGCAAGATATATTTTGGTGTTACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAGATACAATGGCTATTTAGGTGCACAGGATTCTATCGACCAATTACCACCAGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTGATTTTAGTCAATATGATGATCAAAAAAATGAAACTAGTACACAAACATATGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                               thuringiensis strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                           /product=74
513. .2294
/*tag= b
                                                                                                                                                                                                                                                                   /product-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.2%;
                                                                                                                                                                                         SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2425
                                                                                                                                                                                                                                                                                                                                                              train PGS1208.
/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP.
                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                          Ξ
                                                                                                                                                                                                                                                                     ថ្ង
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.2; D
Pred. No. 0.25
0; Mismatches
                                                                                                                                                                                                                                                                                                                 BtPGS1208
                                                                                                                                                                                                                                                                     BtPGS1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The larvae are known as white
    used
                                                                                                                           producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 25;
                                                                                                                                                                                                                                                                                                                 protoxin
                                                                                                                             toxin
                                                                                                                             active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s, or
3011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ဗ္ဗ င္ဗ
                  S
                                                        밁
                                                                                       Ş
                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                         Query Match 2.5
Best Local Similarity 44.5
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1430 TTATGTAGAAACTAGACCTAGTATAGGATCTAATGATACAATCACTTCCCCCATTTTATGG 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      together with the btPGS1245 gene (Q05680). Sequence 2425 BP; 872 A; 366 \text{ C};
                                                                                                                                                                                                                                                 Claim 13; Page 25-27; 38pp; English.

The sequences given in 038653-55 encode lepidopteran-active toxins. These sequences were used within a Ti or Ri plasmid, to transform plant cells. Whole plants can then be regenerated from the transformed cells. The toxin may also be produced by cloning bacillus thuringiensis (Bt). It may then be applied directly to
                                                                                                                                                                                                                                                                                                                                           pradfish GA. Uyeda KA;
WPI; 93-10056/12.
P-PSDB; R33769.
Controlling Lepidopteran pests - using compsn. of Bacillus thuringiensis strains or plants or microorganisms transformed with their toxin genes with their toxin genes claim 13; Page 25-27; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bt isolate 43F coding sequence. Lepidopteran-active; toxin; Ti; Bacillus thuringiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1550 TATAGCTAATACAGACATAGCGGCTTTTCCGGATGGCAAGATATATTTTTGGTGTTACGAA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1490 AGATAAATCTATTGAACCTATACAAAAGCTAAGCTTTGATGGACAAAAAGTTTATCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q38654 standard; DNA; 1953
Q38654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1730 AACAGATGAACCACTTGAAAAAGCA 1754
                                                                                                                                                                                                                   the plant locus.
Sequence 1953 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1992; U07697.
12-SEP-1991; US-758020.
09-SEP-1992; US-941650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MYCO ) MYCOGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 TTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              614 TACTTATTGTCTAAAAGTTAAAGCA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494 GGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGA 433
                                                                              314 TTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAAACACTTCTTCATGGTATGA 373
374 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAAGATACAATGGCTATTTAGGTGCACAGGATTCTATCGACCAATTACCACCAGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAGAAAGGATTGAAAATTTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTTGATTTTAGTCAATATGATGATCAAAAAAAATGAAACTAGTACACAAACATATGATTC 1669
                                                    TTATGTAGAAACTAGACCTAGTATAGGATCTAATGATACAATCACTTCCCCATTTTATGG 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%;
                                                                                                                                            2.98;
                                                                                                                                                                                                                 679 A;
                                                                                                                         Score 38.6; DB 1;
Pred. No. 0.68;
0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40.2; DB 1;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ri; plant; cell;
                                                                                                                                                                                                                   320 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 G;
                                                                                                                                                                                                                   347
                                                                                                                                                                                                                   <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2425;
                                                                                                                                                             Length 1953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bt;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       758 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                           0
```

```
Ş
                                                                                                      Ş
                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                 Ş
                                                        망
                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                               1269
                                                                                                                                                                                                                                                                                                                                                                    1149 AGATAAATCTATTGAAGCTATACAAAAGCTAAGCTTTGATGGACAAAAAGTTTATCGAAC 1208
                                                                                                                                                                                                                494
     TACTTATTGTCTAAAAGTTAAAGCA 638
                                                                                                                                                                                                             GGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGT 553
                                                                                                                                                                                                                                                                                                                    AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTG 493
                                                        AAAAAGATACAATGGCTATTTAGGTGCACAGGATTCTATCGACCAATTACCACCAGAAAC 1388
                                                                                                      AGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGAC 613
                                                                                                                                                               AGTTGATTTTAGTCAATATGATGATCAAAAAAATGAAACTAGTACACAAACATATGATTC 1328
                                                                                                                                                                                                                                                                   TATAGCTAATACAGACATAGCGGCTTTTCCGGATGGCAAGATATATTTTGGTGTTACGAA 1268
```

Search completed: June 1, 2000, 11:12:25 Job time: 19086 sec

AACAGATGAACCACTTGAAAAAGCA 1413

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic - nucleic search, using sw model
            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.2
39.4
38.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    June 1, 2000, 05:53:48 ; Search time 49.94 Seconds (without alignments) 3495.593 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1
1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCAGGGATCTGCGGCGGC.....ATACCTCTAAATGAGGTACC 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
         22784
27784
27784
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
27884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5 (c) 1993 - 2000 Compugen
   US-08-307-588-1
US-08-371-454-1
US-08-471-453-1
US-08-471-453-1
US-08-471-453-1
US-08-328-256-8
US-08-315-468-5
US-08-315-468-5
US-08-92-00040-1
US-07-991-8678-8
US-08-943-087-8
US-08-481-332-8
US-08-483-112
US-08-483-483-112
US-08-483-483-112
US-08-483-577A-112
US-08-853-659A-10
US-08-853-659A-63
US-08-853-659A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ltd
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 14, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 112, Appli
Sequence 113, Appli
Sequence 114, Appli
Sequence 115, Appli
Sequence 116, Appli
Sequence 5, Appli
Sequence 63, Appli
Sequence 63, Appli
Sequence 63, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-08-307-588-1
```

## ALIGNMENTS

```
Sequence 1, Application US/08307588
Patent No. 5919433
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: WEYER, Francois
APPLICANT: WEYER, Francois
APPLICANT: PLAVE, ITAL
APPLICANT: PLAVE, ITAL
APPLICANT: POYEY, Michael G.
TITLE OF INVENTION: MCNOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: MCNOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 2007
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TITE: ILM PC Compatible
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TITE: STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/307.588
FILING DATE: 30-MAR-193
APPLICATION NUMBER: PCT/EP3/00770
FILING DATE: 30-MAR-193
APPLICATION NUMBER: PCT/SP3/00770
FILING DATE: 31-MAR 1952
ATTORNED/ACENT INFORMATION:
NAME: SAXE, Bernhard D.
REFERENCE/DOCKET NUMBER: 128/3/117/GUPL
TELEFONGUNICATION INFORMATION:
TELEFONGUNICATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 178/3/117/GUPL
TELEFONGUNICATION INFORMATION:
TELEFONGUNICATION INFORMATION:
TELEFONGUNICATION INFORMATION:
TELEFONGUNICATION INFORMATION:
TELEFONGUNICATION INFORMATION:
TELEFONGUNICATION OF SED 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LEMBIR: 13/4 DASE PAIR
SECURATION OF SED 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LEMBIR: 13/4 DASE PAIR
SECURATION OF SED 1D NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERIS
```

```
õ
                     밁
                                      õ
                                                              В
                                                                               δÃ
                                                                                                     B
                                                                                                                        Š
                                                                                                                                             В
                                                                                                                                                                Ş
                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                      γ
                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                     밁
                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-307-588-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1343; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                781
                                                                                                             781 ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                              721
                                                                                                                                                                                      661
                                                                                                                                                                                                         661
                                                                                                                                                                                                                             601
                                                                                                                                                                                                                                                 601
                                                                                                                                                                                                                                                                    541
                                                                                                                                                                                                                                                                                        541
                                                                                                                                                                                                                                                                                                             481
                                                                                                                                                                                                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                         421
                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                     361 CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACGACCCTAG
                   TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                          CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                          ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                            CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                       CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                                                                                                                                                              TIGGIGICTATAGICCAGTACAITGIATAAAGACCACAGTIGAAAAIGAACTACCICCAC
                                                                                                                                                                                                                                     TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACCTACTTACGTCATGGAAAA
                                                                                                                                                                                                                                                                  ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                                           CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTCGTCGCCGTGGGCCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                   ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                                                                                                    TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                                          TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCAGGGATCTGCGGCGCGCCCAGATGATGGTCGTCCTCGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27..1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1343;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
 1020
                                                                                                                        840
                                                                                                   840
                                                                                                                                                                780
                                                                                                                                                                                                                           660
                                                                                                                                                                                                                                               660
                                                                                                                                                                                                                                                                                       600
                                                                                                                                                                                                                                                                                                                              540
                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                    960
                                                             900
                                                                                900
                                                                                                                                            780
                                                                                                                                                                                   720
                                                                                                                                                                                                       720
                                                                                                                                                                                                                                                                   600
                                                                                                                                                                                                                                                                                                            540
                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
RESULT 2
US-08-307-588-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
NAME: SAXE, BETTHARD D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 1728

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5309
TELEPHONE: (202)672-5399
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1755 base pairs
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Applic
Patent No. 5919453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: RECEPTOR, ITILE OF INVENTION: RECEPTOR, ITILE OF INVENTION: INTERFERO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1261
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9:
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            STREET: 300
CITY: Washi
STATE: D.C.
ZIP: 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARATACCTCTARATGAGGTACC 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATACCTCTAAATGAGGTACC 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08307588
                                                                                                                                                                                                                                                                                                                                                                                                                         3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BENOIT, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MONOCLONAL ANTIBODIES AGAINST THE INTRECEPTOR, WITH NEUTRALIZING ACTIVITY INTERFERON
                                                                                                                                                                           EP 92400902.0
                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 500
                                                                                                                                                                                                                                                                                                  #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1200
```

double

```
; STRANDEDNESS:
; TOPOLOGY: 11ne
; MOLECULE TYPE: D
; FEATURE:
; FATURE: CDS
; NAME/KEY: CDS
; LOCATION: 27...
US-08-307-588-3
                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                          멼
                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                        δÔ
                                                                                                                                                                      Ş
                                                                                                                                                                                      밁
                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                g
                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                               밁
         Ş
                         밁
                                    ő
                                                   밁
                                                              S
                                                                              밁
                                                                                          Ş
                                                                                                        밁
                                                                                                                  δ
                                                                                                                                  밁
                                                                                                                                            S
                                                                                                                                                          밁
                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1334; Conserv
                                                                                                                                                                                                                                                                                                            181
                                                                                                                     601
                                                                                                                                   541
                                                                                                                                                             481
                                                                                                                                                                         481
                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                          121
                                                    721
                                                                               661
                                                                                            661
                                                                                                         601
                                                                                                                                                541
                                                                                                                                                                                                    421
                                                                                                                                                                                                                361
                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                       121
                                       781
                                                                 721
                          781
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                             CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                   TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAAGCAGCACTACTTACGTCATGGAAAA 660
                                                                                                                                                                    ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                     TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
ACCATTTGTATAAATGGAAACAAATACCTGACCTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                         ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                             CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                               TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                         TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC 720
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
27..1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                              99.3%; Score 1334;
100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                         M1smatches
                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                               600
                                                                                                                                                                         540
                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                           60
 900
              900
                                                                              720
                                                                                                                                   600
                                                                                                                                                            540
                                                                                                                                                                                      480
                                                                                                                                                                                                   480
                                                                                                                                                                                                                420
                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                         0
```

```
RESULT 3
US-08-471-454-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1,
Patent No. !
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: OF JONE PC COMPATION:
APPLICATION NUMBER: FR 89/13770
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 10-OCT-1989
ATTORNEY/ACENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LUTFALLA, GEORAPPLICANT: GRESSER, ION
TITLE OF INVENTION: CDNA
TITLE OF INVENTION: THE #
TITLE OF INVENTION: PREP#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MOGENSEN, KI APPLICANT: UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAATACCTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Application 5731169
                                                                                                                                                                                UMBER: US/08/471,454
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08471454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knud
                                                                                                                                                                                                                             Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges
                                                                                                                                      07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ы
                                                                                                                                                                                                                                                                                                                                                                           р
С
                                                                                                                                                                                                                              #
                                                                                                                                                                                                                                                                                                                                                                                                                                        FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960
```

```
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-471-454-1
                              S
                                                 В
                                                               S
                                                                                   밁
                                                                                                 Ş
                                                                                                                    В
                                                                                                                                    Š
                                                                                                                                                       밁
                                                                                                                                                                    õ
                                                                                                                                                                                        밁
                                                                                                                                                                                                         Š
                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                              ᅜ
                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
Ş
                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 1332; Conserv
                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                                                                    713
                                                                                                     661
                                                                                                                      653
                                                                                                                                     601
                                                                                                                                                       593
                                                                                                                                                                       541
                                                                                                                                                                                         533
                                                                                                                                                                                                           481
                                                                                                                                                                                                                           473
                                                                                                                                                                                                                                            421
                                                                                                                                                                                                                                                              413
                                                                                                                                                                                                                                                                                               353
                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                 293
841
                                 781
                                                  773
                                                                   721
                                                                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۳,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCAGGGATCTGCGGCGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                                                                                                                         ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                           CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                 CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT 780
                                                                                  TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                      CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                    ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                        TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                                                   CTCCTCANANAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                                                                                                                                                                                                                                                                                                                ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                  ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                         ATGCAAACATGACCTTTCAAGTTCAAGTGGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAA
                                                                                                                                                       ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1330.8;
Pred. No. 0;
'0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                840
                                                                                                    720
                                                                                                                                                                                                         540
                                                                                                                                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                    712
                                                                                                                                     660
                                                                                                                                                       652
                                                                                                                                                                      600
                                                                                                                                                                                        592
                                                                                                                                                                                                                                           480
                                                                                                                                                                                                                                                                             420
                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                  292
                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                   232
                                                                                                                                                                                                                          532
                                                                                                                                                                                                                                                             472
                                                                                                                                                                                                                                                                                              412
                                                                                                                                                                                                                                                                                                                                352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-466-974-
                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                         믔
                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                    Sequence 1.
Patent No.
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                         1321
                                                                                                                                                                                                                                                                                                                                                                          1313
                                                                                                                                                                                                                                                                                                                                                                                                            1253
                                                                                                                                                                                                                                                                                                                                                                                                                             1201
                                                                                                                                                                                                                                                                                                                                                                                                                                              1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1013
                                                                                                                                                                                                                                                                                                                                         1373
                                                                                                                                                                                                                                                                                                                                                                                          1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      901
```

```
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          893
                                                                                                                APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAATACCTCTAAA 1334
|||||||||||||
GAAATACCTCTAAA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTA

    Application US/08466974
    5861258

                                                                                                                                                                                                                                                                                                                                                                                                                                MOGENSEN, Knud E. UZE, Gilles LUTFALLA, Georges
                                                                                                                                                                                                                                                                                                                                                                                                                     GRESSER,
                                                                                                         06-JUN-1995
N: 435
ON TON
                                                                                                                                                                                                                                                                                                              VANDERHYE P.C.
GLEBE ROAD
                                                                                                                                                                            Release #1.0,
                                                                                                                                                                             Version
                                                                                                                                                                               #1.25
                                                                                                                                                                                                                                                                                                                                                                                         FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            960
                                                                                                                                                                                                                                                                                                                                                                                           THE
```

960-7

```
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
US-08-466-974-1
õ
                     밁
                                    Š
                                                             В
                                                                               Š
                                                                                                        밁
                                                                                                                       S
                                                                                                                                                  밁
                                                                                                                                                                    Š
                                                                                                                                                                                          밁
                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 960-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1332; Conserv
                                                                                                                                                                                                                 481
                                                                                                                                                                                                                                      473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
                                                              713
                                                                                                          653
                                                                                                                             601
                                                                                                                                                   593
                                                                                                                                                                       541
                                                                                                                                                                                             533
                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                               413
                                                                                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                                                                                          353
                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                   293
                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                       173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
 781
                                         721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                        CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCAGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                    CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACAT
                                                             CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTGGGATCTGCGGCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAG
                                                                                                                                                                                                                                     AAGTACATTTAGAAGCTGAAGATAAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGA
                                                                                                                   TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA
                                                                                                                                                             ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATTTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                                        ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAAT
ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAA
                                                                                                         TCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA
                                                                                                                                                   ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                                                             ATTGGATAMAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1330.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112
                                                                                                                             660
                                                                                                                                                                                                                 540
                     832
                                         780
                                                                                   720
                                                                                                                                                  652
                                                                                                                                                                       600
                                                                                                                                                                                             592
                                                                                                                                                                                                                                      532
                                                                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                                               472
                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                                          412
                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                   352
                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
 840
                                                              772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

```
GENERAL INFORMATION:

APPLICANT: MOGENSEN, KNUD E.

APPLICANT: UZE, Gilles

APPLICANT: LUTEALLA, Georges

APPLICANT: LUTEALLA, Georges

APPLICANT: GRESSER, ION

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                皮
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-471-453-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1 Patent No.
APPLICATION NUMBER: US/08/
FILING DATE: 06-7UN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 15-7UN-1992
APPLICATION NUMBER: FR 89/
FILING DATE: 20-0CT-1989
                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1013
                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAATACCTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACTICCICCAGICTITAACATIAGATCCCTTAGIGATICATICCATAICTATAICGGIG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAACTGATGTTA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAAAGCTGAATAAAAGCAGTGTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAG 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Application US/08471453 5886153
      MBER: FR 89/13770
20-OCT-1989
                                                US 07/900,642
                                                                                                                                            #1.25
                                                                                                                                                                                                                                                                                                                                                        FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               952
```

```
Ş
                                                        õ
                                                                               용
                                                                                               S
                                                                                                                     В
                                                                                                                                       S
                                                                                                                                                            밁
                                                                                                                                                                           Š
                                                                                                                                                                                                 밁
                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: US-08-471-453-1
              δõ
                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BYENE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: 101141 5418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1332; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                       593
                                                                                                                                                                                                    473
                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                          413
                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                 353
                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                   601
                                                                                                                                        541
                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                        293
                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                233
                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                   CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                            ACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAAC
                                                                                                                                                          TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                                        TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT 120
                                                  TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                           AAGTACATTTAGAAGCTGAAGATAAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                                                                TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTT
                                                                                                                                                                                                                                                                                                                                                             TGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAT
                                      TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                  AAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
                                                                                                                                                                                                                                         CTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1330.8; 
; Pred. No. 0; 
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                              540
                                                                                                                                        600
                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
 832
                                       772
                                                          720
                                                                               712
                                                                                                 660
                                                                                                                     652
                                                                                                                                                            592
                                                                                                                                                                                                  532
                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                         472
                                                                                                                                                                                                                                                            420
                                                                                                                                                                                                                                                                                412
                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                      352
                                                                                                                                                                                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                                                                              292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: REAMOVISKI, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, IT:
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-328-256-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08328256 Patent No. 5643749
                                                                                         ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/328,2
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATACCTCTAAA 1334
||||||||||||||
GAAATACCTCTAAA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAAACAAAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAAACCAG 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                             us/08/328,256
                                                                                                          Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      840
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT: 7
US-08-328-256-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sin
Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Applic Patent No. 5643749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                           ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-CCT-1993
                                                                  NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                       FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                    TELEPHONE: 202 -
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACCAAAAACCAGGAAATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAAACCAGGAAATACC 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08328256
                                  248633
                                                                                                                                                                                                                                                                                                                                                                                                                                        E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABRAMOVICH, Carolina RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVEL, Michel
                                                                                                                       REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 126; DB 1; Pred. No. 1.7e-26;
                                                                                                      5,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-328-256-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-315-468-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                         TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1953 base pairs
                 MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-375-600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1218 CCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAA 1266
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/808, FILING DATE: 16-DEC-1991 ATTORNEY_AGENT INFORMATION: NAME: Sallwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IIILE OF INVENTION: Process for Controlling Scarab Pests
IIILE OF INVENTION: with Bacillus thuringiensis Isolates
                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/315,468 FILING DATE: CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/014,941 FILING DATE: 01 FEB 1993 APPLICATION NUMBER: 07/828,430 FILING DATE: 30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCACTGACTGTATATTGTGTGAAAGCCAGAGCACCACCACCATGGATGAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%; P 49; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08315468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foncerrada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michaels, Tracy Ellis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                       double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 49;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                            07/808,316
                                                                                                                                                                                                                                       MA73.C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 1; Luc...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

ORGANISM:

: Bacillus thuringiensis tolworthi

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-315-468-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-943-087-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Sir
Matches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastEEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1089 TTATGTAGAACTAGACCTAGTATAGGATCTAATGATACACTTCCCCCATTTTATGG 1148
                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
08/803,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1389 AACAGATGAACCACTTGAAAAAGCA 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1149 AGATAAATCTATTGAACCTATACAAAAGCTAAGCTTTGATGGACAAAAAGTTTATCGAAC 1208
                            APPLICATION NUMBER: 08/8 FILING DATE: 20-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1329 AAAAAGATACAATGGCTATTTAGGTGCACAGGATTCTATCGACCAATTACCACCAGAAAC 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1269 AGTTGATTTTAGTCAATATGATGATCAAAAAATGAAACTAGTACACAAACATATGATTC 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1209 TATAGCTAATACAGACATAGCGGCTTTTCCGGATGGCAAGATATTTTTGGTGTTACGAA 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 TACTTATTGTCTAAAAGTTAAAGCA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   554 AGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGAC 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 TTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGA 373
                                                                                                                                                                                                                                                                                                     STREET: 1201 Ea
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE:
                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7, Application US/08943087
5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli XL1-Blue (pM1,98-4), NRRL B-18291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Farrah, Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43F
                                                                                                                                            US/08/943,087
32,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40.2; DB 1; Length 1953; Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
```

```
; NAME/KEY: Coding Sequence; LOCATION: 1...1659; OTHER INFORMATION: US-08-943-087-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US92-00040-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.9%;
Best Local Similarity 49.8%;
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9200040 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 ACGGATGAGAAGTCCAT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 GCTGAAGATAAGGCAAT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 GAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTC---ATGGTATGAG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 GGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTAT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 AAGGITACTTATACTGTGCAGTATTTTATTTATGGGCAGAAGAAGTGGCTGAATAAGTCA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Slaney, Annette C.
ITLE OF INVENTION: BACILLUS THURINGIENSIS CTYTIIC(b) TOXIN
ITLE OF INVENTION: GENE AND PROTEIN TOXIC TO COLEOPTERAN INSECTS
                                        APPLICATION NUMBER: FILING DATE: 199201 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 206-442-66
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1659 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                         CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Panit
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGGGCGGTTTTATCCTTTTCTAGAGACGCAGATTGGCCCGCCGGAGGTGGCGCTGACT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCAGTATTATGCCAAGGTTAAGGCCATTTGGGGGACGAAGTGTTCCAAGTGGGCTGAG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTGTCGAAATATCAATCGAACCTATTGTGATCTTTCTGCTGAGACTTCTGATTATGAG 315
                                                                                                                                                                                                                                         19103
                                                                                                                                                                                                                                                         Pennsylvania
U.S.A.
                                                                                                                                                                                                                                                                                                                         1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rupar, Mark J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Donovan, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                      Panitch Schwarze Jacobs & Nadel c/o A.S
                                                                 19920103
                                                                                                                            Release #1.0,
  US 07/649,562
                                                                                      PCT/US92/00040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39.4; DB 4; Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
; LOCATION:
PCT-US92-00040-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-991-8678-8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.9%;
Best Local Similarity 44.9%;
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/07991867B Patent No. 5476781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1292 AGATAAATCTACTGAACCTGTACAAAAGTTAAGCTTTGATGGACAAAAAAGTTTATCGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1232 TTATGTAGAAACTAGACCTAGTATAGGATCTAGTAAGACAATTACTTCCCCCATTTTATGG 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 215-757-1590
                                                                                                                                                                                                                                                             APPLICANT: Moyer, Richard w.
APPLICANT: Hall, Richard L.
APPLICANT: Gruddl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1352 TATAGCTAATACAGACGTAGCGGCTTGGCCGAATGGCAAGATATATTTTGGTGTTACGAA 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
REGISTRATION NUMBER: 276
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1532 AACAGATGAACCACTTGAAAAAGCA 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTG 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 TTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614 TACTTATTGTCTAAAAGTTAAAGCA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID STRANDEDNESS: double TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                         STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAGAAACAATGGCCATGTAGGTGCACAGGATTCTATTGACCAATTACCACCAGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTTGATTTTAGTCAATATGATGATCAAAAAAATGAAACTAGTACACAAACATATGATTC 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTTTGGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGT 553
                                                                                                                                    32606
                                                                                                                                                                        Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2430 base pairs
JCLEIC ACID
                                                                                                                                                                                                         2421 N.W. 41st Street, Suite A-1
                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
144..2099
US/07/991,867B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7205-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.6; DB 6; Length 2
Pred. No. 0.17;
0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Р1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                              RESULT 12
US-08-107-755A-8/c
                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                         멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                            Sequence 8, Application US/08107755A Patent No. 5721352
                                                                             GENERAL INFORMATION:
                   APPLICANT:
                                                         APPLICANT:
```

```
US-07-991-867B-8
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 904-3/2-3800
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 1
FILING DATE: 30-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 9:
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                   1022 ACTICCTCCAGICTITAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                1202 AGTTCCTAATTTGAAACCACTGACTGTAT 1230
                                                                                                   1142 TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAACTGATGTTAC 1201
                                                                                                                                                                      1082 TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          962 AAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCT 1021
                                                                                                                                     755 ATGTTTTCTGGCAAAACAACAGAATTGAT
                                                                                                                                                                                                                                                                                                                                              y Match 2.8%;
Local Similarity 46.1%;
hes 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECUMAN 904 -372-5800 --- TD NO:
                                                                  TTTTTGAAAAATATATCAAATAATAAAAAAAATGTCGATAGAATTAATAATTGGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amsacta moorei entemopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS complement (234..782)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       852..1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (18..218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBER: US 07/657,584
19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 07/827,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO 92/14818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UF114.C3
                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1;
Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                  145; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Length 1511;
                                                                                                                                                                                                                                                                                                                                                   0
```

Gaps

0

816

T: Moyer, Richard W. T: Hall, Richard L. T: Gruidl, Michael E. INVENTION: No. 5721352el Entomopoxvirus

Expression System

MBER OF SEQUENCES: 4
RRESPONDENCE ADDRESS:

DDRESSEE:

E: David R. Saliwanchik 2421 N.W. 41st Street, Suite A-1

Gainesville

Florida

COUNTRY:

```
Ş
                                             뮍
                                                                    Ş
                                                                                                   밁
                                                                                                                             Š
                                                                                                                                                         ₽
                                                                                                                                                                                   õ
                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                             ;
US-08-107-755A-8
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 124; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NECEMBER 100 FOR SEQ ID NO:
1202 AGTICCTAATTIGAAACCACTGACTGTAT 1230
                                                                                                                                                                                   1142 TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAATTATCGAGAAAAAAACTGATGTTAC 1201
                                                                                                                            1082 TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                    875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRIGINAL SOURCE:
                                       815 TTTTTGAAAAATATATCAAATAATAAAAAAAAATGTCGATAGAATTAATAATTGGTCCT 756
                                                                                                                                                                                                                                 962 AAATAACACATCTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCT 1021
                                                                                                                                                        ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0: FILING DATE: 19-FEB-1991 TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08)107,755A FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 30-JA
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RANDEDNESS:
                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (904)
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                          CDS
852..1511
                                                                                                                                                                                                                                                                                                                                                                                                   complement (234..782)
                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amsacta moorei entemopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (18..218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US 07/657,584
19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBER: US 07/827,658
30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372-5800
                                                                                                                                                                                                                                                                                   2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω..
                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UF114.C2
                                                                                                                                                                                                                                                                                   Score 37; DB 2
Pred. No. 0.38;
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                DB 2; Length 1511;
                                                                                                                                                                                                                                                                       145;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                      Gaps
                                                                                                 816
```

```
밁
US-08-544-332-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08544332 Patent No. 5935777
                                                                                                                                                                                                                                                                                                    TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                  FEATURE
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 ATGTTTTCTGGCAAAACAACAGAATTGAT 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: WO 92/14818 FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0'FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                  NAME/KEY:
                                                                                   NAME/KEY:
                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                LOCATION:
                                                                                                                   LOCATION:
                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                       ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Gerard H. Bencen
P: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                  SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                       Bencen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.
                 CDS
852..1511
                                                                                   CDS
                                                                complement (234..782)
                                                                                                                 complement (18..218)
                                                                                                                                                                Amsacta moorei entemopoxvirus
                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                     JMBER: US 07/657,584
19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JMBER: US 07/827,685
30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                     Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us 07/991,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/107,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/544,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5935777el Entomopoxvirus Expression System
                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ħ
                                                                                                                                                                                                                                                                                                                                                                      UF114.C4
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-487-890A-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, very control bata:

APPLICATION UMBER: US/08/487,890A FILING DATE: 07-JUN-1993

CLASSIFICATION 1435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968

APPLICATION NUMBER: US 08/148,968
                                               TELEFAX: (416) 595-1163
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1202 AGTTCCTAATTTGAAACCACTGACTGTAT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1082 TCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT 114
                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  962 AAATAACACATCTTTTTGGTCTGAAGAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 147
                                                                                                                                       NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                         FILING DATE: 08-NOV-1993
TORNEY/AGENT INFORMATION:
                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Toronto
   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTAC 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTTTTCTGGCAAAACAACAGAATTGAT 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTTGAAAAATATATCAAATAATAAAAAAAAAATGTCGATAGAATTAATAATTGGTCCT 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112, Application US/08487890A
o. 5708149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6th Floor, 330 Unviersity Avenue
              1951 base pairs
ucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loosmore, Sheena
Harkness, Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murdin, Andrev
Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray-Owen, Scott
Yang, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chong, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schryvers, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.18;
                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                     US/08/487,890A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                         1038-466 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 1..1890
US-08-487-890A-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-478-435-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 29-DEC-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1706 AAGTA 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1646 ATTTTGTAATAGATGGTAACAATAGTCAAACTGGAAATACCCAAATTAATATTAAAACTG 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1586 GAATTAATGCAGACTTTAAAAATAATGATAATGCCTTCAAAGGTACAGCAACCGCAGAAA 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1526 TTACCGATAAAAAGCTAACAGGCGAATTAAAACGAGCCGATAATCAAAATACCGTATTTA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: FEATURE:
                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 AACTA 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649 CGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATG 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589 AAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTA 648
                                                                   APPLICATION NUMBER: US OF FILING DATE: 08-NOV-1993
                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 08-NOV-1994
                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92;
                                                                                                                                                                                                                                                                                                                                                                                                         M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Sim & McBurney
Suite 701, 330'University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08478435
                                                                                                                                                                                                                                                                                                                                                                                                                         Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murdin, Andrew
Klein, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gray-Owen, Sco
Yang, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schryvers, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harkness, Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                               Michael
   NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferrin Receptor Genes : 147
                                                                                      US 08/148,968
                                                                                                                                         US 08/175,116
                                                                                                                                                                                                             US 08/337,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scott
                                                                                                                                                                                                                                                                               US/08/478,435
                  24,973
1038-462 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36.2; DB Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
```

```
Š
                                                                                                               밁
                                                                                                                                      Ş
                                                                                                                                                                В
                                                                                                                                                                                       Ş
                                                                                                                                                                                                                    밁
Search completed: June 1, 2000, 11:11:03 Job time: 19035 sec
                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 1..1890
US-08-478-435-112
                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 36.2; DB 4; Length 1951; Best Local Similarity 49.7%; Pred. No. 0.72; Matches 92; Conservative 0; Mismatches 93; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                           1706 AAGTA 1710
                                                                                                                                                             709 AACTA 713
                                                                                                                                                                                                                                                                   ..
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0% Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic search, using sw model
                                                                                                                                                                                                         4857316 seqs, 2026611650 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            June 1, 2000, 05:52:42; Search time (without 8912.632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-240-675-1
1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4,5
Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGGGATCTGCGGCGGC.....ATACCTCTAAATGAGGTACC 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_est5:*
em_est6:*
em_est7:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_est1:*
em_est2:*
em_est3:*
               gb_est1: *
gb_est3: *
gb_est4: *
gb_est4: *
gb_est5: *
gb_est6: *
gb_est6: *
gb_est7: *
gb_est10: *
gb_est111: *
gb_est111: *
gb_est112: *
gb_est13: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_est9
                                                                                                                                                                                                                                                                                                                                                                em_est18:*
em_est19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_estl1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_est10:*
                                                                                                                                                                                                                                                                                                                                                                                                           em_est16:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         em_est14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_est13:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_est12:*
                                                                                                                                                                                                                                                                                                                                                                                               em_est1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610.76 Seconds alignments) Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9714632
 Result
                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
%
Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_est25:
em_est26:
gb_est33:
gb_est34:
gb_est35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est31:
gb_est32:
em_est20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est26:
gb_est27:
gb_est28:
                                                                                                                                                                                                                                                                                                                                                                                          em_gss4:*
gb_gss5:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_est27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_est21:
                                                                                                                                                                                                                                                                                                                                    gb_gss8:
                                                                                                                em_gss10:
em_gss11:
gb_gss10:
gb_gss11:
gb_gss11:
em_gss12:
gb_gss12:
gb_gss13:
gb_gss14:
gb_gss14:
gb_gss14:
                                                                                                                                                                                                                                                              em_gss9
                                                                                                                                                                                                                                                                                                                                                                              gb_gss6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_est30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_est29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_est24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_est23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est29
                              SUMMARIES
```

Database :

Searched:

Run

K GH G	ALIGNMENTS  RESULT 1 AW366810/c AW366810 538 bp mRNA EST 04-FEB-2000 DEFINITION CM1-HT0152-041099-021-f06 HT0152 Homo sapiens cDNA, mRNA sequence. ACCESSION AW366810.1 GI:6871460  VERSION AW366810.1 GI:6871460	43.4  43.2  781  82 CNSOOPPO  42.8  3.2  579  92 AQ965871  42.8  3.2  597  92 AQ965869  42.8  3.2  597  92 AQ965869  42.8  3.2  1201  83 CNSO167M  42.6  3.2  1201  83 CNSO161D  42.6  3.2  1101  82 CNSOOXAE  43.8  1108  82 CNSOOXAE  41.6  3.1  1101  82 CNSOOLTT  41.6  3.1  1101  83 CNSO127S  41.6  3.1  1101  83 CNSO127S  41.6  3.1  1101  83 CNSO127S  41.6  3.1  1101  83 CNSO127S	53.4 4.0 387 21 T96832 y 53.2 4.0 1101 82 CNS0039G AL063921 48.6 3.6 1204 83 CNS018M5 AL106581 48.6 3.6 697 83 CNS018M5 AL09511 45.4 3.4 1101 82 CNS003B6 AL064084 45.4 3.4 1101 82 CNS00EVL AL0659706 44.6 3.3 1001 82 CNS00EVL AL09706 44.6 3.3 1010 82 CNS00EVL AL098706 44.6 3.3 1001 82 CNS00EVL AL098706 44.6 3.3 1001 82 CNS00EVL AL098706 44.8 3.3 1001 82 CNS00EVL AL098706 44.8 3.3 1001 82 CNS00EVL AL098639 44.2 3.3 1001 82 CNS00EVL AL098639 44.3 3.3 1001 82 CNS00EVL AL098639 44.3 3.3 1001 82 CNS00EVL AL098639 44.2 3.3 1001 82 CNS00EVL AL098639 43.8 3.3 928 82 CNS00EVL AL0985639 43.6 3.2 1101 83 CNS017KX	Match Length   538   36.9   558   456   556   557   55
Qy 1101 ACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCA 1160	Db 298 CAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGAATAAACAATCCTTTTTGG 239  981 TCTGAAGAAGTTTAACTTTGATACATCATACAAGCATCCTACTCTCAAGTCTTTTAAC 1040	538 741 478 801 418 861 358	Site_2: Smal; A min1-1LDrary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  BASE COUNT 157 a 87 c 107 g 187 t ORIGIN  Overy Match 36.9%; Score 495.4; DB 80; Length 538; Best Local Similarity 95.2%; Pred. No. 2.7e-111; Matches 511; Conservative 0; Mismatches 26; Indels 0; Gaps 0; Oy 681 CATTGTATAPAAGACCACAGTTGAAPATGAACTACCTCCACCAGAAPATATAGAAGTCAGT 740	Tel: +55-11-2704922  Fax: +55-11-2707001  Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM1&t2=CM1-HT0152- 041099-021-f0&t3=1999-10-04&t4=1) Seq grimer: puc 18 FORWard High quality sequence start: 19 High quality sequence stop: 538. Location/Qualifiers 138  FEATURES  source /organism="Homo sapiens" /db_xref="taxon.9606" /clone_lib="HT0152" /dev_stage="Adult" /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

```
SOURCE
ORGANISM
                                           용
                                                                        Ş
                                                                                                                      밁
                                                                                                                                                         Ş
                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
  õ
                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                      665 TGTCTATAGTCCAGTACATTGTATAAAAGACCACAGTTGAAAATGAACTACCTCCACCAGA 724
                                           325
                                                                                                                          384
                                                                                                                                                                                                    444
                                                                                                                                                                                                                                         725
                                                                                                                                                                                                                                                                                   504
                                                                                                                                                               785
                                                                                                                                                                                                                       AAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGC 784
TCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                         AAACATGACCTTTCAAGTTCAGT-GCTCCACGCCTTTTTAAAAAGGAATCCTGGAACCCA
                                                                                TTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTT
                                                                                                                                                             AAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCA 844
                                                                                                                                                                                                    AAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGC
                                                                                                                                                                                                                                                                                 TGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGA 445
                                                                                                                                                                                                                                                                                                                                                                  503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
Unpublished (1995)
On Sep 12, 1996 this sequence version replaced
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. Er from Amersham High quality sequence stop: 418.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Eutheria; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA258405.1 GI:1893676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence
AA258405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.B. clones 260232-265223, 340488-34549, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:667961"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                36.6%;
                                                                                                                                                                                                                                                                                                                                                           Score 491.4; DB 30;
Pred. No. 2.6e-110;
Pred. No. 2:6e-110;
                                                                                                                                                                                                                                                                                                                                                                indels
                                                                                                                                                                                                                                                                                                                                                                                                   Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g1:1393828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetal heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                              904
                                                                                                                        326
    96
                                         266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                ۲
```

```
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
AW292343/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뭕
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1145 TTGGGAAAACACTTCAAATGCTGAG 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1085 AAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATTTT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCCATTCCATATCTATATCGGTGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACT 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW292343 456 bp mRNA EST 16-JAN-2000 UI-H-BI2-agw-a-10-0-UI.sl NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2725554 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortlum/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188431.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW292343.1 GI:6698979
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 455)
NCI-CGAP http://www.ncb1.nlm.nlh.gov/ncicgap.
NCI-CGAP http://www.ncb1.nlm.nlh.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: M13
/clone=lib="NCI_CGAP_Sub4"
/clone=lib="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with is a subtracted library derived from the note in a subtracted library derived from BI. BI constitutes a
mixture of 21 normalized or subtracted NCI_CGAP_F128,
NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_LO15, NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_RX1012,
NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_RX101,
NCI_CGAP_LO12, NCI_CGAP_EX103, NCI_CGAP_RX101,
NCI_CGAP_LO12, NCI_CGAP_BT03, NCI_CGAP_LO15,
NCI_CGAP_LO12, NCI_CGAP_LO19, NCI_CGAP_LO15,
NCI_CGAP_LO12, NCI_CGAP_LO19, NCI_CGAP_LO16,
NCI_CGAP_LO10, NCI_CGAP_LO19, NCI_CGAP_LO16,
NCI_CGAP_LO10, NCI_CGAP_LO19, NCI_CGAP_LO16,
NCI_CGAP_LO10, NCI_CGAP_LO19, NCI_CGAP_LO16,
NCI_CGAP_LO10, NCI_CGAP_LO16, NCI_CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2725554"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
```

```
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                          RESULT 4
AI458581/c
                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 447; Conserv
                         ORGANISM
                                                                                                                                                                                                                                                                                                                                       1164 GCTGAGAGAAAAATTATCGAGAAAAAAA 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              804 CAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 CAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTT 803
                                                                                                                                                                                                                                                                                                                  36
                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGTGATCCAGGATTATCCACTGATTTATGAAATTATTTTTTTGGGAAAACACTTCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATT 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                    CCTGTGATCCAGGATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCATACTTCCTCCAGTCTTTAACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTGGTCT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAA 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACG
                                                                                                                                                                                                                                                                                                                GCTGAGAGAAAAATTATCGAGAAAAAAA 9
                                                                                                                                                AI458581 571 bp mRNA
tj97d01.x1 NCI_CGAP_Lu24 Homo sapiens
similar to gb;J03171 INTERFERON-ALPHA
                                                                                                             mRNA sequence.
AI458581
Homo sapiens
Eukaryota; M
                                                                     AI458581.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI_CGAP_Kid3 pool 1: LLAM 334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-132391), 1456008-1456775, 1500552-1505255) NCI_CGAP_Kid5 pool 1: LLAM 338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-332831, 1471368-147290, 1492104-1493255) NCI_CGAP_Lu5 pool 1: LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4 pool 1: LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1477743) NCI_CGAP_PF12 pool 1: LLAM 2457-2459, 101192-1101959, 1217928-1220615) NCI_CGAP_CO10 pool 1: LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 986759, 1101192-110195), 1217928-1220615) NCI_CGAP_CO10 pool 1: LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144594-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_LIB-NCI_CGAP_Lu5
  Metazoa;
                                                                                        GI:4311160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.2%;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 446.4; DB 79; Length Pred. No. 2.7e-99; Indels 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 79; Length 456;
                                                                                                                                                    CDNA clone IMAGE:2149441 3' RECEPTOR PRECURSOR (HUMAN);,
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1103
                                                                                                                                                                                                                                                                                                                                                                                                      37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                    Š
                                                                                                   δÕ
                                                                                                                                                    В
                                                                                                                                                                                            γQ
                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                 밁
```

밁

Ş 밁

밁 Ş 밁 γ В Ó В Š 밁 Ş

SOURCE

δ B Š

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
1059 TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAAACAGGCCTGTGATCCAGGAT 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                1119 TATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATT 1178
                                                                                                                                                      328
                                                                                                                                                                                                                                                                                                            999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820 TTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAA 879
                                                                                                                                                                                                                                                         388 GATACTGAAATACAAGCTTTCCTACTTCCAGTCTTTAACATTAGATCCCTTAGTGAT
                                                                                                                                                                                                                                                                                                                                                          448 CCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTTGGTCTGAAGAGATAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                     940 TCCGCGTACAAGCATCTGATGGAAATAACACATC-TTTTTGGTCTGAAGAGATAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                505 ATG-CAAAACTACCCAGTGTGTCTTTCCTC-AAACGTTTTCCAAAAAGGAATTT-CCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                880 ATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAAACGTTTTCCAAAAAGGAATTTACCTTC 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              562 TTTTTAAAAAGGATCCTGGAACC---ATTGGTATAATGNAACNAATACCTGACTGTGAAA
                                                                                                                                                                                                                                                                                    GATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCCTTAGTGAT
                                                  TATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATT
                                                                                                                                                      TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jun 5, 1998 this sequence version Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 571)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 425
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-*Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LU5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soares and M. Fatima Bonaldo.
97 c 106 g 194 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:2149441"
/clone_lib="NCI_CGAP_Lu24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 414.8; DB 4
Pred. No. 1.6e-91;
0; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gi:3187434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                         1058
                                                                                                                                                                                                                                                                                                                                                                                                             998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506
                                                                                                                                                                                                                                                         329
                                                                                                                                                                                                                                                                                                                                                            389
1238
                                                                                                                                                      269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      υ
Vi
```

S

8

õ

밁

밁

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
AW292342/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1239 AAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTATGTGAGAAAAACCAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATGTGAGAAAACAAAACCAGGTCAGA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGCCAGAGCACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tunor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188430.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW492342 403 bp mRNA EST 16-JAN-2000
UJ-H-BIJ-agw-a-09-0-WJ.Sl NCI_CGAP_Sub4 Homo sapiens cDNA clone
IMAGE:2725552 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail cDNA Library Preparation: M.B. Soares Lab Clone distribution: M.B. Cocker clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW292342.1 GI:6698978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer: M13 Forward
/db_xref="taxon:9506"
/clone="IMAGE:2725552"
/clone=lib="NCI_CGAP_Sub4"
/clone="IMAGE:2725552"
/clone=lib="NCI_CGAP_Sub4"
/lab_bost="Plub (Life Technologies)"
/lab_bost="Plub (Life Technologies)"
/lab_bost="rector: p773D-Pac (Pharmacia) with a modified
/note="Vector: p773D-Pac (Pharmacia) with a subtracted library
/note="Vector: p773D-Pac (Pharmacia) with a subtracted library
/note="Vector: p173D-Pac (Pharmacia) with a modified
/note="Vector: p173D-Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
```

Ş 밁 Q В Ş 밁 δÃ

밁

Ş 밁 80 밁 Š

멍

```
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                           1037
                                                                                                                                        163
                                                                                                                                                                                                                                                977
                                                                                                                                                                                                                                                                                     283
                                                                                                                                                                                                                                                                                                                                                                                                                               403 TCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATG
3
                                                                                                                                      TAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGG
                                                                                                                                                                                                                                                                                                                                                                         TCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATG
                                                                   TTCAAATGCTGAGAGAAAATTATCGAGAAAAAA 1191
                                                                                                                                                                                                                                                                                     TTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                                                                            GAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGT
TTCAAATGCTGAGAGAAAAATTATCGAGAAAAAAA 9
                                                                                                                                                                                                            TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Discovery. Genome Research 6, 791-806.]
TAG_LIB=NCI_CGAP_Lu5
TAG_TISSUE-lung
TAG_SEO-CAAC"
1 63 c 80 g 142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CloneIDs 1257096-1258631, 1469064-1470983, 1475992-1476743) NCI_CGAP_Fr22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI_CGAP_C010 pool 1 : LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 395; DB 79;
Pred. No. 1.1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                164
                                                                                                                                                                                                                                                    1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856
                                                                                                                                                                             1096
                                                                                                                                           104
                                                                                                                                                                                                                                                                                                                                                                                                                                 344
                                                                                                                                                                                                                                                                                     224
                                                                                                                                                                                                                                                                                                                         976
                                                                                                                                                                                                                                                                                                                                                            284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

RESULT AA308713 LOCUS ACCESSION VERSION KEYWORDS REFERENCE SOURCE DEFINITION AUTHORS ORGANISM l (bases 1 to 383)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Balt, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Man-Wai, C., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., White, O., Sutton, G., Brandon, R.C., Man-Wai, C., Fine, L.D., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Clayton, R.A., Cline, Titzhugh, W.M., Fritchman, J.L., Geophagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonaid, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., AA308713 AA308713.1 GI:1961043 EST. AA308713 383 bp mRNA EST 18-APR-1997 EST179523 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to interferon, alpha/beta receptor (GB:X60459), mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Mammalia;

```
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNT
                                                                                                                                                     301
                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
                                                                                                                                                                                                                                                                                                                                                               256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.2%;
Local Similarity 98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                سو
                                                                                                                                                                                                                                                                                AGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAAATCTCCTCAAAAAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGCTCCCAGATGATGGTCGTCCTCCTGGGCGCGACCCTAGTGCTCGTCGCCGTGG 75
                                            -TTGACTCATTTACACCATTTCG
                                                                                                                                                                                   ATGAAGAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCG
                                                                                                                                             ATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence wature 377 (6547 Suppl), 3-174 (1995)
12140200
On Sep 12, 1996 this sequence version replaced g1:1392985.
Other_ESTS: THC171186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bioinformatics
The Institute:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrite, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Kaymond, L., Kunsch, C., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, J., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Philippe, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="KM12SM"
/cell_line="KM12C(HCC)metastasis
/note="Vector: pBluescript SK-; specific S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="ATCC (inhost):112545"
/db_xref="taxon:9606"
/clone_lib="HCC cell line (matastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="ATCC (inhost):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="colon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 c
                                                                      397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 365.8; DB 3
Pred. No. 1.6e-79;
); Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research
, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s into mouse
Site_1: EcoF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ouse (liver)"
EcoRI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                 375
                                                                                                                                                                                                                                                                                                                                                       315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                             360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195
                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                      B
                                                                                                                                                                                                     Ş
밁
                                                    οy
                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AA258750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
   120
                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                             66 GTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCT
                                                                                                                                                                                                                                                                                                              1 GGGATCTGCGGCGG-TCCCAGATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTC
                                                                                                                                  CAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGAT
                                         CAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (195-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zr62b09.rl Soares_Nhi
similar to gb:J03171
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq.primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Sep 12, 1996 the
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA258750.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA258750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Pooled human melanocyte, fetal heart,
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:667961"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NhHMPu_S1 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERFERON-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 341.2; DB 30 pred. No. 1.7e-73; 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2ST 17-MAR-1997 cDNA clone IMAGE:667961 5'
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
```

and

ŏ

Marra, M.

Mammalia;

밁 Š В Š 망 Š

밁 õ

186

δ

В δÃ В õ

В

Length 380;

1;

Gaps

۲,

65

59

185

179

245

125

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
AA447894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
   밁
                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                Matches
                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                1056 GATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACAGGCCTGTGATCCAG 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAG 305
                                                                278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DU4 DP; mRNA EST 04-JUN-1997 zxlla06.rl Soares_tottal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786130 5' similar to gb:J03171 INTERFERON-ALPHA RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos Kucaba,T., Lacy,M., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., white,Y., Wylle,T., Waterston,R. and Wilson,R. Washd-Merck EST Project 1997
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1290666. Contact: Wilson,RK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -26m13 rev2 ET from Amersham
High quality sequence stop: 464.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA447894.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      numan.
                                                                             Similarity
                                                                                                                                                            168
                                                                Conservative
                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:786130"
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:5983749"
                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                    /lab_host-"DH10B"
                                                                             20.7%;
                                                              0
                                                                             Score
Pred.
                                                                Mismatches
                                                                             277.4;
No. 7.4
                                                        /.4e-58;
1;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further information.
                                                                                          Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contact the
                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jost, S.,
 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239
                                                              0
```

```
REFERENCE
AUTHORS
TITLE
BASE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI863225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                      COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGTATGTGAGAAAACAAAACCAGGAAATACCTCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGTATGTGAGAAAACCAAAACCAGGAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGAC 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1135299.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI863225 444 bp mRNA EST 26-AUG-1999 tz39a08.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2290934 3's similar to gb:J03171 INTERPERON-ALPHA RECEPTOR PRECURSOR (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AI863225
                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                             R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome S

Clone distribution: NCI-CGAP clone distribution i

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           High
                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI863225.1 GI:5527332
                         140
                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 420.
                  /lab_host="PH10B"
// lab_host="PH10B"
// note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall / Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall / Site_2: NotI; This library represents the normalized version of NCI_CGAP_Brn35. Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.19 kb. Tumor types include: meningioma, oligodendroglioma, astrocyt (grade II), medulloblastoma, astrocytoma (grade IV). Constructed by Life Technologies."

Constructed by Life Technologies."
                                                                                                                                                                                                                  /clone="IMAGE:2290934"
/clone_lib="NCI_CGAP_Brn52"
/tissue_type="tumor, 5 pooled (see description)"
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing Cente information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ph.D., Michael
                                                                                    astrocytoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        þe
```

Query Match
Best Local Similarity 100
Matches 271; Conservative

20.2%;

Score 271; DB 61; pred. No. 2.7e-56; 0; Mismatches 0;

Length 444; indels

0

Gaps

?

```
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T96831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 TGAGAAAACAAAACCAGGAAATACCTCTAAA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAGCACACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAGAAAACAAAACCAGGAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAATTATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTGATTTATGAAATTATTTTTTGGGAAAAACACTTCAAATGCTGAGAGAAAAATTTATCGA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T96831 269 bp mrNA EST 27-MAR-1995
ye51d09.r1 Soares fetal liver spleen lNFLS Homo sapiens cDNA c.
IMAGE:121265 5' similar to gb:J03171 INTERFERON-ALPHA RECEPTOR
                                                                                                                                                                                                                                                                                    High quality sequence stops: 210 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 687 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T96831
T96831.1 GI:735455
                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Insert Size: 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 269)
                                                                                                                                                                                                                                                    quality sequence stop: 210.
Location/Qualifiers
              /db_xref="taxon:9606"
/clone="IMAGE:121265"
                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:473810"
                                                                                                                                               /sex="male"
                                                                                                                                                            /clone_lib="Soares fetal liver spleen INFLS'
                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
    vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                   63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
AW435471/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 233; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849 TATA 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTA
                                                                                                                                                                                    Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                       451 Eckstein Medical Research
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                 Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                 Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                 On Jul 8, 1999 this
                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                 discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                          Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia)
                                                  /clone_lib="UI-R-BJ0p"
                                                                                /db_xref="taxon:10116"
                                                                                               /strain-"Sprague-Dawley
                                                                                                              /organism="Rattus norvegicus"
                                                                                                                                             Location/Qualifiers
                                                                /clone="UI-R-BJ0p-afu-h-02-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.3%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                     æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                      Building
   (Pharmacia) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
```

modified

```
611 GACTACTTATTGTCTAAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCTTTCCAAGTTCAGTGGGCTCCACGCCTTTTTAAAAAGGGATCCGGGGAAACCATTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCTTT-CAAGTTCAGT-GGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAAACCATTTG 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGCAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATATGCAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATAT 730
                                                                                                                                                                                                                                                                                                                                                                                         UI-R-BJOp-afu-h-02-0-UI.sl UI-R-BJOp Rattus norvegicus UI-R-BJOp-afu-h-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. S1 c 49 g 75 t 1 others
                                                                                      sequence version replaced
                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                   approaches
  Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
City,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                     ៩
                                                                                                                                                                                     facilitate
  IA 52242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2000
                                                                                                                                                                                                                                                      Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                   gene
  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           clone
```

```
ACCESSION
VERSION
KEYWORDS
SOURCE
     JOURNAL COMMENT
                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA168022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 282; Conserv
                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1123 CACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATC 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAATACAAGCTTTCCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCAT 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGTACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATA 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATG 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAATGGGACCACGCATTTGCAAACATGACCTTCAAAGCACAGTGGATCCCTGTCTATT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTT 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACTCATTTACGAAGTCATCTTTTGGGAAAACACTTCCAATACTGAGAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCAAAAATACACTCTCCTTCCTCCCGGTCATTGCTGTCACCCCCACGGGGGACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTACAAGCCTCAGATGGAAATAACACGTCCTTTTGGTCTGAAGAGAAACTTATTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAGACTACACACTGTGTATCTCCTCGAGAGACTTTCCACACAGGAACTTTCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                         AA168022 563 bp mRNA EST 12-FEB-1997 ms66c03.rl Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:616516 5' similar to gb:M89641 Mus musculus interferon alpha/beta receptor (MOUSE); mRNA sequence
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 563)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuqu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Tholdson, M., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
  Unpublished (1996)
On Sep 12, 1996 this
                                              Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                            Theising, B., Wylie, T., Lennon, G.,
                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                AA168022.1
                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ0p library is a subtracted library derived from the UI-R-AA1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, UI-R-AB1, and UI-R-AG1 libraries: These libraries represent tissues from rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, and ventricle at 16.5 dpc, AV canal at 15 dpc, and ventricle at 13 dpc. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6. 791-806, 1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_LIB-UI-R-BJOp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :_TISSUE=AV canal at 16.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                · 116 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 185; DB 81;
Pred. No. 3.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
  version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTGTAAGGACAGCAAATGTAATG
                                                                                            Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110;
replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                       Dietrich, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.
```

S 밁 S 밁 Š В Š 밁 S 밁 Š 밁 Š

RESULT

TITLE

RESULT

```
δÃ
                                                                                                                                             γQ
                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                               망
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                       Š
                                                          밁
                                                                                                                    융
                                                                                                                                                                                밁
                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 323
                                                                                                                                                  1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                              1040
                            1220 ACTGACTGTATATTGTGTGAAAGC 1243
                                                                                                                                                                                                                                             258
                                                                                                                                                                                                                                                                           980
                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                   138
476
                                                                                                                                                                                                                                                                                                                                    920
                                                                                                                                                                                                                                                                                                                                                                                                                                                            800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       743 CCAAAATCAGAACTATGTTCTTAAATGGGATTA---TACATATGCAAACATGACCTTTCA 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                     CACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATTTTTTGGGAAAAACACTTC 1155
                                                                                                                                                                                                                                                                                                                        CCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCAAGGAAGAGCTATGTCCTGAAATGGGACTACATTGCGTCTGCAGACGTGCTCTTCAG
                                                                                         AAATGCTGAGAGAAAATTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACC 1219
                                                                                                                                                                                TGTCACCGCCATGAGTGACACCTTGCTTGTTTATGTC-------
                                                                                                                                                                                                             CATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAA 1099
                                                                                                                                                                                                                                             GTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCCAGTCTTTAA 1039
                                                                                                                                                                                                                                                                                                                                                                 ACCAATACCAACCTGTGCAAATGTCCAGACTACGCACTGTGTCTTTTCTCAAGATACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAA
                                                                                                                     CTGTCAGGACAGCACATGTGATGGACTCAATTACGAAATCATCTTTTGGGAGAACACTTC
                                                                                                                                                                                                                                                                                                      CTACACAGGAACGTTCTTCTCCATGTACAAGCCTCAGAGGGAAATCACACATCCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                              ACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                             GGCACAGTGGCTTCCTGGCTATTCAAAAAGCAGTTCTGGAAGCCATTCAGATAAATGGAA
                                                          CGATACTAAGATAAGCATGGAGAAGGATGGCCCAGA-GTTCACGCTCAAGAGCTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further MGI:377340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:616516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #937317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lssue_type="carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lone_lib="Stratagene mouse embryonic carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 174.4;
Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                  ----- AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                   356
                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                        979
                                                                                                                                                                                                                                                                                                                                                                                                 919
                                                                                                                                                                                                                                                                                                                                                                    197
                                                                                                                                                                                                                                                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                            475
                                                                                                                       416
                                                                                                                                                                                                                                                                                                         257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cel1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ω</u>
```

```
ACCESSION
VERSION
KEYWORDS
     KEYWORDS
SOURCE
ORGANISM
                                                      ACCESSION
VERSION
                                                                                                     LOCUS
DEFINITION
                                                                                                                                    RESULT 14
AI178178/c
                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ684103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                553 TAGAAGAAAGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGA 612
                                                                                                                                                                                                     341
                                                                                                                                                                                                                                                              281 CTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATA
                                                                                                                                                                                                                                                                                  613 CTACTTATTGTCTAAAAGTTAAAGCAGCACCTACTTACGTCATGGAAAATTGGTGTGTCTATA 672
                                                                                                                                                                                                                                                                                                                                 221 TATAGGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGA 280
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                  GTCCAGTACATTGTATAAAGACCACAGTTGAAAATGA 709
AII78178

AII78178

EST221843 Normalized rat p clone RPLCN21 3' end, mRNA AII78178

AII78178

EST.

Rattus sp.

Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2162 row: L column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ684103 528 bp DNA GSS 28-JUN-1999
HS_2162_B1_F08_T7C CIT Approved Human Genomic Sperm Library D
Sapiens genomic clone Plate=2182 Col=15 Row=L, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ684103.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ684103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ıuman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 528
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: sperm; Vector: pBeloBACll; BAC Clones
E-Coli DH10B"
85 c 87 g 172 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-2162 Col=15 Row-L"
/clone_1ib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:5260086
                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%;
95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                  mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                Score 145.8; DB 85;
Pred. No. 1.4e-25;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 g
                                                                                                                    mRNA
                                                                                                     Bento
                                                                                                   EST
o Soares
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                 Rattus sp. cDNA
                                                                                                                   20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    528;
                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holzman,T.,
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
```

```
RESULT 15
CNS0039G/c
                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
COMMENT
                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              843 CATTTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCCTCCGGTCATTGCTGTCACCCCCACGGGGGACTCCTTGCTTTATGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACCTGAAATACAAGCTTTCCTA 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTCAGACAAATGGAAACCAATACCTACCTGTGCAAATGTGCAGACTACACACTGTGTA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAACACGTCCTTTTGGTCTGAAGAGAAAACTTATTGATTCTCAAAAATACACTCTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCCTCGAGAGACTTTCCACACAGGAACTTTCTTCTCCGTGTACAAGCCTCAGATGGA 146
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                          AL063921
AL063921.1
                                                                                                                                                                                                                                                                                                                                                                CNS0039G 1101 bp DNA GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712, Medical Center Drive,
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tlgr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                    fly),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat Genome Project:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 310)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M.,
Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Index
                                                                                                                                                                                                                                                                                                                                                genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus sp."
/db_xref="ATCC (inhost):2033250"
/db_xref="haxon:10118"
/clone="RPLCN21"
/clone="RPLCN21"
/clone="Normalized rat placenta, Bento, Notee="Organ: placenta; Vector: pT7T3Pac;
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .310
                                                                                                                                                                                                                                                                                                            GI:4941778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation of a Rat EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 128.8; DB Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20850,
                                                                                     segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quackenbush, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1042 WWWWWWATWDTWWDKWWWWATAAKTDTAWTWWRTAWRADWAGRDRGAGKRDRDAATDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      862 WGWADADWWTWDAAADDWWADDRWDAWANKWDDAWAWGARTADRRDWGDRAGKRGGARKR 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            922 KADDDCAGDKDDGKKDADDDTDGTKDDDDKDKWDDWDKAKGTWGDATWAWAATDWWW 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCT 166
                                                                                                           562
                                                                                                                                                              581
                                                                                                                                                                                                                    622
                                                                                                                                                                                                                                                                                                                            682
                                                                                                                                                                                                                                                                                                                                                                               461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           982 GAGRRDGGRKRKDKKDRKDGDDDKKGGKKKKAAKAAKWATKWWDDWDWDKDWKWDGAKDR 923
                                                                                                                                                                                                                                                                    742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATT--ACTAGTACCAAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 4.4%; Score 58.6; DB 82; Local Similarity 18.9%; Pred. No. 0.00034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
TWAAWTAAAWAAAAAWAATTTTTTTTT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDRKRADDKRDAADDRDDAATWTTWTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDR 743
                                                  ACTACTTACGTCATGGAAAATTGGTGTCTAT 671
                                                                                                           CAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAAGTTAAAGCAGC 640
                                                                                                                                                                                                              WAKWDWKTRADRWDRWAADTWTDARKADRDWAKARAWRARRDRARAARADRRWTTKGKTT
                                                                                                                                                                                                                                                                                                                          RDRATWDRTDAWWADAAWWTTTDTDTDDWDKRDRRRKGARRRRTTARAAWDWWTWKAWD
                                                                                                                                                                                                                                                                                                                                                                            CATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                     DRAGTAGRKWRRTWKRRWKRRDTRWDDADADDTARDDRRRRGDDGADAGKGKKTGRKRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAG----TGATACA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="end : TET3"
64 c 131 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Brosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone="BACR08K10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                    563
                                                                                                                                                                                                                                                                                                                                                                                                                                     683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      983
                                                                                                                                                                                                                                                                                                                          623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
```

뮻 Ş 밁 Ş ₽

Ş

Search completed: June Job time: 16908 sec

1, 2000, 10:34:30

á

밁

Š 밁 B S 당 Š

```
PIR; S14930; S14930.
PIR; S26402; S26402.
PIR; A34425; A34425.
HSSP; P02833; ISAN.
                       DNA_BIND
VARSPLIC
VARSPLIC
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K., Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.; "Lineage-restricted expression of homeobox-containing genes in human hematopoletic cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowney P., Corral J.C., Detmer K., Lebeau M.M., Deaven L., Lawrence H.J., Largman C.;
Lawrence H.S. Largman C.;
"A human Hox 1 homeobox gene exhibits myeloid-specific expression alternative transcripts in human hematopoietic cells.";
Nucleic Acids Res. 19:3443-3449(1991).
                                                                                                                                                                                                                                                                                           EMBL; X58430; -; NOT_ANNOTATED_CDS.
EMBL; M30599; AAA386066.1; -.
EMBL; S69027; AAD14030.1; -.
EMBL; S69029; AAD14031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acampora D., D'Esposito M., Faiella A., Pannese M., Migliaccio E., Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.; "The human HOX gene family."; Nucleic Acids Res. 17:10385-10402(1989).
                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>+</del> <del>+</del> <del>+</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 404-486 FROM N.A. MEDLINE; 90046832.
             CONFLICT
                                                                                       DOMAIN
                                                                                                                             DOMAIN
                                                                                                                                         Transcription
                                                                                                                                                                   PFAM; PF00046;
                                                                                                                                                                           PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                      PRINTS; PRO0024; HOMEOBOX
                                                                                                                                                                                                                  MIM; 142957
                                                                                                                                                                                                                                TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94145486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 435-473 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 422-487 FROM N'A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl.
                                                                                                                                                     iomeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: TWO ISOFORMS; HOX-A10-1/PL1 (SHOWN HERE)
HOX-A10-2/PL2; ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE ABD-B FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90098876.
                                                                                                                                                 DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                            T01713; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acad: Sci. U.S.A. 86:8536-8540(1989).
             181
219
227
366
422
423
403
435
437
                                                                                                                         regulation; Alternative splicing.
                                                                                                                                                                   homeobox;
                         192
223
236
371
481
402
405
435
 54733
 ¥.
         DSL -> MCQ (IN ISOFORM HOX-A10-2).
L -> S (IN REF. 2).
L -> F (IN REF. 2).
R -> P (IN REF. 2).
                                                            MISSING (IN ISOFORM HOX-A10-2)
                                                                           HOMEOBOX
                                                                                      POLY-ALA.
                                                                                                    POLY-PRO.
77C6F675916552F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                γď
                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e
E
                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                             ö
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on ::
          333322222222111111
333222222222222244
43220987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
                                                                             100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May 31, 2000, 19:06:34; Search time 42.08 Seconds (without alignments) 225.716 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-240-675-2_COPY_27_427
2141
1 GKNLKSPQKVEVDIIDDNFI....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188963 seqs, 23686106 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKNLKSPQKVEVDIIDDNFI.....AHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                           B
     R2184495
R11958
R111958
R2184496
R2184486
R2184486
R21804
W211804
W211804
W211807
W211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ᅜ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188963
Plasmid pBABLUE hu
Gamma-IFN-R-GBP 13
Rat receptor tyros
Human LDL receptor
Gamma interferon r
Deleted in Colorec
Human Down syndrom
Human Down syndrom
Soluble human inte
Rabbit LDL recepto
Interleukin-10 rec
Mouse IL-10 recept
                                                                                                                                                                                                                                                                                                                          IFN-gamma receptor
Zcytor7 cytokine r
Human IFN-gamma ac
IFN-gamma receptor
Human cytokine rec
Human cytokine rec
Human cytokine rec
Gamma interferon r
Gamma interferon r
Extracellular doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete interfero Sequence of a soul Human interferon r Human IFN receptor Spliced-deleted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFN receptor extra Spliced-deleted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble interferon
Sequence of a soul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRFB4 protein. New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembranal int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human alpha-interf
```

ť		43			_	_	_		36	
,	103	104.5	104.5	104.5	104.5	105.5	105.5	107	107	107
	4 .	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5. O	5.0
į	л л -	1447	600	600	596	1370	878	753	427	426
F	۔ د	ب د	ш	سر	ب	4سو	Н	Н	μ	ᆫ
3000	24 / CCG	R68553	R92526	R78610	R78616	P60005	R78608	W83927	W24973	W09822
timinati (D+) +O+ nac	TENTAL TOTAL TENTAL	Deleted in colorec	Fas antigen #1. Im	Expression vector	Expression vector	Sequence encoded b	Murine IL-3 recept	Human T85 protein.	Human interleukin-	Human interleukin-

## ALIGNMENTS

Qy 301 EIQAFLLPPVFNIRSLSDSFHIY	Qy 241 KRNPGNHLYKWKQIPDCENVKTT(	Qy 181 LTSWKIGYYSPYHCIKTTVENELJ 	Qy 121 SPGTKDSVMWALDGLSFTYSLLII	Qy 61 CNFSSLKLNVYEEIKLRIRAEKEI	Qy 1 GKNLKSPQKVEVDIIDDNFILRWI 	Query Match  Best Local Similarity 100.0%;  Matches 401; Conservative	R14487 ID R14487; AC R14487; AC R14487; AC R14487; DT 16-JAN-1992 (first entry) DE Soluble interferon-alpha/bett KW IFN; autoimmune disease; gra: OS Homo sapiens. PN FR2657881-A. PD 09-AUG-1991. PF 05-FEB-1990; O01298. PA (EUBI-) LAB EURO BIOTECHNO. PI Eld P, Gresser I, Lutfalla G. PI Tovey MG, UZe G; DR N-PSDB; Q1439. PT New water-soluble polypeptide PT New water-soluble polypeptide PT spata - used to treat e.g. lu PT aplastic anaemia, diabetes me PS Claim 2; Page 45; 52pp; Frence CC The transmembrane and cytopla CC have been deleted to obtain a CC receptor. Potentially immunos CC are also claimed as are hybr: CC are also claimed as are hybr: CC see also Q14240. SQ Sequence 436 AA;
EIQAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTPVIQDYPLIYEIIFWENTSNAERKIIE 360	KRNDGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLKVQASDGNNTSFWSEEIKFDT 300 	TSWKIGVYSDYHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFL 240 	SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180	NFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120 	GKNIKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFDYOKTGMDNWIKLSGCONITSTK 60	Score 2141; DB 1; Length 436; Pred. No. 2.3e-185; 0; Mismatches 0; Indels 0; Gaps	indard; Protein; 436 AA.  (first entry) (refron-alpha/beta receptor.  A.  A.  () () () () () () () () () () () () ()

```
B 5
                                                                                                                                                            δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                             Š
                                                                                                                                 밁
                                                                                                                                                                                    В
                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                               닭
                                                                                                                                                                                                                                                   δ
               Ş
                                             밁
                                                              õ
                                                                                           밁
                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                Š
 멂
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
with a hi
                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned CDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases and transplant rejection Claim 2; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Water soluble polypeptide(s) strongly bind interferon(s) and beta - useful as immunosuppressants, for treating au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tovey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R28495 standard; Protein; 436
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 APR-1991; F00318.
17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
ELID P. Gresser I, Lutfalla G, Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1991;
                                                                    301
                                                                                           267
                                                                                                                                         207
                                                                                                                                                               181
                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                  241
                                                                                                                                                                                                            121
 387
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                              GKNLKSPOKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                          KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                       KKTDYTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                              401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92-382110/46.
                                                         EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                              EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                         Score 2141; DB 1;
Pred. No. 2.3e-185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mogensen
                                                                                                                                                                                                                                                                                                                               0
                       401
                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           auto:immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha
                                                                                                                                                                                                                                                                                                                                                      436;
                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                   146
                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386
                                              386
                                                                     360
                                                                                            326
                                                                                                                  300
                                                                                                                                        266
                                                                                                                                                              240
                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                               0
```

```
Ş
                                                  밁
                                                                      δÃ
                                                                                                   밁
                                                                                                                          Š
                                                                                                                                                       밁
                                                                                                                                                                           δÃ
                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                γQ
                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                    Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 2141; DB 1; Best Local Similarity 100.0%; Pred. No. 3.3e-185; Matches 401; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis Disclosure; fig 4; 30pp; French.
This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 144 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-1991.
19-OCT-1990; 1
20-OCT-1989; 1
(CNRS) CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mogensen KE, Uze G
WPI; 91-148740/20.
N-PSDB; Q11701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human alpha-interferon Human alpha IFN; IFN aç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9105862-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R11958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1991
 387
                                                                                                                             241
                                                                                                                                                                                 181
                                                                                                                                                                                                          147
                        361
                                                  327
                                                                          301
                                                                                                    267
                                                                                                                                                       207
                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                              GKNLKSPQKVEVDIIDDNEILRWNRSDESVGNVTESEDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                     CNESSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                               SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                             CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                targetting.
                                                                                                                  KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                        KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                      KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                         SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FR-013770.
S CENT NAT RECH SCI.
Uze G, Lutfalla G, Gresser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rferon receptor protein.
IFN agonists; antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti tumour
                         401
 427
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                 240
                                                                                                                                                                                                            206
                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                              146
                                                                                                      326
```

R14488 ID R AC R

R14488 standard; R14488;

Protein;

B

RESULT

```
δÃ
                                                                                                                                                       밁
                                                                                                                                                                            õ
                                                                                                                                                                                                     밁
                                                                                                                                                                                                                       Ñ
                                                                                                                                                                                                                                              멍
                                                                                                                                                                                                                                                                    ş
                                                                                                                                                                                                                                                                                              용
                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         용
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 401; Conserv
                                   R28496 stand
R28496;
31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also 014239.
31-MAR-1993 (first entry)
Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EUBI-) LAB EURO BIOTECHNO
Eid P, Gresser I, Lutfalla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-1992 (first entry)
Complete interferon-alpha/beta receptor.
IFN; autoimmune disease; graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q14240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                      361
                                                                                                                                                            327
                                                                                                                                                                                 301
                                                                                                                                                                                                        267
                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                            بر
                                                                                                                                                       KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                          CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                 KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                     KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                         CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                   GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91-319778/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MG, Uze G;
                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 001298.
FR-001298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label transmembrane
458.557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                           000
                                                          557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Į,
                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2141; DB 1;
Pred. No. 3.3e-185;
); Mismatches 0;
                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection; histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                               360
                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                266
                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
RESULT
R42635
ID R4
AC R4
AC R4
DT 20
DE HI
KW IE
KW CC
KW CC
KW PS
KW 1M
OS HC
FT dd
                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                             γQ
                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases and transplant rejection

Claim 3; Fig 2; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100
Matches 401; Conservative
                                           Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythemato psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1992.
17-APR-1991;
17-APR-1991;
                                 Homo sapiens.
                                                                                                                                                               R42635 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Water soluble polypeptide(s) strongly bind and beta - useful as immunosuppressants, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EUBI-) LAB EURO BIOTECHNOLOGIE.
Eid P, Gresser I, Lutfalla G, Meyer F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tovey M, Uze G;
                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                   327
                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                              EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE 360
                                                                                                                                                                                                                                                                                                                                                                                KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                     KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                 KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0/46.
Location/Qualifiers
1. .436
                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2141; DB 1;
Pred. No. 3.3e-185;
Mismatches 0;
                                                                                                                                                                 ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nd interferon(s) alpha
for treating auto:immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                               erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                   266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
```

```
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
RRESULT
RR75356
ID RR
AC RV
AC AC RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δŌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EUBI-) LAB
Benoit P, M
WPI; 93-3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-563487-A.
06-OCT-1993.
31-MAR-1992;
31-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neutralising activity against human type I interferon, used for therapy and diagnosis pisclosure; Fig 3; 21pp; English. Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human sequence are claimed. The antibodies are useful for treatment prophylaxis of disorders involving cell proliferation and/or v
                                                                                                                                                                                                                                        R75356 standard;
R75356;
16-OCT-1995 (fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; R42635.
Monoclonal antibody
                                     W09507716-A.
23-MAR-1995.
16-SEP-1994;
17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                       Human IFN receptor.

IFN receptor; interferon receptor; interferon-alpha; interferon.beta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection.
   (EUBI-)
Benizri
                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                             387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                                                                                    327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I-) LAB EURO BIOTECHNOLOGIE IT P, Maguire D, Meyer F, 93-312951/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIQAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                           KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                      sapiens
                                                                                                                                                                                                                       IFN receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100
01; Conservative
   EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557
 4; E03114.
3; EP-402279.
B EURO BIOTECHNOLOGIE 9
Tovey MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400902.
EP-400902.
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
                                                                                                               1. .436
/label=
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ៥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - extracellular_domain
"soluble, immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
                                                                                                                   Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon t
t human type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SA.
Plavec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core 2141; DB 1; red. No. 3.3e-185; Mismatches 0;
                         SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type-I receptor

i interferon, u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tovey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                form
                                                                                                                                                                                                                                                                                                                                                                                                                  401
                                                                                                                                                                                                                                                                                                                                                                                 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of IFN-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NG
MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r - having
used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human
an IFN-R
nt and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
SCCCCPTTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QY
                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                           멇
 밁
                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-131187/17.

N-PSDB; Q86458.

Compsn. of monoclonal antibodies against interferon useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.
The amino acid sequence of human interferon class I given in R75356. A recombinant soluble form of the domain of this receptor (R71723) has been used to ra immunomodulatory monoclonal antibodies.

Sequence 557 AA;
                                                               AU9475977-A.
11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES & DEV C
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                      Key
domain
                                                                                                                                                                                                  spliced-deleted
Interferon alph
New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon (Example 2; Fig 7; 46pp; English. Novel splice-deleted interferon alpha-receptor (IFNAR) form 1 (W21805) is characterised by a new domain (5) which follows an
                                             Abramovich C, Ratovitski WPI; 95-200634/27
                                                                                                                                                                                                                    W21805;
23-SEP-1997
                                                                                                                                                                                                                                        W21805
                                                                                                                                  domain
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                       387
                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                            327
                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                      207
                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                           147
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                          EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                     EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                 KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                           KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                  alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                  /label= Extracellular_dc
/note= "comprises amino
transmembranal IFNAR"
428. 434
                                                                                                                                                                                                            interferon
                                                                                                                                                                        Location/Qualifiers
1. .427
                                                                                                                                                                                                                                        Protein;
                                                                                                                         /label=
                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.8%;
                                                                            8
                                                                                                                          S_domain
                                                                                                                                                                                                                                         434
                                                                           LTD.
                                                         'n
                                                                                                                                                                                                    alpha-receptor IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2137; Di
Pred. No. 7.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                         ₿
                                                          Revel
                                                          Z
                                                                                                                                                      _domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
'.6e-185;
                                                                                                                                                       1-427
                                                                                                                                                                                                                                                                                                            401
                                                                                                                                                                                                                                                                                         427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor is extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                        of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                 360
                                                                                                                                                                                                                                                                                                                                                                     326
                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

```
WATEROUTH WATERO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end-deleted extracellular domain when compared to transmembranal IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNS alpha and beta in cells, telssues and organisms, or for diagnostic purposes.
                                                                                                                                          11-MAY-1995.
20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA) YEDA RES 6 DEV CO LTD.
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembranal interferon alpha-receptor Interferon alpha-receptor; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W21804 standard; Protein; W21804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
  New mammalian soluble interferon alpha-receptor forms inhibiting, modulating or modifying the activities of Disclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR)
                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                               Abramovich C, Ratovitski E,
WPI; 95-200634/27.
                                                                                                                                                                                                                                                                       AU9475977-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 400; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                  /label=
437. .45
                                                                                                                                                                                                                                                                                                                                        /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                         /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.8%;
                                                                                                                                                                                                                                                                                                                    . 557
                                                                                                                                                                                                                                                                                                                                                               .457
                                                                                                                                                                                                                                                                                                                                        Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                      Extracellular_domain
                                                                                                                                                                                                                                                                                         Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2136; DB 1;
Pred. No. 6.5e-185;
0; Mismatches 1;
                                                                                                                        Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                          interferon(s)
                                                                        used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

```
Q
                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    皮
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ននននននន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 400
                                                                                                            16-SEP-1994; E03114.
17-SEP-1993; EP-40279.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE S
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
N-PSDB; 086457.
                                                                                                                                                                                             Homo sapiens.
W09507716-A.
23-MAR-1995.
Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.2A-2B; 105pp; English. A recombinant soluble form of the human interferon class I receptor protein extracellular domain, given in R71723, was expressed in either E. coli or COS cell hosts. The protein was used to raise immunomodulatory monoclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          purposes
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                                                                                                                   IFN receptor extracellular domain.
IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulato
                                                                                                                                                                                                                                                                                                      R71723 standard;
                                                                                                                                                                                                                                                                             16-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                           387
                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                            EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                        KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                              EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity 99.8
400; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2136; DB 1;
Pred. No. 9.4e-185;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                        ζ
                                                                                                                                                         SA
                                                                                                                                                                                                                                       immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                               386
                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
```

Query Match
Best Local Similarity
Matches 398; Conser

Conservative

99.6%;

Score 2132; I Pred. No. 1.5e 3; Mismatches

DB 1; L.5e-184; 0

Length 436;

0

Gaps

```
WARESULT WAR
             Inhibiting, modulating or modifying the activities of interferon(s)

PS Example 3; Fig 7; 46pp; English.

CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2

CC (W21806) is characterised by a double deletion when compared to

CC characterised by a double deletion when compared to

CC shortened by 6 amino acid residues and is followed by a truncated

CC intracellular domain. There is no transmembrane region. The amino

CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.

CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR

CC splice-deleted forms 1 (see also W21805) and 2 may regulate the

CC antagonists or by regulating IFN activities. They can be expressed

CC in host cells and used to inhibit, modulate or modify the

CC activities of IFNs alpha and beta in cells, tissues and organisms,

CC corrections of the composes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                           AU9475977-A.
11 -MAY-1995.
20 - OCT - 1994: 075977.
24 - OCT - 1993: IL - 107378.
(YEDA) YEDA RES & DEV CO LTD.
(ABRAV) ABRAMOVICH C.
ADTAMOVICH C. RATOVITSKI E. R
MPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spliced-deleted interferon alpha-receptor Interferon alpha-receptor; IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W21806;
23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W21806 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKNLKSPQKVEVDIIDDNEILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKTOVTVPNLKPLTVYCLKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
     diagnostic purposes 
ce 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Intracellular_domain /note= "comprises amino acid: transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Extracellular_domain note= "comprises amino acid residues 422-427 of transmembranal IFNAR" 420. . . 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481-557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
          PS Claim 2; Page -; 79pp; English.

CC This sequence is the human CRFB4 sequence, DNA encoding it is used in the crecombinant DNA (I) of the invention. (I) comprises a sequence (S1) CC encoding the interleukin-10 (IL-10) receptor (ILLOR) and a sequence (S2) encoding the interleukin-10 (IL-10) receptor (ILLOR) and a sequence (S2) concoding CRFB4, both operably linked to expression control sequences. CC cells containing (I) may be used to identify agonists/antagonist of IL-10. Agonists are potentially useful, e.g. for preventing allograft crejection, as vaccine adjuvants, for treatment of photosensitivity. CC infiammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, and crivity useful for increasing immune responses against tumours, and continuous parasites (especially intracellular pathogens) and CC for preventing organ rejection. A vector containing (I) is used to creatore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses a dysfunctional ILlOR and is able to bind IL-10 but not to transduce a csignal. Antisense CRFB4 sequences (especially ribozymes), can inhibit CL IL-10 activity in cells. Antibodies specific for CRFB4 are used to company the company of the company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-1997; U12455.
17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
Kotenko SV, Pestka S;
WPI; 98-110590/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection; vaccine; photosensitivity; inflammation; autoimmune disease; septic shock; immune response; organ rejection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRFB4 protein CRFB4; interl
                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA - comprises sequences encoding interleukin-10 and CRFB4 linked to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V19874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W52296 standard;
                                                                                                                                                                                                                                                                                                                                                                                  rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9802542-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thes 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNIPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2084;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
3.9e-180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۲.
```

```
RAESULA RAESUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ភិនិនិង
                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                             from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be may be used to treat pathological conditions associated with endogenous IFN-gamma production.

Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA. Agonists/antagonists may be administered parenterally, orally or rectally especially by intravenous injection or directly into a tumour or allograft.
                                                                                                                                                                                                                                                                                                                                                                    Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage Claim 3; Fig.2A; 86pp; English.

The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BOEH/) BOEHNI R.
(HEMM/) HEMMI S.
Aquet M, Boehni R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFN-gamma receptor beta-subunit.
Interferon-gamma receptor beta subunit;
interferon-gamma-antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aguet M, Boehni F
WPI; 95-224321/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1994; U14277
09-DEC-1993; US-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09516036-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R75782 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 DRNKAGEWSEPVCEQTTHDETVP
                                                                             y Match 9.3%;
Local Similarity 30.1%;
hes 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSWKIGVYSPVHCIKTTVENELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      090808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- Extracelular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abel- Transmembrane_anchoring_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                           ; Score 199; DB 1; 1; pred. No. 3.5e-10; 38; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 220; DB 1;
Pred. No. 4.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muIFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
```

Ş

63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS

121

96

156

LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT

4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62

LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD

밁

97

δÃ

Matches Query Match Best Local

85; Similarity

Conservative

75;

Score 180; DB 1; Pred. No. 3.8e-08; 5; Mismatches 166

166;

66;

Gaps

15;

Length 553; Indels

8.4%;

В

```
WRESULT TO THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                        PT Novel human Zeytor7 DNA encodes a type 2 cytokine receptor - useful for treating renal, neural, pancreatic and prostatic diseases SC laim 1; Pages 55-59; 72pp; English.

Claim 1; Pages 55-59; 72pp; English.

Chis represents the Zeytor7 cytokine receptor. Zcytor7 is a ligand-binding receptor polypeptide and is a novel member of the type 2 cytokine receptor family (CRF2). An expression vector containing the Zcytor polynucleotide, operably linked to transcription promoter, a sequence encoding a transmembrane and intracellular domain, or both, and a transcriptional terminator can be used to transform host cells for the transcriptional terminator and be used to transcriptions of the Scytor7 gene and to isolate ligands binding to it. Zcytor7 is preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Agonists of Zcytor7 can be used to stimulate proliferation and differentiation of cell in these organs. The antagonists and agonists can also be used in the treatment of renal, neural, pancreatic and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams RL, Farrah T. Whitmore TE; WPI; 98-480798/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1998; U03029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
(ZYMO ) ZYMOGENETICS INC.
(ZYMO ) ZYMOGENETICS INC.
NAMES RL, Farrah TM, Jelmberg AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9837193-A1.
27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zcytor7 cytokine receptor polypeptide.
Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas Zcytor7; cytokine receptor family; CRF2; prostate tissue; nervous tissue; type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue; agonist; cell proliferation; renal disease; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W79159 standard; Protein; W79159;
   Sequence
                                   diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V57515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neural disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY -- KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF----IDGSWHRLLEPNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te= "extracellular (ligand-binding) domain:
    sequence claimed in claim !"
    .553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kho CJ, Lok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreas;
tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
```

```
RESULT 15
R71035
AC R71035
AC R71035
DT 11-CFF
DE HUMAN
OS HOMO S.
PN W05905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
  밁
                                             δÃ
                                                                                                      밁
                                                                                                                                                   Ş
                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                        용
                                                                                                                                                                                                                                                                                                                                                                      Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-1995.
22-AUG-1994; U09438.
20-AUG-1993; US-110119.
(UYNE-) UNIV NEW JERSEY.
Cook JR, Donnely RJ, Em.
Pestka S, Schwartz B, So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suppressing tumours in mammals with accessory factor 1 (AF-1) for interferon gamma, specifically induction of class I HLA antigens, including use of AF-1 DNA in gene therapy Disclosure; Fig 21A; 114pp; English.

The sequence is that of human interferon-gamma accessory factor-1. Incorporation of AF-1 into immune and tumour cells re-establishes normal function with elimination of malignant cells. Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q84697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09505847-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R71035 standard; Protein; R71035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 95-106679/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IFN-gamma accessory facto
Interferon-gamma; AF-1; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             771035;
11-OCT-1995 (first entry)
Accessory factor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 VIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV--TVPNLKPLTVY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278
                                                                                                                                                                                                                  141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 PPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESLSRTIPPDKTVIEY 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213
                                                      214
                                                                                                         194
                                                                                                                                                               160
                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
254 GTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE 292
                                                                                                                                                                                                                                                                                                                           85
                                                                                                                                                                                                                                                                                                                                                                                 52
                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LKSPOKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYOKTGMDNWIKLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FLFSVMGYSIYRYIHVGKEKHPANLI---------LIYGNEFDKRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCTQITATECDFTAASPSAGFPMDFNV----TLRLRAELGALHSAWVTMPWFQHYRNVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APEKWKRNPEDLPVSMOQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT
                                                                                                   SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMADASTELQQVILISV
                                                                                                                                                                                                            GPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR
                                                                                                                                                                                                                                                               GPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS 159
                                                                                                                                                                                                                                                                                                                                                                         GCQNITSTKCNFSS------LKLNVYEEIKLRIRAEKENT-SSWYEVDSFTPFRKAQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                  LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFKYTDSK-----WFTADIMSIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V----PAEKIVINFITLNISDDSKIGHQDMSLLGKSSDVSSLND------PQPSGNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLRVQASDGNNTSFWSEEIKFDTEI --- QAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
                                                                                                                                                         RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVENELPPPENIEVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGTK------DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                       -----QNQNYVLKWDYTYANMTFQVQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%;
22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Emanuel S, Soh J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 148; DB 1; Length 337;
; Pred. No. 1.4e-05;
49; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kotenko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mariano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĭM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                         253
                                                                                                                                                                                                            1,93
                                                                                                                                                                                                                                                                                                                        140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
```

Search completed: June 1, 2000, 00:40:12 Job time: 20018 sec

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the r
score greater than
and is derived by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.
100.
100.
100.
97.
22.
20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62 'Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145308 segs, 14437401 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GKNLKSPQKVEVDIIDDNFI.....AHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-675-2_COPY_27_427
2141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/18a/5A_COMB.pep:*
/cgn2_6/ptodata/1/18a/5B_COMB.pep:*
/cgn2_6/ptodata/1/18a/ECTUS_COMB.pep:*
/cgn2_6/ptodata/1/18a/pcTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000, 00:00:26; Search time 23.82 Seconds (without alignments)
243.048 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                  US-08-328-256-11
US-08-328-256-12
US-08-328-256-10
US-08-471-454-2
US-08-471-453-2
US-08-471-453-2
US-08-471-453-2
US-08-471-277-3
PCT-US94-11277-4
PCT-US94-11277-4
PCT-US94-11277-6
PCT-US94-11277-6
PCT-US94-11277-6
PCT-US94-11277-6
PCT-US94-11277-6
PCT-US94-11277-6
PCT-US94-11277-6
PCT-US94-11277-6
PCT-US94-11277-6
US-08-943-087-18
US-08-943-087-18
US-08-943-087-24
US-08-943-087-24
US-08-943-087-24
US-08-943-087-24
US-08-943-087-24
US-08-943-087-24
US-08-943-087-38
US-08-943-087-38
US-08-943-087-38
US-08-943-087-38
US-08-943-087-38
US-08-943-087-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, App.
Sequence 2, Appl.
Sequence 10, App.
Sequence
                  Sequence
                                                                                                                     Sequence
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                      e 2, Appli
e 2, Appli
e 3, Appli
e 4, Appli
e 4, Appli
e 4, Appli
e 5, Appli
e 6, Appli
e 6, Appli
e 7, Appli
e 16, Appli
e 16
```

180 8.4 553 2 US-08-943-087-44 180 8.4 553 2 US-08-943-087-46 180 8.4 553 2 US-08-943-087-46 180 8.4 553 2 US-08-943-087-56 167.5 7.8 221 2 US-08-943-087-54 166.5 7.8 221 2 US-08-943-087-52 165.5 7.7 221 2 US-08-943-087-52 163.5 7.6 221 2 US-08-943-087-60 160.5 7.5 221 2 US-08-943-087-60 160.5 7.5 221 2 US-08-943-087-8 146 6.8 337 4 PCT-US94-14277-8 147 6.6 574 2 US-08-940-713-2 118 5.5 489 4 PCT-US93-11110-1 118 5.5 489 4 PCT-US93-11110-1 118 5.5 1005 2 US-08-469-537A-103 117.5 5.5 2214 1 US-08-727-034-7 110 5.1 2213 1 US-08-727-034-3	8.4 553 2 U	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
.4 553 2 U.S. 553 2 U.S. 6 5231 2 U.S. 6 523	.4 553 2 US-08-943-087-44 .4 553 2 US-08-943-087-46 .4 553 2 US-08-943-087-48 .1 221 2 US-08-943-087-56 .8 221 2 US-08-943-087-54 .8 221 2 US-08-943-087-52 .7 221 2 US-08-943-087-52 .7 221 2 US-08-943-087-52 .6 221 2 US-08-943-087-58 .8 337 4 PCT-US94-14277-8 .8 337 4 PCT-US94-113-2 .5 489 4 PCT-US94-1110-1 .5 1005 2 US-08-943-9537A-103 .5 2214 1 US-08-727-034-7 .1 2213 1 US-08-727-034-3	110	117.5	118	118	118	142	146	160.5	163.5	165.5	166.5	167.5	172.5	180	180	180
000000000000000000000000000000000000000	2 US-08-943-087-46 2 US-08-943-087-46 2 US-08-943-087-56 2 US-08-943-087-54 2 US-08-943-087-52 2 US-08-943-087-52 2 US-08-943-087-52 2 US-08-943-087-52 2 US-08-943-087-52 2 US-08-943-087-58 4 PCT-US94-14277-8 4 PCT-US94-1110-1 5 5221789-1 1 US-08-727-034-7 1 US-08-727-034-3	5.	5 5		5.5	5 5	6.6	6. 8	7.5	7.6	7.7	7.8	7.8	8.1	8.4	8.4	8.4
	US-08-943-087-44 US-08-943-087-46 US-08-943-087-56 US-08-943-087-54 US-08-943-087-52 US-08-943-087-52 US-08-943-087-60 US-08-943-087-60 US-08-943-087-60 US-08-943-087-60 US-08-943-11110-1 US-08-943-11110-1 US-08-727-034-7 US-08-727-034-3	2213	2214	1005	489	489	574	337	221	221	221	221	221	221	553	553	553
US-08-943-087-44 US-08-943-087-46 US-08-943-087-56 US-08-943-087-56 US-08-943-087-52 US-08-943-087-52 US-08-943-087-52 US-08-943-087-52 US-08-943-087-58 PCT-US94-14277-8 US-08-943-087-13-2 PCT-US94-11110-1 5221789-1 5221789-1 5221789-1 US-08-469-372-034-7 US-08-727-034-3	-08-943-087-44 -08-943-087-46 -08-943-087-56 -08-943-087-56 -08-943-087-50 -08-943-087-52 -08-943-087-52 -08-943-087-58 -08-943-087-58 -08-943-087-60 -08-943-087-60 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-943-087-6 -08-727-034-3	μ.	<u>س</u>	N	ທ	4	N	4	N	N	N	N	N	N	N	N	N
	Sequence	US-08-727-034-3	US-08-727-034-7	US-08-469-537A-103	5221789-1	PCT-US93-11110-1	US-08-906-713-2	PCT-US94-14277-8	US-08-943-087-58	US-08-943-087-60	US-08-943-087-52	US-08-943-087-50		US-08-943-087-56			-08-943-087

## ALIGNMENTS

```
; LENGTH: 434 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08328256 Patent No. 5643749
                      Query Match
Best Local (
                                                                                                                                                                                                                              TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/328,2
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY_AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                NAME: BROWDY, Roger L. REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
STREET: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #a∟
D.C.
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 Seventh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BROWDY AND NEIMARK
9 Seventh Street, N.W.,
                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/328,256
Score 2141; DB 1;
Pred. No. 9.4e-214;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                      Length
                                          434;
```

Š

1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60

Matches 401;

Similarity

Conservative

0

Indels

0

Gaps

Š 밁 õ

밁 Š 밁 õ

В

Š

В

В

Š

0

```
RESULT 2
US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08307588 Patent No. 5919453
                                                                                                                                                                                                      APPLICATION NUMBER: PCT/EP93/00770
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28.665
REGISTRATION NUMBER: 28.665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                            TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BENOIT, PATTICK
APPLICANT: MEYER, Francois
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, MICHAel G.
TITLE OF INVENTION: MONCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acid
TYPE: amino acid
                                                                                                                         REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 05-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: V
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTEQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Foley & Lardner 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BENOIT, Pact Parties P
                   436 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER: US/08/307,588
05-DEC-1994
                                                                                                                                                                                        17283/117/GUPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
; MOLECULE TYP
US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멇
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                      COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
NAME: BROWDY, ROGER TE.
REGISTRATION NUMBER: RES. 5610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
  REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: REVEL, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LTSWKIGYYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 419 Seve
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100 nes 401; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTESFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0, Application US/08328256
5643749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 Seventh Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BROWDY AND NEIMARK
9 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2141; DB Pred. No. 9.5e-2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
```

386

360 326 300

240

```
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                           US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08471454 Patent No. 5731169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
                                                                                                                                                                                                                                        APPLICANT: GRESSER, ION
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
            CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                         ADDRESSEE: NIXON & V
                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                    CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 KKTDYTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPGTKDSYMWALDGLSFTYSLLIWKNSSGYEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                            E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                          PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                               LUTFALLA, Georges
                                                                                                                                                                                                                                                                                                                              MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202-737-3528
06-JUN-1995
                                                                                                                                                                                                                                                                                                                illes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
          US/08/471,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ج
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2141; DB 1;
Pred. No. 1.4e-213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                        Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

```
멇
                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                   US-08-466-974-2
                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-471-454-2
                                                                                                                                                                                              Patent No. 5861258 GENERAL INFORMATION:
                                                                                                                                                                                                                                 Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/1370
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 557 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                      TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING I
                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                      NUMBER OF SEQUENCES:
                                                                                                                               APPLICANT:
                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                        387
                                                                                                                                                                                                                                                                                                                                                     361 KKIDVIVPNLKPLIVYCVKARAHIMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 100.0%;
Local Similarity 100.0%;
tes 401; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTSWKIGYYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                          EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                         EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acids
                                                                                                                                                                                                                                 Application US/08466974
                                                                                                                       LUTFALLA, Geo
                                                                                                                                                          MOGENSEN, Knud E. UZE, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S: Single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                           Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2141;
Pred. No. 1.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4e-213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

146

120 98 60

386

300 266 240 206 180 Gaps

```
RESULT 6
US-08-471-453-2
; Sequence 2, Application US/08471453
; Patent No. 5886153
                                                                                                                     Š
                                                                                                                                                  밁
                                                                                                                                                                         Ş
                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                     멍
                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: US-08-466-974-2
                                                                                             윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    327
                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                             147
                                                                                             387
                                                                                                                                                                               301
                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 401; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                          KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT 300
                                                                                                                                                                                                                                                                 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                         KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE 360
                                                                                                                                                                                                                                                                                                                          SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2141; DB 2; 100.0%; Pred. No. 1.4e-213; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

```
Ş
                                                                                                       밁
                                                                                                                                         δÃ
                                                                                                                                                                               В
                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                           뮍
Š
                                   망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 401; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-0CT-198
ATTORNEY/ACENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/COURTET NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                               301
                                       267
                                                                                                           207
                                                                                                                                                                                                                                                     TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 NOI
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                           27 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                1 GKNIKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
                                                        KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYFLIYEIIFWENTSNAERKIIE
                                                                                                         LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFL
                                                                                                                          LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFL
                                     KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRESSER, ION
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2141; DB 2; 100.0%; Pred. No. 1.4e-213; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #1.25
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                           266
                                                                                                                                                                                                                                                                                                                             86
                                                                         300
                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
문
                             Ş
                                                                      밁
                                                                                                    Ş
                                                                                                                                         밁
                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   몆
                                                                                                                                                                                                                                                                                                         US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Applic
Patent No. 591945:
                                                                                                                                                                                                                Matches 401;
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)672-539 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MEYER, Francois,
APPLICANT: MAGUIRE, Deborah
APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT AFFLUCTION NUMBER: US/Ub/Sv., FAPPLICATION NUMBER: US/Ub/Sv., FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 92400902.0 FILING DATE: 31-MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: SAXE, Bernhard D. REGISTRATION NUMBER: 28,665 REFERENCE/DOCKET NUMBER: 17283/117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/1
FILING DATE: 30-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                   121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                     61 CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                         27 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
ZIP: 20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                            1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
SPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                  CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                    TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08307588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BENOIT, Patrick
                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Foley & Lardner
                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17283/117/GUPL
                                                                                                                                                                                                                               Score 2141; DB 2;
Pred. No. 1.4e-213;
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25 (EPO)
                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                              <u>.</u>.
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE
                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386
                                                                                                                                                                                                          0
                밁
                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멍
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                 1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTESFDYQKTGMDNWIKLSGCQNITSTK 60
                                                                                                                                                                                                                                                                LENGTH:
                GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 86
                                                                                                    Similarity
                                                                                       Conservative
```

```
; MOLECULE TYPE: US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08328256 Patent No. 5643749
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/328,256
FILLING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILLING DATE: 24-OCT-193
ATTORNEY_AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                    TELLEFAX: 248633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                 TELEPHONE: 202 - TELEPHONE: 202-737-3528
                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
                                                                                                                                                           amino acid
                                                                                                                                                                            496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 Seventh Street, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                          linear
                                                                                                      protein
                                                                                                                                         single
                  97.6%;
                                                                                                                                                                                                                                                                                                                       REVEL-13
Score 2089; DB 1,
Pred. No. 2.9e-208;
                                                                                                                                                                                                                                                                                                       25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
                                  Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266
```

Indels

8

٠,

```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US94-14277-3
                                                                       ; TOPOLOGY: PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application PC/TUS9414277
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
CLASSIFICATION:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34.659
REFERENCE/DOCKET NUMBER: 866PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: RECEPTOR Subunit Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: "C"
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 KKTDVTVPNLKPLTVYCVKARAHTMDE-----SDAVCE 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                            TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPGTKDSVYWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNESSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hemmi, Silvio
Conservative
                                                                                    linear
22.9%; Score 490.5; DB 4;
48.5%; Pred. No. 4e-43;
tive 34; Mismatches 69;
                           Length
 Indels
                            202;
۲,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
 ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
PCT-US94-14277-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
   밁
                         Q
                                                        В
                                                                                   Ş
                                                                                                                                                                                       ; TYPE: ami
; TOPOLOGY:
PCT-US94-14277-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94080
```

```
ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4. Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/164596
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Aguet, Michel
APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PSLKKHSNYSTXQCISTTVANK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LTSWKIGVYSPVHCIKTTVENE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL 180
                       262 TTOCYFPONYFOKGIYLLRYQASDGNNTSFWSEEIKFDTEIQAFLLPPYFNIRSLSDSFH 321
                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 07-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                      1 MPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPGYSKSSSGSHSDKWKPIPTCANVQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ENLKPPENIDXYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDERKWLKXPECQHTTTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
TTHCVFSQDTXYTGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPPPPVITVTAMSDTLL 120
                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                          20.5%;
ilarity 44.0%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT/US94/14277
                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 Kb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  866PCT
                                                                                                                                                                              Score 438.5; DB 4;
Pred. No. 9.7e-38;
Pred. No. 9.7e-38;
S; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blvd
                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                        Length
                                                                                                                                                                       . 49
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
```

w ••

```
망
                                                                                                                                                              8
                                                                                                                                                                                                   밁
                                                                                                                                                                                                                               Ş
                    Ş
                                                         닭
                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                  US-08-683-743-4
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pestka, SI
APPLICANT: Kotenko, S
TITLE OF INVENTION: C
TITLE OF INVENTION: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equence 4, Application US/08683743 stent No. 5843697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
   182 TSWKIGVYSPVHCIKTTVENELP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 V-LFRALLNKTSNFSEKLCE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 IYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLIVYCVKAR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                            67 KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT 124
                                                                                                                            79 -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Ave, Continental Plaza, STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYXNCQDSTCD-----GLNYEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQAR 173
                                                       ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP 196
                                                                                                                                                                                                PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                                                                                                                                                                                                                   POKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66
                                                                                       KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pestka, Sidney
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signey 't
Serguei
CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                      10.3%; Score 220; DB 2; 30.0%; Pred. No. 9.6e-15; tive 41; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/683,743
                                                                                                                                                                                                                                                                                                        Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4th
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                 79
                                                                                                                                                          Ş
                                                                                                                                                                                                В
                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                           B
                                              RESULT 13
PCT-US94-14277-6
                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US94-14277-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US94-14277-2
                Sequence 6, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9414277 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOTTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                           198
                                                                                                                                                              167
                                                                                                                                                                                                 143
                                                                                                                                                                                                                                 109 LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: a
                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                           55 NITSTKCNPSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           29 LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                           4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                          SPETTYCLKVKAAL-LISWKI---GVYSPVHCIKTI 198
                                                                                                                                                                                              VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL 197
                                                                                                                                                                                                                                                                     DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 142
                                                                                                                           KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRNKAGEWSEPVCEQTTHDETVP 219
                                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bohni,
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
Aguet, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aguet, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                 9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,659
                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 199; DB 4; Length 332; Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
```

Indels

32;

Gaps

```
US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
PCT-US94-14277-6
                                                                                                                              Sequence 2, Applicati Patent No. 5945511 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.0%;
Best Local Similarity 29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-530
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bohni, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit Polypeptides
NUMBER OF SEQUENCES: 8
                                                                               APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                              APPLICANT:
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                     124
                             APPLICANT:
                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                 167 SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                   ITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/1 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 07-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  64 DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS 123
                                                                                                                                                                                                                                                                                                                                                                                                                 55 NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LARPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----IDGSWHRLLEPNCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Love, Richard B. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                                                                                                                                                                                                                                                                                                                                                 LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGYEERIENIYSRHKIY--KL 166
                                                                                                                                                                                                                                                   KPYRVYCLQTERQLILKNKKIRPHGLLSNVSCHETT 214
                                                                                                                                                                                                                                                                                                                  VTPGKGSLVIHFSPPFD-----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94080
OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 460 Point San Bruno Blvd
South San Francisco
            I: Jelmberg, Anna C.
I: Adams, Robyn L.
I: Whitmore, Theodore E.
I: Farrah, Theresa M.
INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                 Application US/08943087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 192; DB 4;
Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                    В
                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
 US-08-943-087-14
                                                                                                   S
                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
                                                                                                                                     302
                                                                                                    335 VIQDYPLIYEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1201 R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lunn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
```

В Š В Š В Ş

S

吊

```
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                             171 TYCLKVKAALLTSWKIGVYSPVHCIKTTVENE------LPPPENIEVSVQNQNY 218
                                                                                                                                                                                                                                                                                                                                                                                              157 APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSOCVTN----HTLVLTWLEPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                             122 PGTK-----DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
350 PPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESLSRTIPPDKTVIEY 401
                                                                                                                                                                                                 264 ----FLFSVMGYSIYRYIHVGKEKHPANLI----
                                                                                                                                                                                                                                                                                                 213 LYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKIIFWYVLP----ISITV----
                                                                                                                                              278 LLRVQASDGNNTSFWSEEIKFDTEI----QAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 LSAETSDYEHQYYAKVKAIWGTKCSKWAESGREYPFLETQIGPPEVALTTDEKSISVVLT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 LPKPANITELSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LKSPOKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYOKTGMDNWIKLSGCQNITSTKCN 62
                                                                                                                                                                                                                                           VLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
                                                                                                  V----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLND-------PQPSGNLR 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 553 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: ZymoGenetics, Inc.
1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.4%; Score 180; DB 2; I
20.6%; Pred. No. 3.2e-10;
7ative 75; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/943,087
                                                 -IFWENTSNAERKIIEKKTDV--TVPNLKPLTVY 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    East
                                                                                                                                                                                                    ------LIYGNEFDKRFF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   212
                                                                                                                                                                                                                                                                                                      264
```

Sequence 14, Application US/08943087

```
ş
     밁
                                    Ş
                                                                      밁
                                                                                                  Š
                                                                                                                                         밁
                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Watches 85; Conserve
                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 110
CITY: Seattle
CTATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
                                                               213 LYCVHVESFVPGPPRRAQPSEKQCARTLXDQSSEFKAKIIFWYVLP----ISITV----
                                                                                                171 TYCLKYKAALLTSWKIGYYSPYHCIKTTYENE-----LPPPENIEVSYQNQNY 218
                                                                                                                                    157 APEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN----HTLVLTWLEPNT 212
264 ----FLFSVMGYSIYRYIHVGKEKHPANLI----
                              219 VLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIY 277
                                                                                                                                                                     122 PGTK------DSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYK--LSPET 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 206-442-6627
                                                                                                                                                                                                     97 LSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLT 156
                                                                                                                                                                                                                             63 FSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                          37 LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                         4 LKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/943,087 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jelmberg, Anna C.
Adams, Robyn L.
Whitmore, Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                          8.4%; 5c.
20.6%; Pre
                                                                                                                                                                                                                                                                                                                                            Score 180; DB 2; Length 553;
Pred. No. 3.2e-10;
'5; Mismatches 166; Indels 86; Gaps
----- 301
```

264

15;

```
Š
                                                                                                            밁
          밁
                                                                                                                                                          Š
350 PPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESLSRTIPPDKTVIEY 401
                                                                                                  302 V----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLND------PQPSGNLR 349
                                                  335 VIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV--TVPNLKPLTVY 376
                                                                                                                                                  278 LLRYQASDGNNTSFWSEEIKFDTEI---QAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 334
```

Search completed: June Job time: 15447 sec 1, 2000, 04:17:53

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                               Database :
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 1, 2000, 00:37:00; Search time 64.83 Seconds (without alignments) 362.649 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-2_COPY_27_427
2141
1 GKNLKSPQKVEVDIIDDNFI.....AHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                            168808 seqs, 58629743 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      168808
```

#### SUMMARIES

	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	υ	12	11	10	. 9	. 80	7	6	5	4	ω	N	_	NO.	Result
	110	110.5	111	111	111	111.5	113	113	113	115	115.5	117	117.5	117.5	117.5	118	118	118	122.5	123	123	123.5	148	199	217.5	220	225	966	1384.5	2141	Score	
	5.1					5.2														5.7	5.7	5.8	6.9	9.3	10.2	10.3	10.5		64.7	100.0	Match	Query
	1912	1898	16	83	6831	1896	76	61	1450	26926	658	817	1585	1427	1383	1005	981	489	1451	1526	1375	1443	337	332	349	325	273	590	560	557	Length	
	N	N	N	N	N	N	N	Ŋ	N	۳	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	2	N	2	N	N	88	
	A56178	$\mathbf{r}$	ω	*	w	T08851	0	B49502	A44027	T38344	T16040	A48721	T19121	I51669	A36080	S49015	S51604	A31555	S42167	T13823	T13822	150600	I38500	A49947	JC6311	A47003	G01418	A45283	S27387	A32694	ID	
,	protein-tyrosine-p	eant	hypothetical prote	twitchin - Caenorh	hypothetical prote	Down syndrome cell	protein-tyrosine-p	protein-tyrosine-p	yofibrill	cardiac m	stical pro	titin, muscle - ch	₩	ppressor		receptor tyrosine	receptor-like tyro	interferon gamma r	190K protein - hum	gene	frazzled gene prot	chicke	interferon gamma r		o			alpha/		interferon alpha/b	Description	

45 103.5	44 103.5	43 104	42 104	41 104	40 104.5	39 105	38 105.5	37 105.5	36 107.5	35 108	34 108.5	33 108.5	32 109	31 109.5
4.8	4.8	4.9	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	5,1	5.1	5.1	5.1
1499	896	2311	1239	896	1447	56	1825	878	1372	991	2215	2033	416	575
N	N	<b>ب</b> ــا		μ	N	N	ν	Ь	N	2	N	N	N	N
150212	156563	TVCHSR	A32579	A35782	A54100	S41602	T32828	A40091	A34157	I78843	T00348	T09123	T25036	A49667
protein-tyrosine-p	interleukin-3 rece	kinase-related pro	neuroglian - fruit	cytokine receptor	tumor suppressor p	interferon alpha r	hypothetical prote	interleukin-3 rece	insulin receptor p	receptor protein-t	LR11 protein - mou	hybrid receptor So	hypothetical prote	interleukin-10 rec

# ALIGNMENTS

121 SPGTKOSVMWALDGLSFTYSTLIWKNSSGVEERIENTSRHKIYKLSPETTYCLKYKAAL	Query Match Query Match Best Local Similarity 100.0%; Score 2141; DB 2; Length 557; Best Local Similarity 100.0%; Pred. No. 4.2e-154; Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60	432/1; 48 in	RESULT 1 A32694 A17694 A17694 A17694 A17694 A17694 A17694 A17696 C;Species: Homo sapiens (man) R;Uze, G; Lutfalla, G; Gresser, I. Cell 60, 225-234, 1990 A;Title: Genetic transfer of a functional human interferon alpha receptor into mouse A;Reference number: A32694; MUID:90124632 A;Reference number: A32694; MUID:90124632 A;Reference number: A32694; MUID:90124632 A;Rocession: A32694 A;Molecule type: mRNA A;Residues: I-557 cUZE> A;Recession: A32694 A;Molecule type: mRNA A;Residues: GB:J03171; NID:g184645; PIDN:AAA52730.1; PID:g306914 R;Lutfalla, G. Submitted to the EMBL Data Library, July 1991 A;Description: The structuree of the human interferon alpha/beta receptor gene.

```
interferon alpha receptor type 1 precursor - bovine (Species: Bos primigenius taurus (cattle) C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C:Accession: $27387; $33770 C:Accession: $27387; MUID:93076908 A:Accession: $27387; MUID:93076908 A:Accession: $27387; MUID:93076908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha
A;Reference number: $33770; MUID:93305725
A;Accession: $33770; MUID:93305725
A;Accession: $33770; MUID:93305725
A;Accession: $33770
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-421,'V',423-560 <LIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: lung
C;Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; A;Experimental source: MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                   밁
                                                                                                                                                     Ş
                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F; 25-560/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lim, J.K.; Langer, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence
                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
õ
                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                    146
  359
                                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                             LKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFD
                                                                                                                                                                                                                           LLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAF 239
                                                                                                                                                                                                                                                                                                         S-PGTKDSVMWALDGLSFTYSLLIWKNSSGYEERIENIYSRHKIYKLSPETTYCLKVKAA 179
                                                                                                                                                                                                                                                                                                                                                                                       FSSLKL-NYYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN 62
                                                                                                                        FKKIPGNHSDKWKQIPNCENVTSTHCVFPREVSSRGIYYVRVRASNGNGTSFWSEEKEFN
                                                                                                                                                                                                                                                                                      SPPGTKDSIMWAMDRSSFRYSVVIWKNSSSLEERTETVYPEDKIYKLSPEITYCLKVKAE
                                                                                                                                                                                                                                                                                                                                                                    FSSVELENVFEKIELRIRAEEGNNTSTWYEVEPFVPFLEAQIGPPDVHLEAEDKAIILSI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                               NLK-PENVEIHIIDDNFFLKWNSSSESVKNVTFSADYQILGTDNWKKLSGCQHITSTKCN 85
  IEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401
                                          TEMKTIIFPPVISVKSVTDDSLHVSVGASEESENMSVNQLYPLIYEVIFWENTSNAERKV
                                                                                TEIQAFLLPPVFNIRSLS-DSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI
                                                                                                                                                                                                      LRLQSRVGCYSPVYCINTTERHKVPSPENIQINADNQIYVLKWDYPYENATFQAQWLRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha receptor type 1 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1384.5;
Pred. No. 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the human alpha interferons are determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bovine alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; DB 2;
.5e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: 9432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
                                                                                358
                                                                                                                          325
                                            385
                                                                                                                                                                299
                                                                                                                                                                                                        265
                                                                                                                                                                                                                                                                                      205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                         밁
                                                             δÃ
```

```
interferon alpha/Deta receptor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C;Date: 25-Mar-1993 #sequence_revision 18425; I48426; I48427; I48427; I48428; I48429 C;Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48427; I48428; I48429 B;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E. Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992 Proc. Natl. Acad. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 148, 343-346; 1994
A;Title: Structure of the murine interferon alpha/beta
A;Reference number: I48423; MUID:95047447
A;Accession: I48423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; A;Note: sequence extracted from NCBI backbone (NCBIN:102354, R;Lutfalla, G.; Uze, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A45283; MUID:92262522
A;Accession: A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-590 <UZI
                                                                                                                                                                                                                                                                                                                                               A; Introns: 177/3;
C; Keywords: cytoki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; A;Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 397-424 < RE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 265-375 < RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U06244; NID:g497114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 426-445 <RE6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: I48426
A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 118-125
                                                                                                                                                     Query Match
Best Local Similarity
Matches 192; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                      IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated
                                                                      GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK 60
GENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDEAKWLKVPECQHTTTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-590 <UZE>
                                                                                                                                                                                                                                                                                                                                                   cytokine receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <RE7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <RES>
                                                                                                                                                                                 45.18;
47.68;
                                                                                                                                                                                                                                                                                                                                                       transmembrane
                                                                                                                                                     Score 966; DB 2;
Pred. No. 2.3e-65;
1; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from GB/EMBL/DD3J
                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN: AAA65008
                                                                                                                                                                                                                               Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor-encoding gene:
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID: 9194112
NCBIP: 102357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PID: g755810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID: 9755813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: g755812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g510262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID: g510265
                                                                                                                                                             10;
                                                                                                                                                         Gaps
                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo
```

```
C; Date: 21-Dec-
C; Accession: GC
R; Lutfalla, G.
RESULT 5
A47003
Cytokine receptor family class II protein CRF2-4 precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
C:Accession: A47003
                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A; Reference number: G06935 A; Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine receptor family II, member 4 - C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                     S
                                                                                                                                                                                                                          맑
                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:138168; OMIM:123889
A;Map position: 21g22.1-21g22.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-273 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:CRFB4; CRF2-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
Date: 21-Dec-1996 #sequence_revision
Accession: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references: EMBL:U08988; NID:g571295; PID:g571296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                    197
                                                                                                                                                                                       182
                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 EKDGPEFTLKNLQPLTVYCVQARV-LFRALLNKTSNFSEKLCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 IEKKIDVTVPNLKPLIVYCVKARAHIMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                     TSWKIGVYSPVHCIKTTVENELP 204
                                                                                                                                                                                                                                                             KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL 181
                                                                                                                                                                                                                                                                                                                       KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH-ISPGT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSQKHILPPPPVITVTAMSDTLLVYVNCQDSTCD------GLNYEIIFWENTSNTKISM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSKSSSGSHSDKWKPIPTCANVQTHCVFSQDTVYTGTFFLHVQASEGNHTSFWSEEKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPSLKKHSNYSTVQCISTTVANKMPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEVKAI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAEDKAILVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH
                                                                                                                                                    DRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                                          ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP 196
                                                                                                                                                                                                                                                                                                                                                                         PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS- 79
                                                                                                                                                                                                                                                                                                                                                                                                                PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66
                                                                                                                                                                                                                                                                                                  -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLDDSLHMRFLAPKI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%;
ilarity 30.0%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 225; DB 2; 1
Pred. No. 7.2e-10;
13; Mismatches 87;
                                                                                                                                                  219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-Jun-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7:
```

```
C; Accession: JC6311
R; Glbbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A; Title: CRP2-4:isolation of
A; Reference number: JC6311
A; Accession: JC6311
A; Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K;Lutfalla, G.; Gardiner,
Genomics 16, 366-373, 1993
A;Title: A new member of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멅
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γQ
                                                                В
                                                                                                Ş
                                                                                                                                    밁
                                                                                                                                                                  Š
                                                                                                                                                                                                      В
                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: A new member of the cytokine receptor gene family A; Reference number: A47003; MUID:93300510
밁
                            Š
                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U53696
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-349 <GIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 21q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: 217227; NID: g393378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 DRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                  65 SLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS--
                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LSYRIFQDKCMNTTLTECDFSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL
                                                                                                                                                                                                                                      7 POKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                    --HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPEMQIESLAESLELRFSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSWKIGVYSPVHCIKTTVENELP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI 136
QVQGFLLDQNRTGEWSEPIC-ERTGNDEITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLNYYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT
                              KVKAALLTSWKIGVYSPVHCIKTTVENELPP
                                                                QIENEPET----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSPYDSEVLRNLEPWTTYCI
                                                                                                  ----PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCL
                                                                                                                                                                                                       PEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH-----CKRTASTQCDFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRNLEPWTTYCVQVRGFLP
                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                         10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 220; DB 2; 1 30.0%; Pred. No. 2.2e-09; tive 41; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K.; Uze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clones encoding the human
                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                        Score 217.5; DB 2;
Pred. No. 3.7e-09;
5; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ရ
                                 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g393379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                         Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196
                                                                   189
                                                                                                   174
                                                                                                                                     134
                                                                                                                                                                       122
                                                                                                                                                                                                       77
                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at
```

```
interferon gamma receptor beta subunit - mouse
N;Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific coft
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A49947
R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.
cell 76, 803-810, 1994
A;Title: A novel member of the interferon receptor family complements functi
A;Reference number: A49947; MUID:94170381
A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNĀ A; Residues: 1-332 <HEM> Y A; Cross-references: GB:S69336; NID:9545841; PIDN:AAB30165.1; A; Experimental source: early B-cell line Y16 A; Note: sequence extracted from NCBI backbone (NCBIN:145654, C; Keywords: cytokine receptor
                                                                                                                                                                                        A;Accession: I38501
A;Molecule type: mRNA
A;Residues: 1-63,'Q',65-337 <RE2>
A;Cross-references: EMBL:U05877; I
A;Experimental source: clone pJS3
                                                                                                                                                                                                                                                                                                                                                  A;Title: Identification and sequence of an accessory factor required for activation of A;Reference number: A49946; MUID:94170380
A;Accession: I38500
                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Date: 16-Feb-1996 #sequence_revision
C; Accession: 138500; 138501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                     A; Map position: 21
C; Keywords: cytokine receptor
                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; A;Experimental source: clone pSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-337 < RES>
                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon gamma receptor accessory factor-1 precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                         position: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198
                                                                                                                                                                                                                                                                                                                                                                                                         J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; 5, 793-802, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGMD-NWIKL--SGCQ 54
                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
LKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYQKTGMDNWIKLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTPGKGSLVIHFSPPFD----VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQHYENVTVGPPKNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF - - - - - IDGSWHRLLEPNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                   Similarity 22.3
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                    6.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                             NID: g463551;
                                                 Score 148; DB 2; Length 337; Pred. No. 0.00062; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 199; DB 2; Pred. No. 8.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-Feb-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                PIDN: AAA16956.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBIP:145656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g545842
                                                                                                                                                                                                                                                                                                    PID: g463550
                                                                                                                                                                                                               PID:g463552
                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               functionality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                    52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cofactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                       <u>ا</u>
                                                                                                                                                                                                                                                                                                                                                                                                                              Emanuel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of,
 frazzled ge
C; Species:
                                      RESULT
T13822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 跊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
                                                                                                                                          Ş
                                                                                                                                                                             В
                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                  뮍
                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                    VQ.
                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                           밁
```

```
neogenin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I50600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1443 <VIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: I50600
R;Vielmetter, J.; Kayyem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A;Title: Neogenin, an avian cell surface protein expressed
A;Reference number: A55193; MUID:95105243
A;Accession: I50600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
150600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U07644; NID:g641965; PID:g641966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103
                                            340
                                                                                         699
                                                                                                                                                                                                                                                                    598
                                                                                                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                                                                                                                               482 TQVMIQNLMPETVYVERVVAQNKHGHGE--SSAPLKVAT--QPEVQLPGPAPNIRAYAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 APRDVVATLVSTRFIRLTWRTPVSDPQGDNLTYSIFYTKEG----INRERVEN-TSRPGE 48:
  757
                                                                                                                              286 GNNT---SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHIYIGAPKQSGNTPVIQDY
                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFKYTDSK-----WFTADIMSIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                              GTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPE-NIEVTPGEGSLIIRESSPEDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR
                                                                                      VNGTGPATDWVSAETFESDLDESRVPEVPSSLHVRPLVTSI-VVSWTPPENQNI-VVRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMADASTELQQVILISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVENELPPPENIEVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCTQITATECDFTAASPSAGFPMDFNV----TLRLRAELGALHSAWVTMPWFQHYRNVTV 140
                                                                                                                                                                                                                                                                                                                                                         PTSVTVTWETPLSGNGEIQNYKLYYMEKGQDSEQDVDVAGLSYTITGLKKYTEYSFRVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPOKVEVDIIDDNFI-LRWNR--SDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE
AIGYGI----GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA 796
                                                                                                                                                                                                                                                                                                            ALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVLKWDYTYANMTFQVQWLH
                                       PLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA 382
                                                                                                                                                                                                                     AFLKRNPGNHL-----YKWKQIPDCENVKTTQCVFPQNVFQ--KGI-----YLLRVQASD 285
                                                                                                                                                                                                                                                                    --YNKHGPGVSTQDVVVRTLSDVPSAAPQNLTLEARNSKSIMLHWQPPPA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
89; Conserv
                                                                                                                                                                             GTHSGQITGYKIRYRKYSRKSDVTESVGGTQLFQLIEGLERGTEYNFRIAAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- QNQNYVLKWDYTYANMTFQVQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LKLNVYEEIKLRIRAEKENT-SSWYEVDSFTPFRKAQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 123.5; D
Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminal neuronal d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                      537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                  869
                                                                                                                                                                                                                                                                                                                                                             597
                                                                                             756
                                                                                                                                                                                                                                                                      646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
```

10

gene protein s: Drosophila

fruit fly (Drosophila melanogaster) melanogaster

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1375 <K0
A; Cross-references: El
C; Genetics:
frazzled gene protein, log isoform - fr
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision
C;Accession: T13823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: frazzled
A; Map position: 2
                                                                                                                              Š
                                                                                                                                                            B
                                                                                                                                                                                  Š
                                                                                                                                                                                                                ₽
                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                         맑
                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멼
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: Z17780
A; Accession: T13822
                                                    T13823
                                                                 RESULT
                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 20-Sep-1999 #sequence_revision;
Accession: T13822
::Kolodziej, P.A.: Timpe, L.; Mitchell,
ell 87, 197-204, 1996
:Title: Frazzled encodes a Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448
                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508
                                                                                                                                                                                                                                                                                                                                                                                                                                    889
                                                                                                                                                                                                                                                                       854
                                                                                                                                                                                                                                                                                                                                                     223
                                                                                                                                                                                                                                                                                                                                                                                                          188
                                                                                                                                  364
                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                          794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
wes 101; Conserv
                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GKNLKS-----PQKVEVDIIDDNFI-LRW------NRSDESVG 31
                                                                                                                                                                                                                                                                                                                                                                                                 YARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYVI 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFEG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQK 507
                                                                                                                                                                                                                                                                                                                                                                                                                                 GYKIRYRK--FKDAPOVKSTPANI-RYFELSNLDRNAEYOVKIAAMTVNGSGPFTEWNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL----TSWKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQIT 687
                                                                                                                                 DVTVPNLKPLTVYCVKARAHT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSL
                                                                                                                                                                                                                                                                       PTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY----
                                                                                                                                                                                                                                                                                                                          GRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVDA
                                                                                                                                                             ---REVTVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEET
                                                                                                                                                                                       SDSFHIYIGAPKQSGNTPVIQDYP-----
                                                                                                                                                                                                                  -HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSMSVLNSTYQNVPVTPP-----
                                                                                                                                                                                                                                                                                                                                                                             -----NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLGW 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
ilarity 16.3%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function in vivo as a receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Timpe, L.; Mitchell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:U71001; NID:g1621114; PID:g1621115; PIDN:AAC47314.1
                                                                                                                                                                                                                                                                                              ; Score 123; DB 2;
; Pred. No. 0.33;
68; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
                                    fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       member of the DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-Sep-1999 #text_change 20-Sep-1999
             20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K.J.;
                                                                                                                                                                                       -LIYEIIFWENTSNAER----KIIEKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goodman, C.S.; Fried, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or component of a
             #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VD
            20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                             1016
                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                                     225
                                                                                                                                                                                                                                                                                                                                                                                                                                   744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mediating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jan,
                                                                                                                                                             밁
                                                                                                                                                                                     õ
                                                                                                                                                                                                                  맑
                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                           190K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                              1168
                                                                                                                                                                                                                                                                                                                          1005
                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         599
                                                                                                                                                                                                                                                                                                                                                     225
                                                                                                                                                                                                                                                                                                                                                                                                                                                             188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frazzled
```

```
C; Accession: $42167

R; Vinkemeier, U.; Obermann, W.; Weber, K.;
J. Cell Sci. 106, 319-330, 1993

A; Fitle: The globular head domain of titin
A; Reference number: $42166; MUID:94095665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:KOlodziej, P.A.; Timpe, L.; Mitchell, K.J.; Goodman, Cell 87, 197-204, 1996
A:Title: Frazzled encodes a Drosophila member of the DC A:Reference number: Z17780
A:Accession: T13823
A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-1526 <KOL>
                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 MYTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKNLKS------PQKVEVDIIDDNFI-LRW------NRSDESVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQK 658
                                                                                                                                                                                                                                                                                        MLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                                                                                                                                                                   DVTVPNLKPLTVYCVKARAHT
                                                                                                                                                                                                                                                                                                                                                                                ---REVIVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYSPVHCIKTTVENELP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEWNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL-----TSWKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQIT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFTPFRKAQIG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -IRAEKENTSSWYE-----
                                                                                                                                                                                                                                                                                                                                                                                                                              SDSFHIYIGAPKQSGNTPVIQDYP-----LIYEIIFWENTSNAER-----KIIEKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSMSVLNSTYQNVPVTPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLGW
                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL:U71002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TYANMTFQVQWLHAFLKRN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%;
                                                                                                                                                                                                                                                                                        1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 123; DB
Pred. No. 0.38;
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID:g1621116; PID:g1621117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PPEVHLE-AEDKAIVIHISPGTKDSVMWALD 133
                                                                            Fuerst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PPENIEVSVQNQNYVLKW 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                               0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PGNHLYKWKQIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN: AAC47315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fried,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VD
                                                                                                                            24 - Sep - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L.Y.; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
```

extends

into

the

center

of the

sarcomeric

```
A;Accession: S42167
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule: 1-1451 <VIN>
A;Residues: 1-1451 <VIN>
A;Cross-references: EMBL:X69090; NID:g407098; PIDN:CAA48833.1; PID:g407099
C;Superfamily: skelemin
                                                                                                                                                C;Genetics:
A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                              Interferon gamma receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-reb-1990 #sequence_revision 28-Fe
C:Paccession: A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δĀ
                                                                                                                                                                                                                                                                                                                                A; Title: Molecular cloning A; Reference number: A31555; A; Accession: A31555
                                                                                                                                                                                                                                                                                                                                                                                         R; Aguet, M.; Dembic, Z.; Merlin, Cell 55, 273-280, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-489 < AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                  Ş
                                                                                                                                                                                                                                                                            A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437 GLIEGRSYIFRVRAVNKMGIGFPSRVSEAVAALDPAEKARLKSP---LSTLDWTVIVTEE 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Sinhes 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 DYIIISWKQPAVDGGSPILGYFIDNCEVGTDSW------SQCNDTPVKFARFPVT 436
201 NELPPPENIEVSVQNQNYVLKWDYTYANM--TFQVQWLHAFLKRNPGNHLYKWKQIPDCE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 DNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEI 74
                                                          Local Similarity
hes 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-YKISNLKENMVYQFQVAAMNMAGLGAPSAVSECFKCE 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVKSPRFALFDLAEGKSYCFRVRC----SNSAGVGEPSEATEVTVVGDKLDIPKAPGKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPSEGIVPGPPTDLSVTEATRSYVVLSWKPPGQRGHEGIMYFVEKCEAGTENWQRVNTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGTKDSVMWALDGLSFT----YSLLIWK-----NSSGVEERIENIYS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KL-----RIRAEKENTSSW-----YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDITCLESFRDSMVLGWKQPDKTGGAEITGYYVNYREVIDGVPGKWR----EANVKAVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEII----FWENTSNAERKIIEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TCHGLVTGQS-----YIFRVRAVNAAGLSEYSQDSE-AIEVKAAIAPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTV-----ENELP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSRNTDTSV-----VVSWEESKDAKELVGYYIEANVAGSGKWEPC--NNNPVKTHRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPENIEVSVQNQNYVLKWD------YTYANMTFQVQWLHAFLKRNP-GNHLYKWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 5.7%;
Similarity 19.8%;
91; Conservative (
                                                          Conservative
                                                                                                                                                                                                                                                                       GB:J03143; NID:g184650;
                                                                           5.5%;
                                                                                                                                                                                                                                                                                                                                                 and expression; MUID:89003065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 122.5; DB 2;
Pred. No. 0.39;
66; Mismatches 181;
                                                        Score 118; DB 2
Pred. No. 0.19;
39; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-Feb-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                       0f
                                                                                                                                                                                                                                                                         PIDN:AAA52731.1; PID:g306915
                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                           DB 2;
                                                            102;
                                                                                                                                                                                                                                                                                                                                                                         human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401
                                                                                               Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                       interferon-gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                            10;
```

```
S51604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:S68029
A;Note: the authors translated the codon GAC for residue 170 as Glu
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeate;Seywords: ATP; transmembrane protein
C;Keywords: ATP; transmembrane protein
F;651-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D. Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor-like tyrosine kinase Ehk-1 - rat C;Species: Rattus norwegicus (Norway rat) C;Date: 07-May-1995 #sequence_revision 21 C;Accession: S51604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ᅜ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
ß
                                   Ş
                                                                              B
                                                                                                               Qγ
                                                                                                                                                            밁
                                                                                                                                                                                               Q
                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-981 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S49015; A; Accession: S51604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 QCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFNSSI
                                                                                                                                                              416
                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                        348
                                                                                449
                                                                                                                      313
                                                                                                                                                                                                      253
                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                          310
                                                                                                                                                                                                                                                                                                                                                                                                          272
509
                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ----ACIALVSVRVYYKKCPSVVRHLAVFPD-----TITGADSSQLLEVSGSCVNHSVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKNLKSPQKVEVDII--DDNF-----ILRWNRSDESVGNVT---FSFDYQKTGMDNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LSDSFH--IYIGAPKQSGN-TPVIQDYPLIYEIIFWENTSNAERKIIEKKTD----
                                                                                                                                                                                                                                            PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR---
                                                                                                                                                                                                                                                                                                                                                                KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH------CIKTTVENELPP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKLSGCQNITST----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VTVPNLKPLTVYCVKARA--HTMDEKLNKS-----SVFSDAV 399
                                     WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT 384
                                                                                                                        IRSLSDSFHIYIG---APKQSGNTPVIQ---
                                                                                                                                                                                                                                                                                                                          GFFKASPHSQTCSKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP
                                                                                                                                                                                                                                                                                                                                                                                                          DPPKMHCSAEGEWLV----PIGKCMC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVKTTQCVFPQNVFQKGIYL-LRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVE-----VKNYGVKNSEW--IDACI
FEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART
                                                                              VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY
                                                                                                                                                                                                    QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN 312
                                                                                                                                                                                                                                                                                  ---PENIEVSVQNQNYVLKW-------DYTYANMTFQVQWLHAFLKRNPGNHLYKWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92; Conserv
                                                                                                                                                            -----YLPQQIGLKNTSVMMADPLAHTNYTF-----EIEA-----VNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         two novel members 5; MUID:94067777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 118; DB 2; Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-Jul-1995 #text_change
                                                                                                                   546
                                                                                                                                                                                                                                                                                                                                                                                                          ----KAGYEEKNGTCQVCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor-like tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                              359
                                                                                                                                                                                                                                                                                                                                                                                                          309
                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
                                                                                                                                                                  448
                                                                                                                                                                                                                                                416
                                                                                                                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221
                                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
```

```
A;Molecule type: mRNA
A;Residues: 1-305, 'G', 359-1005 <MA2>
A;Cross references: EMBL:568026
A;Cross references: EMBL:568026
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP: transmembrane protein
C;Keywords: ATP: transmembrane protein
F;675-941/Domain: protein kinase homology <KIN>
F;683-691/Region: protein kinase ATP-binding motif
                                                                                                                  밁
                                                                                                                                                                      Ş
                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                         용
                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor tyrosine kinase Ehk-1 - rat
C; Species: Rattus norvegicus (Norwav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ncogene 8, 3277-3288, 1993

Fittle: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase; Reference number: S49015; MUID:94067777

Accession: S49015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Rattus norvegicus (Norway rat);Date: 14-Jul-1995 #text_change 28-May-1999;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999;Accession: S49015; S51602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:S68024; Note: the authors translated the codon GAC for residue 170; Accession: S51602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.5%; Score 118; DB 2; Length 1005; Best Local Similarity 20.1%; Pred. No. 0.51; Matches 92; Conservative 51; Mismatches 165; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1-1005 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
                                 348 WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT 384
                                                                                                               449 VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 DPPKMHCSAEGEWLV----PIGKCMC-------KAGYEEKNGTCQVCRP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 GRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG---- 221
509 FEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART 546
                                                                                                                                                                      253 QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN 312
                                                                                                                                                                                                                                                                                                                                                      360 PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR--- 416
                                                                                                                                                                                                                                                                                                                                                                                                              206 ---PENIEVSVQNQNYVLKW------DYTYANMTFQVQWLHAFLKRNPGNHLYKWK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 GFFKASPHSQTCSKCPP------HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ----ACIALVSVRVYYKKCPSVVRHLAVFPD----TITGADSSQLLEVSGSCVNHSVTD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH------CIKTTVENELPP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKLSGCQNITST-----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKNLKSPOKVEVDII--DDNF-----ILRWNRSDESVGNVT---FSFDYOKTGMDNW 47
                                                                                                                                                                                                                              -----YLPQQIGLKNTSVMMADPLAHTNYTF------EIEA-----VNG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
```

Search completed: June Job time: 14289 sec

1,.2000, 04:35:09

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                         June 1, 2000, 00:40:17; Search time 34.71 Seconds
(without alignments)
351.842 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83857 seqs, 30454973 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62 'Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKNLKSPQKVEVDIIDDNFI.....AHTMDEKLNKSSVFSDAVCE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-240-675-2_COPY_27_427
2141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
        BB
  INRL HUMAN
INRL SHEEP
INRL MOUSE
CRF4 HUMAN
INS HUMAN
INS HUMAN
INS HUMAN
EAS RAT
INSR RAT
MPSF CHICK
DCC MOUSE
EAS HUMAN
IIOR MOUSE
EAS HUMAN
IIOR MOUSE
EAS HUMAN
IIOR MOUSE
EAS HUMAN
IIOR MOUSE
EAS HUMAN
ILJB MOUSE
INC HUMAN
ILJB MOUSE
NGG DROME
CYRB HUMAN
SPOT HAEIN
SPOT HAEIN
SPOT HAEIN
INRA HUMAN
YHOO TANY
REPO TMY
S230 PLAFO
KISS HUMAN
YHOO TANY
INSR HUMAN
INRL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83857
      P11722
P06213
P48551
P16621
P42701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
mus musculu
homo sapien
mus musculu
homo sapien
mus musculu
homo sapien
mus musculu
homo sapien
homo sapien
homo sapien
haemophilu
homo sapien
haemophilus
homo sapien
haemophilus
homo sapien
haemophilus
homo sapien
saccharomyc
tobacco mos
plasmodium
saccharomyc
sallus gall
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 mus musculu
4 homo sapien
4 homo sapien
6 homo sapien
7 rattus norv
7 rattus gall
8 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) bos taurus
) ovis aries
```

95.5 4.5 2280 1 YCE2_TOBAC 95.4 4.5 2280 1 YCE2_TOBAC 95.4 4.4 918 1 IL6B_HUMAN 94.5 4.4 1068 1 YCE0_MARPO 94 4.4 917 1 IL6B_MOUSE 94 4.4 2628 1 HAGA_PORGI 93.5 4.4 620 1 YMMO_YEAST 93.5 4.4 620 1 YMMO_YEAST 93.5 4.4 1091 1 CIC2_HUMAN 93.5 4.4 1091 1 CIC2_HUMAN 93.4 3 1097 1 LLFR_HUMAN 93 4.3 1101 1 P11G_HUMAN	4.5 925 1 4.4 918 1 4.4 1068 1 4.4 2628 1 4.4 2628 1 4.4 2628 1 4.4 620 1 4.4 1091 1 4.3 1097 1 4.3 1107 1	45
925 2280 918 1068 1 917 1 2628 620 620 1 1091 1101	925 1 PMP2_CAREL P93341 2280 1 YCF2_TOBAC P09976 918 1 IL6B_HUMAN P09976 1068 1 YCF0_MARPO P12221 917 1 IL6B_MOUSE Q00560 2628 1 HAGA_PORGI Q03162 620 1 YMZ0_YEAST Q03162 620 1 CD22_HUMAN P20273 1097 1 CD22_RAT P20273 1097 1 LIFR_HUMAN P42702 1101 1 P11G_HUMAN P48736	93
مر مرامر سر سر مرامر مرامر مرامر	1 PMP2_CAREL. P93341 1 YCF2_TOBAC P09976 1 ILGB_HUMAN P40189 1 YCF0_MARPO P12221 1 ILGB_MOUSE Q00560 1 HAGA_PORGI Q51845 1 YMZ0_YEAST Q03162 1 CD22_HUMAN P42702 1 LIFR_HUMAN P42702 1 LIFR_HUMAN P48736	3
1 PWP2_CABEL 1 YCF2_TOBAC 1 IL6B_HUMAN 1 YCF0_MARPO 1 YCF0_MARPO 1 HAGA_POORGI 1 YMZ0_YEAST 1 CD22_HUMAN 1 CD22_RAT 1 LIFR_HUMAN 1 P11G_HUMAN	P91341 P09976 P40189 P12221 Q00550 Q51845 Q03162 P20273 P54290 P42702	1101
PWP2_CAEEL. YCF2_TOBAC IL6B_HUMAN YCF0_MARPO IL6B_MOUSE HAGA_PORGI YMZ0_YEAST CD22_HUMAN CIC2_RUMAN P11G_HUMAN P11G_HUMAN	P91341 P09976 P40189 P12221 Q00550 Q51845 Q03162 P20273 P54290 P42702	μ
		P11G_HUMAN

### ALIGNMENTS

222222222222222222222222222222222222222	S S S S S S S S S S S S S S S S S S S	77 77 77 77 77 77 77 77 77 77 77 77 77	RESULT INRI_HI IN AC PI
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).  EMBL; J03171; AAA52730.1; EMBL; J03171; AAA52730.1; EMBL; X60459; CAA42992.1; PIR; A33694; A32694. PIR; S17112; S17112.	95059042. 95059042. 21 O., Yan H., Domanski P., Handa R., Small C. O., Yan H., Domanski P., Handa R., Small J., Witte M., Kishnan K., Krolewski J., Mitte M., Kishnan K., Krolewski J., Bidling to and tyrosine phosphorylation of binding to and tyrosine phosphorylation of place to the state of	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE; 90124632.  Uze G., Lutfalla G., Gresser I.;  "Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.";  Cell 60:225-234(1990).  [2]  SEQUENCE FROM N.A.  MEDLINE; 92129376.  Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;  "The structure of the human interferon alpha/beta receptor gene.";  J. Biol. Chem. 267:2802-2809(1992).	LT 1  LHUMAN  INRI_HUMAN  STANDARD; PRT; 557 AA.  P17181;  01-AUG-1990 (Rel. 15, Created)  01-AUG-1990 (Rel. 39, Last sequence update)  15-FEB-2000 (Rel. 39, Last annotation update)  INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).  IFNAR OR IFNAR.  HOMO sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
RESULT INR1_BU II AC QUE DT 0 DT 0 DT 0 DT 0 DE II GN II GN II GN II GN II GN II GN II TOSS BE COSS BE
                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                   유 성
                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 401
         01-OCT-1993 (Rel. 27, C
01-FEB-1994 (Rel. 28, I
01-NOV-1997 (Rel. 35, I
INTERFERON-ALPHA/BETA R
IFNAR OR IFNAR.
                                         INR1_BOVIN
Q04790;
Q1-OCT-1993
Q1-FEB-1994
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                  LT 2
BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transphosphorylation SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                             387
                                                                                                                                                                                                         361
                                                                                                                                                                                                                                      327
                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                          207
                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTK
                                                                                                                                                                           KKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                   KRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDT
                                                                                                                                                                                                                                                                                                                                                         LTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTEQVQWLHAFL
                                                                                                                                                                                                                                                                                                                                                                                                                  CNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPERKAQIGPPEVHLEAEDKAIVIHI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 100.
Similarity 100.
01; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199
481
50
50
50
110
110
1172
172
172
173
314
413
413
413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
437
458
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ξ,
                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436
457
557
2200
486
486
486
486
486
58
58
58
81
110
1172
2254
4416
4416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
63525
                             Created)
Last sequence update)
Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_002717.
G -> A (IN REF. 2).
; 0F6744C8A1ADBE73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2141; DB 1;
Pred. No. 9.5e-154;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <
                                                                                                      560
                                                                                                    ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XB)
                                                                                                                                                                                                          401
                                                                                                                                                                             427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYK2)
TYK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                             (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
                                                                                                                                                                                                                                        386
                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                326
                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                            266
                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

```
SAN TARKARA BARARA BARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; PADACET J.A.;

Lim J.-K., Langer J.A.;

"Cloning and characterization of a bovine alpha interferon "Cloning and characterization of a bovine alpha interferon Biochim. Biophys. Acta 1173:314-319(1993).

-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINE I IFNS TRIGGERS TYROSIME PHOSPHORYLATION OF A NUMBER OF INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-ANI
    CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
Lim J.-K.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X68443; CAA48484.1;
EMBL; L06320; AAA02571.1;
PIR; S33770; S33770.
PIR; S27387; S27387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouchel-Vielh E., Lutfalla G., Mogensen K.E. "Specific antiviral activities of the human determined at the level of receptor (IFNAR) FEBS Lett. 313:255-259(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93076908.
Mouchel-Vielh E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 93305725.
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBURITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I TYPE I III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOXINE FAMILY OF RECEPTORS.
SIMILARITY: BELONGS TO THE CLASS II CYTOXINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                    ; Transmembrane;
1 24
25 560
  422
560
                                                      438
438
459
199
199
172
172
172
173
1313
1313
         ₹
Glycoprotein; Signal.
BY SIMILARITY.
         MW.
                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                        POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                      INTERFERON-ALPHA/BETA RECEPTOR CHAIN.
       -> V (IN REF. 2). 66D76B72861E1D11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.E., Uze G.;
uman alpha interi
NAR) structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A AND BETA. BINDING TO TYPE
N OF A NUMBER OF PROTEINS
IFN-R ALPHA-AND BETA-
            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G.;
interferons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor.";
```

```
Š
                밁
                             Ωy
                                                 밁
                                                                   Ş
                                                                                    Query Match
Best Local S
Matches 258
121
                 86
                                  63
                                                   27
                                                                    ω
                                                  S-PGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA
                          FSSLKL-NYYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                  FSSVELENVFEKIELRIRAEEGNNTSTWYEVEPFVPFLEAQIGPPDVHLEAEDKAIILSI
                                                                                            Similarity
                                                                                     Conservative
                                                                                              64.78;
                                                                                     62;
                                                                                             Score 1384.5; D
Pred. No. 7e-97;
                                                                                      Mismatches
                                                                                                       DB
                                                                                     78;
                                                                                                      ۲.
                                                                                      Indels
                                                                                                       Length
                                                                                     ÿ
                                                                                      Gaps
                                   120
                                                     85
                                                                     62
                                                                                      Ģ
```

```
RESULT 3
INR1_SHEEP
ID 1.NOV
DT 01.NOV
DT 01.NOV
DT 15-FEB
DE (INTERF
GN IFNAR1
OS OVAS a
OC ENTARY
OC CAPTIN
RN [1]
RP SEQUEN
RX MEDLIN
RA HADLI
RY SETUL
RY SETUL
RY SEQUE
RY MEDLIN
RA HADLI
RY SEQUE
RY MEDLIN
RA HADL
RT PAGONE
RY SEQUE
RY SEQUE
RY SEQUE
RY SEQUE
RY MEDLIN
RA HADL
RT PAGONE
RT SOUE
RY SEQUE
RY SEQUE
RY MEDLIN
RY MEDLIN
RY SEQUE
RY SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                           MEDIINE: 98006426."

MEDIINE: 98006426."

Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;

Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and pregnancy.";

Endocrinology 138:4757-4767(1997).

I FUNCTION: RECEPTOR FOR INTERPERONS ALPHA AND BETA. BINDING TO TYPE TONGROUS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INRI_SHEEP STANDARD; PRT; 560 AA. 028589; 095206; 01.NOV-1997 (Rel. 35, Created) 01.NOV-1997 (Rel. 35, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) 1TTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (INTERFERON ALPHA/BETA RECEPTOR-1).
                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Cetartiodactyla; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaluz S., Fisher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97135690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFNAR1 OR IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Endocrinol.
                                                                                                                                                                                                              SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: TYPE I NALL TISSUES EXAMINED EXC
TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXC
CONCEPTUS AT DAY 15 OF PRECNANCY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEKKTDVTVPNLKPLTVYCVKARÅHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEIQAFLLPPVFNIRSLS-DSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKKIPGNHSDKWKQIPNCENVTSTHCVFPREVSSRGIYYVRVRASNGNGTSFWSEEKEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEKRTNFIFPDLKPLTVYCVKARALIENDRRNKGSSFSDTVCE 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRLQSRVGCYSPVYCINTTERHKVPSPENIQINADNQIYVLKWDYPYENATFQAQWLRAF
   X95939; CAA65183.1;
U65978; AAB84231.1;
PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17:207-215(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaluzova M., Sheldri
interferon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheldrick E.L., Flint A.P.F.; eceptor and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IFN-ALPHA-REC)
                                                                                                                               restrictions
tent is in
                                                                                                                                                                    EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae
                                                                                                                                                                                                                                                                                EXCEPT
                                                                                                                                                                                                                          RECEPTORS
                                                                                                                                                                                   a collaboration
                                                                                                              in no way
                                                                                                                                                                                                                                                                                                                                                                             TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205
                                                                                                                                                  9
                                                                                                                                                                                                                        RESULT
   RROCOGEDDAC
                                                                                                                                                                                                                                                                                                                           Ñ
                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γ
                                                                                                                                                                                                                                                                                                 엉
                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 256;
                                                                                                                                                                                   INR1_MOUSE P33896;
                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                    01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
 EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                       326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
                                                                                                                                                                                                                                                                                                                                  359
                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
```

```
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia; Sciurognat
                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTEREERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR
IFNAR1 OR IFNAR OR IFAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEVKPIIFPPVISMKSITDDSLHVSVSASEESENMSVNQLYPLVYEVIFWENTSNAERKV
                                                                                                                                                                                                                                         TEIQAFLLPPVFNIRSLS-DSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI
                                                                                                                                                                                                                                                                                        LKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFD
                                                                                                                                                                                                                                                                                                                                             LITSWKIGYYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAF
                                                                                                                                                                                                                                                                                                                                                                               SPPGTEDSIMWALDRSSFRYSVVIWKNSSSLEERTETVYPEDKIYKLSPEITYCLKVKAE
                                                                                                                                                                                                                                                                                                                                                                                              S-PGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                FSSLKL-NVYEEIKLRIRAEK-ENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                            LEKRTDFTFPNLKPLTVYCVKARALIENDRWNKGSSYSDTVCE
                                                                                                                                                                                        IEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                              LKKIPGKHSNKWKQIPNCENVTTTHCVFPRDIFSMGIYYVRVRASNGNGTSFWSEEKEFN
                                                                                                                                                                                                                                                                                                                               LRLQSRVGCYSPVYCINTTERHKVPSPENVQINVDNQAYVLKWDYPYESTTFQAQWLRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438
438
459
199
199
108
108
109
172
222
222
231
331
331
377
                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437
458
860
220
220
220
255
555
108
857
108
331
331
331
331
331
331
331
331
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC
BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1382.5; DB
Pred. No. 9.9e-97;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
             Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> G (IN REF. 2)
-> D (IN REF. 2)
E7198A1905D4805C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
Muridae;
                                                                                                                590
                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲.
                                                                                                                                                                                                    401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                  (IFN-ALPHA-REC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                             385
                                                                                                                                                                                                                                                     358
                                                                                                                                                                                                                                                                              325
                                                                                                                                                                                                                                                                                                     299
                                                                                                                                                                                                                                                                                                                                265
                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
```

ū

```
Š
                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                    멍
                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                              ð
                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                     밁
                                                                              á
                                                                                                                          밁
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UZE G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
UZE G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;

"Behavior of a cloned murine interferon alpha/beta receptor expressed in homospecific or heterospecific background.";

Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).

1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE I I FINS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-SUBUNITS THEMSELVES.

1- SUBUNITS THEMSELVES.

1- SUBULILAR LOCATION: TYPE I MEMBRANE PROTEIN LIKE DOMAINS.

1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M89641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92262522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:107658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A45283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPSLKKHSNYSTVQCISTTVANKMPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPG
                                                                                                                                                                                                                                          LLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDY-TYANWTFQVQWLHA
                                                                                                                                                                                                                                                                                                                                                                                         CEFSLLDINVYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEAEDKAILVH
                                                                                                                                                                                                                                                                                                                                                                                                                 CNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH
                                        DTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI |:: || :::||: :|: : | | |||||||||||: ::||: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|
                                                                                                                                                     FLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKF
                                                                                                                                                                                                                                                                                                  ISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEVKAI
                                                                                                                                                                                                                                                                                                                            ISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTFSAEYRTKDEAKWLKVPECQHTTTTK
                                                                                                                            YSKSSSGSHSDKWKPIPTCANVQTTHCVFSQDTVYTGTFFLHVQASEGNHTSFWSEEKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192;
  IEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
430
450
78
199
199
109
1181
214
314
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA37890.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590
86
220
220
109
1181
214
214
314
370
409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
; 7EC6DFF370185D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    966;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                               145
                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                          205
                                                     378
                                                                                             358
                                                                                                                                        325
                                                                                                                                                                                298
                                                                                                                                                                                                                          265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
```

```
CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Query Match
Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93300510.

Lutfalla G., Gardiner K., Uze G.
"A new member of the cytokine ro
21 at less than 35 kb from IFNAI
Genomics 16:366-373(1993).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRF4_HUMAN
Q08334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
                                                    DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                               - FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 96054036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                           EMBL; 217227; CAA78933.1; EMBL; U08988; AAA86872.1;
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                    neighbor.";
                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lutfalla G., McInnis M.(
"Structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379
                                                                                                                                                               DOMAIN
                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                             HSSP; P13726
MIM; 123889;
                                                                                                                                                                                                                                                                                                                                                                                                                  function: IS PROBABLY INVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXDGPEFTLKNLQPLTVYCVQARV-LFRALLNKTSNFSEKLCE
                                                                                                                                                                                                                                                   A47003;
                                                                                                                                                                                                                               P13726; 1DAN
123889; -.
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates;
                                                                                                                                                                                                                    Transmembrane;
   Conservative
                                                                                                                                                                                                                                                   A47003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                        Ą,
                                                    19
325
220
249
325
325
37
49
68
102
161
161
161
124
273
37011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                                                                                                                                                                                                                                                                                            institutions as long
             30
                                                                                                                                                                                                                                                                                                                                                                                                                                                .G., Antonarakis
n CRFB4 gene: com
             . 3%;
                                                                                                                                                                                                                    Glycoprotein; Signal.
                                                         Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFNAR.
    41;
                                                       POTENTIAL.
A -> D (IN REF. 2).
FLGHP -> VGRME (IN F
MISSING (IN REF. 2).
M; 66706C79F8514B23 C
  Score 220; DB 1;
Pred. No. 1.2e-09;
1; Mismatches 89
                                                                                                           POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G.;
receptor
                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                    CYTOKINE RECEPTOR CLASS-II EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325
                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene family maps
                                                                                                                                                                                                                                                                                                                              There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ያ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Uze G.;
                                                                                                                                                                                                                                                                                                                     Usage
                                                         CRC64;
                                                                              REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                         Length
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1ts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                  CRF2-4
      12;
     Gaps
                                                                                                                                                                                                                                                                                                                                 90
      7;
```

S

7

PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSL 66

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 6
                            CARBOHYD
CARBOHYD
VARIANT
                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1994 (Rel. 35, Last annotation update)
INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGS_HUMAN P38484;
                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.; "Identification and sequence of an accessory factor required activation of the human interferon gamma receptor."; Cell 76:793-802(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
  SEQUENCE
                                                                   CARBOHYD
                                                                                  CARBOHYD
                                                                                                                                                   DOMAIN
                                                                                                                                                                 CHAIN
                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                     MIM; 147569; -.
PFAM; PF00041; fn3;
                                                                                                                                                                                                                  MIM; 147569;
                                                                                                                                                                                                                             EMBL; U05875; AAA16955.1; EMBL; U05877; AAA16956.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IFNGR2 OR IFNGT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE INTERFEDITE INTERFEDITE TO THE CLASS II CYTOKINE FAMILY OF RECEPTO SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENEXETWINKNYYNSWIYNVQYWKNGIDEKFQIIPQYDFEVLRNLEPWITYCVQVRGFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSWKIGVYSPVHCIKTTVENELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEA-EDKAIVIHISPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENVRMNSVNFKNILQWESPAFAKGNLTFTAQY - - - - LSYRIFQDKCMNTTLTECDFSS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94170380.
                                                                                                                                                                                         Transmembrane;
  337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBROBLAST;
                            28
248
269
269
110
110
137
219
231
  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                            27
247
268
337
268
337
56
85
110
1110
137
219
231
  37834
                                                                                                                                                                         Glycoprotein; Signal; Repeat.
POTENTIAL.
  ₹
                                                                                           INTERFERON-GAMMA RECEPTOR B
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
                            POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
R -> Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
R -> Q.
/FTId=VAR_002718.
18C61B10AD90E509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ζ
                                                                                                                                                              RECEPTOR BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                              OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
```

```
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    跊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   많.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYM1_HUMAN
P52179;
01-OCT-1996
01-OCT-1996
15-JUL-1999
MYOMESIN 1 (
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   Vinkemeier U., Obermann W., Weber K., Fuerst D.O.;
"The globular head domain of titin extends into the center of sarcomeric M band. cDNA cloning, epitope mapping and immunoel microscopy of two titin-associated proteins.";
J. Cell Sci. 106:319-330(1993).
1- FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYOMESIN 1
ASSOCIATED
 DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Ci
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                         EMBL; X69090; CAA48833.1;
                                                                                                                                                                                                                                                                                                                                                                            TISSUE-SKELETAL MU
MEDLINE; 94095665.
                                                              Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYOM1.
                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LKSPOKVEVDIIDDNFILRW-----NRSDESVGNVTFSFDYQKTGMDNWIKLS-----
                                                                                                                                                                                                                                                DEPENDENT:
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
                                                                       ; PF00041; fn3;
; PF00047; 1g; 3
TS; PR00014; FNT
                                                                                                              603508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCQNITSTKCNFSS------LKLNVYEEIKLRIRAEKENT-SSWYEVDSFTPFRKAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FCYYVHYWE--KGGIQQVKGPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPEVHLE----AEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFKYTDSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNISCYETMADASTELQQVILISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPVHCIKTTVENELPPPENIEVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCTQITATECDFTAASPSAGFPMDFNV----TLRLRAELGALHSAWVTMPWFQHYRNVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 (Rel. 34, Created)
6 (Rel. 34, Last sequence update)
9 (Rel. 38, Last annotation update)
(190 KD TITIN-ASSOCIATED PROTEIN) (190
PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
  55544
68266
domain;
16 81
16 51
52 57
58 63
64 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QNONYVLKWDYTYANMTFQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         MUSCLE;
                                                           FNTYPEIII.
omain; Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.9%;
                                                                                                                                                                                                                                                   7 5
                                                                                                                                                                                                                                                  IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
  4 6 6 7 1 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 148; DB 1;
Pred. No. 0.00032;
9; Mismatches 104
                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1451
                                                 ; Thick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                       into the center of immuno
                                                 REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234
                                                           filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KD CONNECTIN-
                                                                                                                                                                                                                                                                                                                                         immunoelectron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -WFTADIMSIGV
                                                                                                                                                                                                                                                             DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                    of the
                                                                                                                                                                                                                                                                                      SI
                                                                                                                                                                                                                                                                                      BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
```

```
INGR. HORAL
INGR. HORAL
ID INGR. H
ID INGR. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                P15260;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                          SEQUENCE FROM N.A. MEDLINE; 89003065. Aguet M., Dembic Z
                                                                                                                                                                                                                                                                                                              INGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388
  receptor.";
Cell 55:273-280(1988).
                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                      'Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                          762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLIEGRSYIFRVRAVNKMGIGFPSRVSEAVAALDPAEKARLKSP----LSTLDWTVIVTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KL-----RIRAEKENTSSW-----YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYIIISWKQPAVDGGSPILGYFIDKCEVGTDSW------SQCNDTPVKFARFPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --VFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEII-----FWENTSNAERKIIEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPENIEVSVQNQNYVLKWD------YTYANMTFQVQWLHAFLKRNP-GNHLYKWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVKSPRFALFDLAEGKSYCFRVRC----SNSAGVGEPSEATEVTVVGDKLDIPKAPGKII
                                                                                                                                                                                                                                                                                                                                                                                                          A-YKISNLKENMVYQFQVAAMNMAGLGAPSAVSECFKCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDITCLESFRDSMVLGWKQPDKTGGAEITGYYVNYREVIDGVPGKWR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TCHGLVTGQS-----YIFRVRAVNAAGLSEYSQDSE-AIEVKAAIAPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSRNTDTSV----VVSWEESKDAKELVGYYIEANVAGSGKWEPC--NNNPVKTHRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTV--
                                                                                                                                      Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
76
290
385
512
613
712
817
918
1138
1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ξ
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
81
289
384
511
612
711
816
816
917
1023
1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1451
                                                                                                                                        Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162452
                                                            Merlin
                                        expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
6.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66;
                                                            ၵ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 122.5; DB 1; Pred. No. 0.18;
                                                                                                                                                          Craniata;
                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                        Hominidae;
                                          of.
                                            the
                                                                                                                                                                                                                                                                                                              489
                                                                                                                                                            Vertebrata;
                                                                                                                                                                                                                                                                                                              ያ
                                          human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181;
                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                401
                                            interferon-gamma
                                                                                                                                                                                                                  (CDW119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                              Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EANVKAVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ENELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
```

g Š

201 27

NELPPPENIEVSVQNQNYVLKWDYTYANM--TFQVQWLHAFLKRNPGNHLYKWKQIPDCE 258

SSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVE----

-VKNYGVKNSEW--IDACI 78

Query Match Best Local S Matches 50

Similarity

5.5%;

50,

Conservative

39;

102; ۲,

Indels

34;

Gaps

10;

Score 118; DE Pred. No. 0.09 99; Mismatches

No. 0.093;

Length 489

```
[2]
DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
MEDLINE; 93183911.
Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta Stueber D. and Stu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zauodny P.J., Narula S.K.;
"Crystal structure of a complex between interferon-gamma soluble high-affinity receptor.";
Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and X-ray crystal structure of the A6 J. Mol. Biol. 273:882-897(1997).
-:- FUNCTION: RECEPTOR FOR INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95342235.
Walter M.R., Windsor W.T.,
  DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERFERON-GAMMA DIMER.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winkler F.K., Robinson J.A.;
"Neutralizing epitopes on the extracellular interferon gamma"
(IFNgammaR) alpha-chain characterized by homolog scanning mut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sogabe S., Stuart F., H
Winkler F.K., Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.9
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                              Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                       209950; -
                                                                                                                                                                                                                                                                                                                                                                                                                                        A31555;
                                                                                                                                                                                                                                                                                                                                                                                                                  1JRH; 25-MAR-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                             J03143; AAA52731.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98035727.
                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stuart F., Henke C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           A31555
      $
domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2.8
                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal; Phosphorylation
         W.
                                                                                                                                                                                                                                                                                                                                   -structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagabhushan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERFERON GAMMA.
    POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
COCF9E574D8F47400 CRC64;
                                                                                                                                                                                                                        INTERFERON-GAMMA RECEPTOR EXTRACELLULAR (POTENTIAL) POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bridges A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ဝ္ဗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by homolog scanning fab-IFNgammaR1-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T.L., Lundell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OWI
                                                                                                                                                                                                                                                                                        RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEX WITH ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTORS BIND ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ິດ
ເ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.J.,
                                                                                                                                                                                                                                                                                          ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lunn C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ດ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

splicing

```
THE RESULT OF STATE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                          EPHRIN-A1, -A2, -A3, -A4 AND -A5.

-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

-I- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

-I- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.

-I- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
HSSP; P00523; 2PTK.

PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00109; TYRKINASE_ATP; FA
PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK.1) (EPH HOMOLOGY KINASE-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPA5_RAT P54757;
                                                                                                                         EMBL; X78689; CAA55357.1; HSSP; P00523; 2PTK.
                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Expression and developmental regulation of Ehk-1, a neuronal Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95206467.
Taylor V., Pfarr S., Mie
Lassmann H., Steck A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression."; Oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE; 94067777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Métazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHAS OR EKH1 OR EHK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFNSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVKTTQCVFPQNVFQKGIYL-LRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VTVPNLKPLTVYCVKARA--HTMDEKLNKS----SVFSDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LSDSFH--IYIGAPKQSGN-TPVIQDYPLIYEIIFWENTSNAERKIIEKKTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miescher G.C., Honegger P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1005 AA
                                                            FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breitschopf H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
Rattus.
                                                                                                                                                                                                .isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                THE NERVOUS
                                                                                                                                                                                                                   for
                                                                                                                                                                                                           commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316
                      밁
                                                                                               멍
                                                                                                                                  Š
                                                                                                                                                                        밁
                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                      449
                                                                                                 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PRAM; PF00041; fn3; 2.
                                                          313
                                                                                                                                    253
                                                                                                                                                                                                                                                       310
                                                                                                                                                                                                                                                                                                                                     272
                                                                                                                                                                                                                                                                                                                                                       103 GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH
                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deceptor;
                                                                                                                                                                          360
                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GKNLKSPQKVEVDII--DDNF-----ILRWNRSDESVGNVT---FSFDYQKTGMDNW
                  VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY
                                                        IRSLSDSFHIYIG---APKQSGNTPVIQ-------DYP----LIYEIIF
                                                                                                                                                                                                ---PENIEVSVQNQNYVLKW------DYTYANWTFQVQWLHAFLKRNPGNHLYKWK
                                                                                                                                  QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN
                                                                                                                                                                                                                                                     GFFKASPHSQTCSKCPP------HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP
                                                                                                                                                                                                                                                                                          KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH-----CIKTTVENELPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG----
                                                                                                                                                                        PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR---
                                                                                                                                                                                                                                                                                                                              DPPKMHCSAEGEWLV----PIGKCMC------KAGYEEKNGTCQVCRP
                                                                                                                                                                                                                                                                                                                                                                                                            ----ACIALVSVRVYYKKCPSVVRHLAVFPD-----TITGADSSQLLEVSGSCVNHSVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                IKLSGCQNITST-----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00069; pkinase; 1.
PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ξ
                                                                               | : |
--YLPQQIGLKNTSVMMADPLAHTNYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170
566
578
669
708
979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otein kinase; ATP-binding; Phosphorylation;
Glycoprotein; Signal; Alternative splicing
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSCCECGCGRASSICAN
SPLICED FORMS).
D -> E (IN REF. 2
G -> A (IN REF. 2
T -> I (IN REF. 2
I -> I (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB
Pred. No. 0.24
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESDPPTMACTR -> G (IN SPLICED FORMS).
RPPSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLICED FORMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCNSHAGVCEECGGHVRYLPQQIGLKNTSVMMADPLAHTNY TFEIEAVNGVSDLSPGTRQYVSVNVTTNQAA -> T (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLICED FORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRRRTQGRGGG -> DADGPRAQASWCHARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE
ATP (BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPHRIN TYPE-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAED42C99693C574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGRASSLCAVAHPSLIW ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN SPLICED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G
                                                                                               EIEA----
```

R (IN

Gaps

21;

(IN

- VNG

448 312

508

416 252

359 206 309 161

271

384

```
á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                PRINTS; PRO0014; ENTYPEIII.

PRINTS; PRO0109; TYRKIMASE.

PROSITE; PS00107; PROTEIN_KIMASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KIMASE_TYR; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS50011; PROTEIN_KIMASE_DOM; 1.

PROM; PF00041; fn3; 1.

PFAM; PF000575; Furin-11ke; 1.
                                                                                                                                                 EMBL; U80631; AAB3896
EMBL; U80630; AAB3896
EMBL; U80629; AAB3896
PIR; A36080; A36080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSR_RAT STANDARD; PRT; 1383 AA. P15127; P97681; O1-APR-1990 (Rel. 14, Created) O1-APR-1990 (Rel. 14, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR).
PFAM; PF01030;
Transferase; Ty
Glycoprotein; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 90231337.

Goldstein B.J., Dudley A.L.;

"The rat insulin receptor: primary structure and conservation tissue-specific alternative messenger RNA splicing.";

Mol. Endocrinol. 4:235-244(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSR
                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348
                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LICAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN TYROSINE PHOSPHATE. ENZYME REGULATION: AUTOPHOSPHORYLATION ACTIVATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THIS I
                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART
                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                            PROTEIN KINASES
                                                                                                                                                                                              M29014; AAA41441.1;
                                                                                                                                        P06213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tam J.W.O
                                                                                                                                                                                                                                                                                                                             the Swiss Institute of Bioinformatics
 0; Recep_L_domain; 1.
Tyrosine-protein kinase; Receptor; Transmembrane;
; ATP-binding; Phosphorylation; Signal; Repeat.
                                                                                                                                                                         AAB38968.1; JOINED AAB38967.1; -.
                                                                                                                                           1IRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1383
                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546
                                                                                                                                                                                                                                                                                                                              and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                 commercial
                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                               밁
                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                           δÃ
                                                          Ş
                                                                                    밁
                                                                                                        8
                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                       481 NDIALKTNGDQASCENELLKFSFIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQN
                                                                                                                                                                                                                              567
                                                                                                                                                                                                                                                   112
                                                                                                                                                                                                                                                                         541
                 362
                                        747
                                                              330
                                                                                     889
                                                                                                           279
                                                                                                                                  650
                                                                                                                                                        226
                                                                                                                                                                               590
                                                                                                                                                                                                      172
                                                                                                                                                                                                                                                                                                 56
                                                                                                                                                                                                                                                                                                                                              17 DNFILRWNRSDESVGNVTFSFDYQKTGMDN------
                                                                                                                                                                                                                                                                         VTEFDGQDAC------GSNSWTVVD
                                                                                                                                                    YANWTFQVQWLHAFLKRNPGNHLYKW-KQIPDCENVKTTQCVFPQNVFQKGIYL-----
    KTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                     TSSGNGAEDTRPSRKRRSLEEVGNVTATTPTLPDFPNISSTI--APTSHEEHRPFEKVVN
                                                                                    PPFESDDSQKHNQSEYDDSASECCSCPKTDSQILKELEESSFR-KTFEDYLHNVVFVPRK
                                                                                                                                                                               YAIFVKTLVTFSDERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDP
                                                                                                                                                                                                    YCLKVKAALLTSWK---IGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKW---DYT
                                                                                                                                                                                                                              NDPKSQTPSHPG-----WLMRG-----
                                                                                                                                                                                                                                                 EDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETT
                                                                                                                                                                                                                                                                                               IT----STKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEA
                                                                                                        --LRVQASDGNNTSFWSEEI-----KFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQ
                                                                                                                                   NGNIT------KGLKLPSRTWS
                                                                                                                                                                                                                                                                                                                                                                     Similarity 19.0
86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.5%;
19.0%;
                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                                 Score 117.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
```

DB 1; 146;

1383

Indels 171; Length

Gaps

19;

----WIKLSGCQN

----IDPPQ---RS

566

171

111

540 55

.....LKPWTQ

649

225 589

TPVIQDYPLIYEIIFWENTSNAERKIIEK---

362

329 687 279

```
CHAIN
PROPEP
                                                                                                                       1
27
761
764
764
958
979
619
849
1024
1030
1058
1160
1160
11000
1000
.9 L ->
                                                                                                                                                             FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASP
                                                                                                           INTERCHAIN POTENTIAL.
                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                            PHOSPHORYLATION (AUTO-).
IMPORTANT FOR BIOLOGICAL
BY SIMILARITY.
                                                                                                                                                                                             INSULIN RECEPTOR, ALPHA-SUBUNIT REMOVED IN MATURE FORM.
INSULIN RECEPTOR, BETA-SUBUNIT.
EXTRACELLULAR (POTENTIAL).
            POTENTIAL.
                        POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                 POTENTIAL
                                                                                                                                               SIMILARITY
                                                                                                                                                           (BY SIMILARITY).
> M (IN REF. 2).
4B919566902A944A CRC64;
                                                                                                                        (BY SIMILARITY).
                                                                                                                                    ACTIVITY
```

밁

```
RESELLA SE LA COLLA COLL
       g
                                          Š
                                                                                                 밁
                                                                                                                                            δÃ
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A44027; A44027.
HSSP; P56276; 1TLK.
PFAM; PF00041; fn3; 5.
PFAM; PF00047; 19; 3.
PRINTS; PR00014; FNTYPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHICK
                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPSF_CHICK Q02173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pectoralis M-protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D11474; BAA02033.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete primary structure and tissue expression of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Panaka T., Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93015907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
       422
                                                                                                    373
                                                    63
                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE. DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE CONTENT IS GRADUALLY INCREASED THROUGHOUT THE OVO DEVELOPMENT AND REACHED ITS PEAK AFTER HATCHING.
SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: IS A STRUCTURAL
       DAPVKICKYPVTGLYEGRSYIFRVRA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESLVISGLRHFTGYRIELQACNQDSPEERSGV
                                                  FSSLKLNVYEEIKL-----RIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAED-
                                                                                                                                            SPOKVEV-DIIDDNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLSGCQNITSTKCN
                                                                                                 APMDVKCHDANRDYVIVTWKPPNTTSQNPVIGYFVDKCEVGLENWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J., Yanagisawa M., Imamura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , STRIATED MUSCLE.
                                                                                                                                                                                                                                                                                                                   142
368
496
597
797
1002
11225
1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267:20302-20310(1992).
S A STRUCTURAL CONSTITUENT OF MYOFIBRILLAR M-BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PECTORALIS MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29, Createu,
29, Last sequence update)
38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                   364
464
693
794
799
1095
1205
1312
                                                                                                                                                                                                                    5.3%;
                                                                                                                                                                                                                                                                                                                   163400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITUTE
                                                                                                                                                                                                                                                                                                              IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        munoglobulin domain.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                    Score 113;
Pred No. 0.
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                 E313C7D39FE6CAC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kasuya Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         837
                                                                                                                                                                                                                    DB 1;
.92;
       VNSAGISRPSRVSEPVAALDPVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ⋧
                                                                                                                                                                                                                                           Length 1450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakurai T.
                                                                                                                                                                                              132;
                                                                                                 OCN.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                  114
                                                                                                 421
                                                                                                                                                 62
                                                                                                                                                                                              25
  REAL TO SEE TO PERSON TO SEE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _MOUSE
DCC_MOUSE
P70211;
EMBL; X85788; CAA59786.1;
HSSP; P56276; lTLK,
MGD; MGI:94869; DCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BALB/C; TIS MEDLINE; 96112625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooper H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
```

```
EL SUBMITTED (JUN-1996) to the EMBL/GenBank/DDBJ databases.

1 - FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.

2 - - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ARE PRODUCED FROM CONTROL PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM THE SAME GENE BY THE USE OF ALTERNATIVE INITATION SITES. A THIRD COMMENT OF THE SAME GENE BY THE USE OF ALTERNATIVE INITATION SITES. A THIRD COMMENT OF THE SEMBLE ONLY IN THE EMBRYO IS PRODUCED BY ALTERNATIVE SPLICING.

2 FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO AT HIGH LEVELS IN THE EMBRYO. EXPRESSED AT HIGH LEVELS IN THE CONTAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN COMPLETORY OF LEVELS FOUND IN TESTIS, HEART AND THYMUS.

3 EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.

3 EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.

3 EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning of the mouse homologue of the deleted in colorectal can gene (mDCC) and its expression in the developing mouse embryo."; Oncogene i1:2243-2254(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QESEAIK----VQAALTCPSYPHGITLLNCDGHSMTLGWKAPKYSGGSPILGYY 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FWSEEIKEDTEIQAFLLPPVF -- NIRSLS - DSFHIYIG -- APKQSGNTPVIQDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KAIVIHISPG----TKDSVMWALDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKG-IYLLRVQASDG---NNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSEITEPIQPQDIVVVPSAPGRVVATRNTKTSVVVQWDKPKHEENLYGYYIDYSVVGSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVHCIKTTVENEL - - - PPPENIEVSVQN - - QNYVLKWD - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPLTYFIEKSMVGSGSWQRVNAQVAVKSPRYAVFDLAEGKPYVFRV----LSANKHGISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERTQTVHVDEGRKIVISKDD----LEGDIQIPGPPTNVHASEISKTYVVLSWDPPVPRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse).
etazoa; Chordata; Craniata; Vertebrata; Mammalia;
etazoa; Chordata; Craniata; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPANH----KPI----NYNR----FVVHGLETGEQYIFRVKAVNAVGFSENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSFTYSLLIWKN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - YTYANMTFQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
```

( 명

3.1.3.48) (R-PTP-

Mammalia;

Η.,

Streul1

X :

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                            Š
                                                                                                                                                                                                                 용
                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                       8
õ
                             밁
                                                   Š
                                                                                          &
                                                                                                                    Š
                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.:
Best Local Similarity 21.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00041; fn3; PFAM; PF00047; ig; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                      483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431
                                                                                                                                                                                                                                                                               594
                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                        116
                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPQKVEVDIIDDNFI-LRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKCNF
                                                                                                                                                                                                                                                                                                                                                           GSLQLTVGNLKPEAMYTFRVVAYN--EWGPGESSQPIKVATQPELQVPGPVENLHA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APRDVLPVLVSSRFVRLSWRPPAEAKGNIQTFTVFFSREGDNRERALNTTQP----
                                                                                                                                                                                   LHAFLKRNPGNHLYKWKQIPDCENV----KTTQCVFPQ-----NVFQKGIYLLRVQAS
                                                                                                                                                                                                                                                N-----YVLK-----TFQV-----
                                                                                                                                                                                                                                                                               YTLRFLA--YNRYGPGVSTDDITVVTLSDVPSAPPQNISLEVVNSRSIKVSWLPPPSGTQ
                                                                                                                                                                                                                                                                                                                                       --VSTSP-TSILITWEPPAYANGPVQGYRLFCTEVSTGKEQNIEVDGLSYKLEGLKKFTE
                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLKL---NVYEEIKLRIRAEKENTSSWYEVDSFTPFRKA----QIGPPEVHLEAEDKA
                                                PVIQD------YPLIYEIIFWENTSNAERKIIEKĶTDVTVPNLKPLTVYCV-----KAR
                                                                                                                         DGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYI------
                                                                                                                                                       ---YTAETPENDLDE-SQVPDQPSSLHVRPQTNCIIMSWTPPLNPNIVVRG-YIIGYGVG
                                                                                                                                                                                                                   NGFITGYKIRHRKTTRRGEMETLEPNNLW-YLFTGLEKGSQYSFQVSAMTVNGTGPPSNW
                                                                                                                                                                                                                                                                                                            YCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN----
                                RSITDPTDPVDYYPLLDDF-
                                                                                            -SPYAETVRVDSKQR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1098
1123
154
154
254
345
426
525
525
722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       840
941
161
161
261
352
352
352
318
478
628
819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940
1042
1117
212
310
400
400
299
318
478
628
838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                            --YYSIERLESSSHYVISLKAFNNAGEGVPLYESATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR SUPPRESSOR PROTEIN DCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   itiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
n; Alternative
                                   - PDVSTPMLPPVGVQAVALTHEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal; splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOFORM).
                                                                                                                                                                                                                                                                                                             Ω-----
                                                                                                                         -GAP-KQSGNT
                                                                                                                                                                                                                                                WQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LONG F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                           171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                              593
                                                                                                                                                                                                                                                                                                                                                                                                          537
                                                                                             814
                                                                                                                                                           765
                                                                                                                                                                                                                     710
                                                                                                                                                                                                                                                   235
                                                                                                                                                                                                                                                                                  651
                                                                                                                                                                                                                                                                                                             216
                                   861
                                                              381
                                                                                                                            333
                                                                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
PTPD_HUMAN
        밁
                                                  PROSITE: FULL
PEAM; PF00047; 19; 3.
PFAM; PF000102; Y_phosphatase; 2.
PFAM; PF00102; Y_phosphatase; 2.
PFAM; PF00102; Y_phosphatase; 2.
PFAM; PF00102; Y_phosphatase; 2.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine phosphatase delta. Evidence for tissue-specific expression of alternative human transmembrane protein-tyrosine phosphatase delta isoforms.", J. Biol. Chem. 270:6722-6728(1995).
    DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOY-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR
                                                                                                                                                                                                                                                               EMBL; L38929; AAC41749.1;
EMBL; X54133; CAA38068.1;
PIR; S12052; S12052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 390-1912
TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pulido R., Krueger N.X., Serra-Pages C., "Molecular characterization of the human protein-tyrosine phosphatase delta. Evide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTPRD
                                                                                                                                                           PROSITE; PS50056; PROSITE; PS50055;
                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphatases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krueger N.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 95204468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                     PRINTS; PR00700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Structural diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             862 VSWADNSVPKNOKTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DI
TISSUES DUE TO ALTERNATIVE SPLICING.
PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR PHON THE TRANSMEMBRANE SEGMENT.
SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (
SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (
LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOM
AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN TYROSINE + ORTHOPHOSPHATE
                                                                                                                                                                                                                                      601598;
                                                                                                                                                                                                                                                   P18052; 1YFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9:3241-3252(1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91006018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                        FNTYPEIII.
PRTYPHPHTASE
                                                                                                                                                           TYR_PHOSPHATASE_1; 2:
TYR_PHOSPHATASE_2; 2:
TYR_PHOSPHATASE_PTP;
        20
1912
1265
1290
1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito H.;
evolution
                                                                                                                                                                                                                                                                                     . .
      EXTRACELLULAR (POTENTIA POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                   PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of human receptor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito
                                                                                                Transmembrane;
                                   INE PHOSPHATASE (POTENTIAL).
```

+

H(2)0

DIFFERENT

DOMAIN ٦ ۲

DOMAINS),

G

Duplication;

```
RESULT 14
IION_MOUSE
ID IION_M
AC 061727
DT 15-JUL
DT 15-DEC
DE INTERL
GN ILIORA
OS MUS mu
OC EUKARY
OC EUKARY
OC EUKARY
OC EUKARY
OC EUTHER
RN [1]
RP STRAIN
RX MEDLIN
RX MEDLIN
RA HO A.S
RT "A recc.
CC -1- FU
                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 60
                                                                                                                110R_MOUSE STANDARD; PRT; 575 AA.

Q61727;
Q61727;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).

VILIORA OR IL10R.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
EXTE
MEDLINE: 94068585.

HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., M. Ho A.S.-Y., Interferon To raceptor for interfeukin 10 is related to interferon Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).

-1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6 X AJ F1; TISSUE-HEMATOPOIETIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                    977
                                                                                                                                                                                                                                                                                                                                                               363
                                                                                                                                                                                                                                                                                                                                                                                                                                                     907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 LSPETTYCLKVKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSPVHCIKTTV-ENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNH
                                                                                                                                                                                                                                                                                                                               TIMTLIGLKPDTTYDVKVRAHT
                                                                                                                                                                                                                                                                                                                                                TDVTVPNLKPLTVYCVKARAHT
                                                                                                                                                                                                                                                                                                                                                                                                                  PPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSN-----AERKIIEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVKEISIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGPLOGYRLKFGRKDMEPLTTLEFSEKEDHFTATDIHKGASYVFR----LSARNKVGFGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQPETSYSLTVTAYTTKGDGARSKPKLVSTTGAVPGKPRLVINHTQMNTALIQWHPPVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 115
118 225
232 318
320 414
417 513
516 606
509 708
18 1017
25 916
18 1017
75 1618
19 125
3 1553
4 1844
5 1178
832
1138
1137
724
832
1139
139
139
139
139
139
139
139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EEVPTG - - - FPQNLHSEGTTSTSVQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%;
22.9%;
                                                                                                                                                                                                                                                                                                                                                              384
                                                                                                                                                                                                                                                                                                                                998
                                                                                                                                                                                                                                                                                                                                                                                         ----GIITKYTLLYRDI-----NIPLLPMEQLIVPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110; DB
Pred. No. 2.2;
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN-TYROSINE |
PROTEIN-TYROSINE |
PROTEIN-TYROSINE |
BY SIMILARITY.

CLEAVAGE (POTENTIL
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
MISSING (IN KIDNEMISSING (IN KIDNEMISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SING (IN KIDNEY ISOFORM).
SING (IN KIDNEY ISOFORM).
SING (IN KIDNEY ISOFORM).
SING (IN FETAL BRAIN ISOFORM).
A: 2.5-FOLD REDUCTION IN CLEAVAGE.
3AE8CBCD3218ZE26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------ALLTSW--KIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---OW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                      Mammalia;
Mus.
                             Moore K.W.;
on receptors
   AFFINITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                        976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247
RESULT
EPAS_HU
ID PS
AC PS
AC PS
DT 01
DT 01
DT 15
DT 15
DT EF
DE XI
DT T1
DT T7
DE XI
DE XI
DE XI
DE TY
OS HC
                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:96538;
                                                                                                                                                                                                          325
                                                                                                                                                                                                                                       294
                                                                                                                                                                                                                                                                     267
                                                                                                                                                                                                                                                                                               251
                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                           206
                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242
263
204
50
66
113
113
182
238
```

```
EPAS_HUMAN STANDARD; PRT; 1037
PS4756;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence upda
15-JUL-1998 (Rel. 36, Last annotation up
15-HILL TYPE-A RECEPTOR 5 PRECURSOR (EC 2
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KIN
TYROSINE KINASE HEKT).
EPHAS OR EHK1 OR HEK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L12120; AAA16156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                 EEIKFDTEIQAFLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDEVIL-----TVDSVTLKAMDGIIYGTIHPPRPTITPAGDEYEQVFKDLRVYKISIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKNLKSPQKVEVDIIDDNFILRW----NRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNI
                                                                                                                                                                                                                                          GKPSLQTEESQFLLP
                                                                                                                                                                                                                                                                                                              -- KLPTVLVFKKPHDFFPANPLCPETPDAIHIVDLEVFPKVSLELRDSVLHGSTDSGFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDKAIVIHISPGTKDSV-MWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QALSCDLTTFTLDLYHRSYGYRARVRAVDNSQYSNWTTTETRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSTKCNFSSLKLNVYEE---IKLRIRA-EKENTSSWYEVDS-FTPFRKAQIGPPEVHLEA
: |: :: |::| : |:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSELKNATKRVKQETFTLTVPIGVRKFCVKVLPRLESRINKAEWSEEQCLLITTEQY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTELPSPSYVWFEARFFQHILHWKPIPNQSESTYYEVAL----KQYGNSTWNDIHICRKA
                                                                                                                                                                                                                                                                                                                                                                                                                     PENIEVSVQNQNYVLKWDYTYANMTFQV-------QWLHAFLKRNPGNHLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 20.075; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   -----FTVTNLSILVISMLLFCGILVCLVLQW----YIRHPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PET-----TYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL10RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575
2241
575
225
50
50
1113
1182
238
6424
                                                                                                                                                                                                                                          339
                                                                                                                                                                                                                                                                          308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal.

POTENTIAL.

INTERLEUKIN-10 RECEPTOR.

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Œ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                     annotation update)
ECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENT:
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.5
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                           update)
                                                                                                                                                1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 ...
                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                               -VFQKGIYLLRVQASDGNNTS-FWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                              324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
                                                                                                                                                                                                                                                                                                                                               293
                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Similarity

5.0%; 20.3%;

Score 108; DB Pred. No. 1.4;

Length 1037;

23;

```
PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.

PFAM; PF00036; SAM; 1.

PFAM; PF00036; SAM; 1.

PFAM; PF00336; SAM; 1.
                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                           DOMAIN
NP_BIND
BINDING
ACT_SITE
                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                        EMBL; X95425;
                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                 SIGNAL
                                                    CARBOHYD
                                                                                                                                       DOMAIN
                                                                                                                                                TRANSMEM
                                                                                                                                                          DOMAIN
                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                   Transferase;
 SEQUENCE
                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                          600004;
                                                                                                                                                                                                                                                                                                                                                      L36644;
P00523;
                                                                                                                                                                                         Transmembrane;
 1037
                     25
574
595
675
675
681
707
707
264
299
366
423
436
436
436
436
436
436
436
                                                                                                                                                                                                     Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                       CAA64700.1; -.
                                                                                                                                                                                                                                                                                                                                                               AAA74245.1; -.
 ₽
                                                                                                                                     1037
573
594
1037
 114784
                                                                                                                                                                             otein kinase; ATP-binding; Phosphorylation;
Glycoprotein; Signal; Alternative splicing
POTENTIAL.
  ₹.
                              POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                   POTENTIAL.
                     SCCECGCGRASSLCAVAHPILIW -> R
                                                                                    POTENTIAL.
                                                                                               SIMILARITY.
  FC2C46C959AFB699 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions in as its content is in
                       (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
```

```
Ş
                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                            밁
                                                                                                                                                                                                                         δÃ
                                                                                          Q
                                                                                                                              닭
                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                          밁
 믕
                            20
                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 94
                                                               444
                                                                                                                               411
                                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                            308
                                                                                                                                                                                                                                                                                            162
                                                                                                                                                                                                                                                                                                                          270
                                                                                                                                                                                                                                                                                                                                                       103 GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH 161
                                                                                                                                                                                                                                                                                                                                                                                         219 ----ACIALVSVRVYYKKCPSVVRHLAVFPD----TITGADSSQLLEVSGSCVNHSVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 GRNIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG----
                               342
                                                                                              307
                                                                                                                                                            247
                                                                                                                                                                                              358 PSAPRNAISNVNETSVFLEWIPPADTGGRKDVSYYIACKKCNS-----HAGVCEECGG
                                                                                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKNLKSPQKVEVDII--DDNF-----ILRWNRSDESVGNVT---FSFDYQKTGMDNW 47
                                                                                                                                                                                                                                                                                         KIYKLSPETTYCLKVKAALLISWKIGVYSPVH-----CIKTTVENELPP-----
                                                                                                                                                          HLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFL
                                                                                                                                                                                                                          ---PENIEVSVQNQNYVLKW------DYTY-----ANMTFQVQWLHAFLKRNPGN 246
                                                                                                                                                                                                                                                                                                                                                                                                                       IKLSGCQNITST-----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI 102
                                                               ---VNGVSDLSPGARQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIIL
                                                                                                                                                                                                                                                            GFFKASPHIQSC------GKCPPHSYTHEEASTSCVCEKDYFRRESDPPTMACTRP
                                                                                                                                                                                                                                                                                                                            EPPKMHCSAEGEWLV----PIGKCMC-----
EYEIKHFEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART 544
                          IYEIIFWENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT
                                                                                              LPPVFNIRSLSDSFHIYIG---APKQSGNTPVIQ-------DYP----L
                                                                                                                              HV---RYLPRQSGLKNTS-------VMMVDLLAHTNYTF------EIEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 159;
                                                                                                                                                                                                                                                                                                                            ----KAGYEEKNGTCQVCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 162;
                                   384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                               357
                                                                                                                                                                                                                                                                                                                               307
                                                                                                                                                                                                                                                                                                                                                                                                                                                            219
                                                                                                                                                                                                 410
                                                                                                                                                                 306
                                                                                                                                                                                                                                                                                               206
                                                                                                   341
                                                                                                                                   444
```

FOX G.M., Hoist P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
Basu R., Welcher A.A.;
Basu R., Welcher A.A.;

"cDNA cloning and tissue distribution of five human EPH-like receptor
protein-tyrosine kinases.";

Oncogene 10:897-905(1995).

-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.

MEDLINE; 95206782. TISSUE-BRAIN SEQUENCE OF 25-1037 FROM N.A.

Submitted (JAN-1996) Miescher G.C. TISSUE-BRAIN; SEQUENCE FROM N.A.

៥

the EMBL/GenBank/DDBJ databases

<del>'</del> -<del>:</del>

TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED

ALTERNATIVE PRODUCTS: A NUMBER ALTERNATIVE SPLICING.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARI

VARIANTS ARE PRODUCED

ВУ

IN THE NERVOUS

SYSTEM

Search completed: June Job time: 14313 sec ۲, 2000, 04:38:50

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seg length: 0
Maximum DB seg length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 08
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
               110
112
113
114
117
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
             668.5
216.5
119.5
1183.5
1123.5
1123.5
1123.5
1123.3
1123.3
1123.3
1123.3
1123.1
117.5
1117.5
1117.5
1117.5
1117.5
1117.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPTREMBL_12:*
             US-09-240-675-2_COPY_27_427
2141
1 GKNLKSPQKVEVDIIDDNFI.....AHTMDEKLNKSSVFSDAVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              June 1, 2000, 00:39:48; Search time 69.16 Seconds
(without alignments)
402.010 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_mhc: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_fungi: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_human: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
          1526
1461
1461
1427
1585
2214
817
1264
26926
1377
          4445544554455445554455544
        O9YHWO
O63953
O9YGC8
O9YGC8
O9YGC9
O9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225878
O9yhw0 gallus gall
Q61190 mus musculu
Q63953 mus musculu
Q63953 mus musculu
Q9ygc8 gallus gall
Q9yw6u9 gallus gall
Q9yw6u9 gallus gall
Q94537 drosophila
Q94537 drosophila
Q94538 drosophila
Q94538 drosophila
Q94539 homo sapien
Q01365 xenopus lae
Q17859 caenorhabdi
Q92673 homo sapien
Q01794 gallus gall
Q91767 manduca sex
Q09946 caenorhabdi
Q10466 homo sapien
Q01763 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
```

	13 Q98949 13 Q98949 11 Q98675 11 Q986775 11 Q88307 4 Q9Y6N7 5 Q9Y6N7 4 Q1333 5 Q61141 5 Q61142 11 Q64142 11 Q64146 13 Q90815			108.5 108.5 108.5 108.5 105.5 105.5 105.5 104 104 103.5 103.5	00000004444444 04000000000000000000000
024495 drosophila 029917 sus scrofa 063155 rattus norv 060469 homo sapien 060468 homo sapien 023020 caenorhabdi 023550 caenorhabdi 023551 caenorhabdi 023551 caenorhabdi 024936 homo sapien 04404 r protein-t 095209 oryctolagus 018094 caenorhabdi	5 Q24495 6 Q29117 11 Q63155 4 Q60468 5 Q23520 5 Q23550 5 Q23551 5 Q23551 6 Q23551 6 Q23551 6 Q23551 6 Q23551 7 Q23551 8 Q23551 8 Q23551 8 Q23551 9 Q2551 9 Q251 9	1767 572 1445 1571 1596 6048 6048 6831 7160 484 1898 2213 421	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	113 111.5 111.5 111.5 111.5 111.5 111 111 1	300000000000000000000000000000000000000

## ALIGNMENTS

RESULT	LT 1
D C	Q9YHWO PRELIMINARY; PRT; 569 AA.
AC	
D.	-1999 (
j i	(TrEMBLrel. 10,
<b>3</b> 5	01-MAY-1999 (TrEMBUrel. 10, Last annotation update)
ລະເ	TENAR!
0 2	Gallus gallus (Chicken)
გ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
8	ianidae: Phasianinae: Gallus.
RN	
ЯP	SEQUENCE FROM N.A.
RC	TISSUE-LIVER;
RA	REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;
RT	the interferon/inter
RT	•
RL	Genome Res. 0:0-0(1999).
DR	EMBL; AF082664; AAD13669.1;
XX	Receptor.
ŞQ	SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;
Quer Best Matc	Query Match 31.2%; Score 668.5; DB 13; Length 569; Best Local Similarity 38.0%; Pred. No. 8.9e-46; Matches 158: Conservative 77: Mismatches 154: Indels 27: Gans 12:
Qy	KVEYDIIDDNFILRWNRSDESVGNYTESEDYQKTGMDNWIKLSGCON
D)	31 NIKSPODIQVYAVNINETIMWNYTGDGT-NVTFSAQYQCFDDLQTSEPEWKELSGCQNVS 89
ОУ	58 STXCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSTTPFRKAQIGPPEVHLEAEDKAI 116
Д	90 HTECDESSAITAYYDTHHIRIRAERREAKSPWSSIFEMIPYEIAQIGPPEIALQSINGAI 149
Qy	GTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKI
дb	150 KINISPPEANQVRKMW-LISVFFKYNVVIWDNSSNV-EKVRSILPIDVINDLAPETTYCL 207
Οу	d.
뫄	208 KVQATVPLEDKGGLESPIHCIKTIRKVNDLLCPTNVRVFALNNKFYLLWDNHYNEHVTYT 267

```
RESI Q61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         명
RESULT
Q63953
ID Q
AC Q
DT 0
DT 0
DT 0
OC DT 0
                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                 밁
                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q61190;

Q1-NOV-1996 (TrEMBLrel. 01, C:

Q1-NOV-1996 (TrEMBLrel. 12, L:

Q1-NOV-1999 (TrEMBLrel. 12, L:

CYTOKINE RECEPTOR FAMILY 2, M:

IL10RB OR CRFB4 OR CRF2-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 186:97-101(1997).

EMBL; U53696; AAC53062.1; -

MGD; MGI:109380; II10rb.

PFAM; PF00041; fn3; 1.

SEQUENCE 349 AA; 39774 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae;
                                                      Q63953;
Q1-NOV-1996 (TremBLrel. 01, 01-NOV-1996 (TremBLrel. 12, 01-NOV-1999 (TremBLrel. 12, 12, 14) Therefore, GAMMA RECEPTOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               061190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIBBS V.C., PENNICA D.;
"CRF2-4: isolation of coproteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                      Q63953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268
                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                               IFNGR2
                                                                                                                                                                                                         175
                                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                       122
            Eutheria;
                                                                                                                                                                                  190
                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WENTSNAERKIIEKKTD---VTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKSCLSKDVEVDPPVTNEIGPPDVKVDISDVLLHIKITPPGGPGNKIMSDLYDFSYQILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOWLHAFLKRNDGNHLYKWKQIPDCENVKTTQC-----VFPQNVFQKGIYLLRVQASDGN
||:| :|| :: ||:: |||: :| : | : | : | | | |||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKNSSDNEEEVKMKETKQTIATVSDLAPSTLYCVKVQA--FSEAYNKSSDFSREEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQYLTGYLKNLYDDYSSKWQKVSGCENITSMKCNLSSVIKPTS----ASYYFRVQAMNEY
                                                                                                                                                                                                                                                                                                                                                  POKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                                                                             KVKAALLTSWKIGVYSPVHCIKTTVENELPP: |: | : | : | : | : | : |
                                                                                                                                                                                                                                                                              --HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPEMQIESLAESLHLRFSAP
                                                                                                                                                                                                                                                                                                   SLKLNYYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-- 122
                                                                                                                                                                                                                                                                                                                           PEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH-----CKRTASTQCDFS
                                                                                                                                                                                 QVQGFLLDQNRTGEWSEPIC-ERTGNDEITP
                                                                                                                                                                                                                                QIENEPET - - -
                                                                                                                                                                                                                                                   ----PGTKDSYMWALDGL--SFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCL
                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
97199375.
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
             ; Metazoa;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                               -WTLKNIYDSWAYRVQYWKNGTNEKFQVVSPYDSEVLRNLEPWTTYCI
            Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                       10.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequ
Last anno
MEMBER 4
                                                                                                                                                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clones
                                                                                                                                                                                                                                                                                                                                                                            Score 216.5; DB
Pred. No. 8e-10;
45; Mismatches 7
                                                           Created)
Last sequence update)
Last annotation update)
(INTERFERON GAMMA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        4AC1802A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
annotation update)
ER 4 (CLASS II CYTOKINE RECEPTOR 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349
                                                                                                                                                                                                           205
                                                                                                                         332
                                                                                                                                                                                  219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                              79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                           Mammalia;
                                                                BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse
                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                SUBUNIT)
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323
                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                     189
                                                                                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                 9
```

```
RESULT OF CONTROL OF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQ DRR PROPERTY OF REAL PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멇
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic organization and promoter analys encoding the second chain of the mouse in Scand. J. Immunol. 44:599-606(1996).

EMBL; U69599; AAC52938.1; JOINED.
EMBL; U69596; AAC52938.1; JOINED.
EMBL; U69596; AAC52938.1; JOINED.
EMBL; U69597; AAC52938.1; JOINED.
EMBL; U69598; AAC52938.1; JOINED.
                                                   REBOUL J., GARDINER K., MONNERON D
"Comparative genomic analysis of the receptor gene cluster.";
Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1; ...
EMBL; AF082666; AAD13671.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9YGC8 PRELIMINARY;
Q9YGC8;
01-MAY-1999 (TTEMBLTel. 1
01-MAY-1999 (TTEMBLTel. 1
01-MAY-1999 (TTEMBLTEL. 1
INTERLEUKIN-10 RECEPTOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
MGD; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-129SV/J;
MEDLINE; 97128072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells.";
Cell 76:803-810(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEMMI S., BOHNI R., STARK G., DI M "A novel member of the interferon functionality of the murine interf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EBENSPERGER C., RHEE S., MUTHUKUMARAN PESTKA S., DEMBIC Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
MEDLINE; 94170381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                         IL10R2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LKSPQKVEVDIIDDNEILRWNRSDES-----VGNVTESFDYQKTGMD-NWIKL--SGCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:107654; Ifi
; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIY--KL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPE-VH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTPGKGSLVIHFSPPFD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
            341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
            <u>β</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ifngr2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.38;
                39062
                                                                                                                                                                                                                                                                                                                                                                                                                                            10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Μ.
.
                ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VFHGATFQYLVHYWEKSETQQEQVEGPFKSNSIVLGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 199; DB Pred. No. 1.9e 88; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DI MARCO F.,
eron receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBF24E9E
            7433D364 CRC32;
                                                                                                                                                                                                   D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ດ
ເ
                                                                                                                                                                                                   UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
1.9e-08;
hes 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family complements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGUET M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                ; Archosauria; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DONNELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                   ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
```

```
멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
               Š
                                                    В
                                                                                   Š
                                                                                                                            밁
                                                                                                                                                           ő
                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                      망
                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gailus (Chicken).
Gallus gailus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Eukaryota; Metazoa; Chordata; Cranidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09W6U9;
01.NOV-1999 (TrEMBLrel. 12,
01.NOV-1999 (TrEMBLrel. 12,
01.NOV-1999 (TrEMBLrel. 12,
GLYCOPROTEIN 130 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEISSEN M., HELLER S., PENNICA D., ERNSBERGER U., F
"The specification of sympathetic neurotransmitter
on gpl30 cytokine receptor signaling.";
Development 125:4791-4801(1998).
EMBL: AJ011688; CAB42084.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 99026068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9W6U9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                                387
                                                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 WKQIPDCENVKTTQC-VFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 CIKTTVENELPPPENIEVSVQNQNYVLKWD---YTYANMTFQVQWLHAFLKRNPGNHLYK
                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCE 401 : | : | | : | : | | : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFNIRSLSDSFHIYIGAP---KQSGNTPVIQDY-PLIYEIIFWENTSNAERKIIE---KK 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVNVKSESGTLHVDFTGPAADREHDKWSLKQYYGSWIYRILYWKKGSN--KKVIHIDTKH
                                                    GKLWVGWTAPNNVLKYVIEWC---LMSNSSDCITEWQTEPG--NI-----QGTYLKG
                                                                                     QNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKG
                                                                                                                            YNVTTTSLTLKLPNGTY----EVTVVAHNRVGA-SPPSVLLIPSSNSKAPVKNIRTLPKD
                                                                                                                                                             HKIYKLS-----PETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN
                                                                                                                                                                                                                                                                              SIQGLRPYTEYVFSIRCMKEDGVGFWSDWSE-----EQIG-----VTTEDKP----
                                                                                                                                                                                                                                                                                                                 SSLKLNVYEEIKLRIRAEKEN----TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIH
                                                                                                                                                                                                                                                                                                                                                      PRNLSYNSGILPTVLKLSWENQISTVVMELKFNIRYRISSDINWMEVPP-EDTASPRTSF
                                                                                                                                                                                                                                                                                                                                                                           PQKVEVD--IIDDNFILRW-NRSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSEILSQLEPWTIYCIQVQG--VIPEWNKTGERSQELCE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VTTNLNVTECDVSSLSVY--GAYVLRVRTEWEDEHSDWA-VVRFKPMADTVIGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLLLCVSGIVPKPRNARISSVNFRSVLLWDPPGVRKGNLSYTVQAKSIFPKQNFNN----
                                                                                                                                                                                                    ----SKGPTIWRTIDVSPSPAFWIVRLMWKALEPFEANGVILQYEVTIRAKPPLSHPPSR
                                                                                                                                                                                                                                       ISPGTKDSVMWALDGLS----FTYSLLIWK-----NSSGV------
                                                                                                                                                                                                                                                                                                                                                                                                                                85; Conservative
---IXLLRVQA---SDGNNTSFWSEEIKFDTEIQAFLLP-----PVFNIRSLSDSFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEART PRIMARY CULTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 PO
102495 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 183.5;
Pred. No. 3.4e
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 133.5; DB 13; Pred. No. 0.013; 7; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. 9DC128C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (E7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB_13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E8);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROHRER H.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phenotype depends
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                       EERIENIYSR
                                                                                                                                                                                                                                                                                                                                                                                                                              105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aves;
                                                                                                                                                                                                                                                                                                                   119
                 321
                                                                                                                            441
                                                                                                                                                                                                      386
                                                                                                                                                                                                                                           160
                                                                                                                                                                                                                                                                              331
                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250
                                                    488
                                                                                         275
                                                                                                                                                                 215
                                                                                                                                                                                                                                                                                                                                                        288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OS GG OS GG RT TO THE RA HIERORY RT TO THE RA HIERO
                                                                  Š
                                                                                                                                        õ
                                                                                                                                                                                 밁
                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                   밁
                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFNAR2.
                                                                                                           333
                                                                                                                                               314
                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       489
                                                                                                                                                                                   291
                                                                                                                                                                                                                       257
                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                    201
                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKARAHT
```

```
Q9YHV9 PRELIMINARY; PRT; 508 AA.
Q9YHV9;
Q19YHV9;
Q19YHV9;
Q19YHXY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
INTERFERON ALPHA/BETA RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative genomic analysis receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL; AF082665; AAD13670.1; -.
HSSP; P13726; 1TFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LIVER;
REBOUL J., GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 I----YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 VDIIDDNF--ILRWN-RSDESVG---NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : | : |
                                                                                                                                                                                                                                                                                                                                                                                        YKLSPETTYCLKV-----KAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                  LPPTHLRKNGKL-----LSLFDIYNKVNYEITLRTVGEEHKRSPEKVTEEPFSIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKLNVYEE----IKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS
                                      WENTSNAERKIIEKKTDVTVPNLKPLT----VYCVKARAH
                                                                                                                         RSLSDSFHIYI----
                                                                                                                                                                      TFECEEITSVEIIY-KEVKKK-----AEGSVGAVSSEDDSDDSESDAM----
                                                                                                                                                                                                               ---CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNI
                                                                                                                                                                                                                                                            DY - - - YGITIAGAICFSIILYVILKCLHL - - - - - - GGYILHKKSLPDTLVFTKMFSYLPF
                                                                                                                                                                                                                                                                                                  NYVLKWDYTYAN-----MTFQVQWLHAFLKRNPGNHLYKWKQIPD----
                                                                                                                                                                                                                                                                                                                                               EELYPNRNYCVSVMVTASLNKHSIPSAWK-----CITTD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFQVVSDEYSAFVQSFVGTEVFNSSLLH----FSPLSETFLGPPEFNLSSCVHCINITIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLTWNHLTVDEQNG----FIRSYTILYKTVDGNETAVS----VDPSKTEXTLSSLTSDTLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIKPFKCYLITVYPLFADGQGSG--
                                                                                 ----SNHDYTRRDIVRRAPQSSDTSPVFVQHSTSSTCDGSSSWVSQNPDDGPEVFE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PGT---KDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQMTSNNFQHILSWRAHSDPTVPTYYRVLYS-----SHSNWKIAKQCSRIVQPFCNLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GARDINER K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ,
EKDTDSEL--LSPLSKVNCTYSLRSRSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57049
                                                                                                                              -GAPKQSGNTPVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MONNERON D., alysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 127.5; DB Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2DC4E498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QSVKAYLQQGRPSKGPTVQTKKVGKAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
418
                                        383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                              -QDYPLIYEIIF
                                                                                                                                                                                                                                                                                                                                                 SVAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                              347
                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                                                                                                                  200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                 313
                                                                                                                                                                                                                                                            290
                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377
                                                                                                                                                                        333
                                                                                                                                                                                                                                                                                                    257
```

```
밁
                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                당
                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                      닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mouse Neogenin, a DCC-11ke molecule, he expressed widely in the adult mouse and Oncogene 15:691-700(1997).

EMBL; Y09535; CAA70727.1; -.
HSSP; P02751; 1TTG.
MGD; MGI:1097159; Neol.
PFAM; PF00041; fn3; 6.
PFAM; PF00044; FNTYPEIII.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 1493 AA; 163159 MW; 98F266
              Q90610 PRELIMINARY; P. Q90610; Cres Ol-NOV-1996 (TrEMBLrel. 01, Lass Ol-NOV-1999 (TrEMBLrel. 12, Lass Ol-NOV-1999 (TrEMBLrel. 12, Lass NEOGENIN (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; C. Neognathae; Galliformes; Phasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P97798;
P97798;
01-MAY-1997
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEOGENIN (NEOGENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     472
                                                                                                                                                                                                                                                                                                                                                                                              695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                       340
                                                                                                                                                                                                                                                                                                                                                                                                                             229
                                                                                                                                                                                                                                                   803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPQKVEVDIIDDNFI-LRWN--RSDESVGNVTFSFDYQKTGMDNWIKLSGCQNITS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIHISPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --TKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVLKW---DYTYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVTIQNLMPATVYIF-----KVMAQNKHGSG----ESSAPLRVET--QPEVQLPGPAPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTKEGVDR----ERVENTSQPGEM
                                                                                                                                                                                                                                                 AIGYGI---
                                                                                                                                                                                                                                                                    VNGTGPATDWLSAETFESDLDETRVPEVPSSLHVRPLVTSI-VVSWTPPENQNI-VVRGY
                                                                                                                                                                                                                                                                                                                                                                                              GQITGYKIRYRKASRKSDVTETLVTGTQL-----SQLI--EGLDRGTEYNFRVAALT
                                                                                                                                                                                                                                                                                                                                                                                                                             ---MTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFRVVA--YNKHGPGVSTQDVAVRTLSDVPSAAPQNLSLEVRNSKSIVIHWQPPSSTTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAYATSPTSITVTWETPLSGNGEIQNYKLYYMEKGTDKEQDIDVSSHSYTINGLKKYTEY
                                                                                                                                                                                                                                                                                                                                                          GNNT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97407661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 (TrEMBLIEL. 03, C
7 (TrEMBLIEL. 03, I
9 (TrEMBLIEL. 12, I
NEOGENIN PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mouse).
|etazoa; Chordata; Craniata; Vertebrata;
|dentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHIYIGAPKQSGNTPVIQDY
                                                                                                                                                                                                                                                   GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.8%;
                    Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125; DB
Pred. No. 0.12
74; Mismatches
                                                                                      Created)
Last sequence update)
Last annotation update)
                  Craniata; Vertebrata; (anidae; Phasianinae; )
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98F26676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1493
                                                                                                                                                               1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                               ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embryogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splice variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                     842
                                                                                                                                                                                                                                                                                       382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
Mus.
                    Gallus
                                       Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                          802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                               RESULT
Q94537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
     ACC OCC OF REAL REAL PROPERTY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
```

```
Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Cell Biol. 127:2009-2020
EMBL; 007644; AAC59662.1;
HSSP; P80362; IMTL.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; ig; 4.
SEQUENCE FROM N.A.
MEDLINE; 970.5076.
KOLODZIEJ P.A., TIMPE L., MITCHEI
AN L.Y., JAN Y.N.;
TARZZIE encodes a Drosophila me
subfamily and is required for CN
Cell 87:197-204(1996).
EMBL; U71001. AAC47314.1;
FLYBASE; FEGNON1592; fra.
PFAM; PF00041; fn3; 6.
                                                                                                                                                                                                                           Q94537;
Q94537;
Q1-FEB-1997
Q1-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Neogenin, an avian cell surface protein expressed neuronal differentiation, is closely related to the suppressor molecule deleted in colorectal cancer.", J. Cell Biol. 127:2009-2020(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE; 95105243.
VIELMETTER J., ROMAN J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN;
                                                                                                                                                            Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                      Drosophila
                                                                                                                                                                                                    FRAZZLED.
                                                                                                                                                                                                                  FRAZZLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                                                                                             340
                                                                                                                                                                                                                                                                                                                                                                                                        699
                                                                                                                                                                                                                                                                                                                                                                                                                                                            646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
                                                                                                                                                                                                                                                                                                                                                    757
                                                                                                                                                                                                                                                                                                                                                                                                                                 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPOKVEVDIIDDNFI-LRWNR--SDESVGNVTFSFDYQKTGMDNWIKLSGCQNITSTKCN
                                                                                                                                                                                                                                                                                                                                                    AIGYGI----GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                                                                                                                                                                                                                                                                                                                                                 PLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA : | | : |: |: |: | | | | | : | : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                  GNNT - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFLKRNPGNHL----YKWKQIPDCENVKTTQCVFPQNVFQ--KGI-----YLLRVQASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLISWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVLKWDYTYANMTFQVQWLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTSVTVTWETPLSGNGEIQNYKLYYMEKGQDSEQDVDVAGLSYTITGLKKYTEYSFRVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APRDVVATLVSTRFIRLTWRTPVSDPQGDNLTYSIFYTKEG----INRERVEN-TSRPGE
                                                                                                                                                                                                                                                                                                                                                                                                        VNGTGPATDWVSAETFESDLDESRVPEVPSSLHVRPLVTSI-VVSWTPPENQNI-VVRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --YNKHGPGVSTQDVVVRTLSDVPSAAPQNLTLEARNSKSIMLHWQPPPA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1443
                                                                                                                                              melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musca; Drosophilidae; Drosophila.
                                                                                                                                                                                                                             (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GTHSGQITGYKIRYRKVSRKSDVTESVGGTQLFQLIEGLERGTEYNFRIAAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHIYIGAPKQSGNTPVIQDY
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                              12,02,
                                                                                             MITCHELL K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DREYER W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 123.5; 1
Pred. No. 0.15
50; Mismatches
                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
                                                        CNS
                                                                                                                                                                                                                                                                                   PRT;
                                                                      member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270877DC
                                                        and
                                                                                                                                                                                                                                                                                   1375
                                                        of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .15;
                                                                                                                                                                                                                                                                                   ₹
                                                                                                GOODMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194;
                                                         axon
                                                                                                                                                                                                                                update)
                                                                      DCC
                                                                                               C.S.,
                                                        guidance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          during
e human
                                                                       immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                  FRIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminal tumor
                                                                                                                                                                  Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                     339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                                                                           756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597
```

```
RAN WARRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SODR
                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                       닭
                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
SEQUENCE FROM N.A.
MEDLINE; 97015076.
KOLODZIEJ P.A., TIMPE L., M
JAN L.Y., JAN Y.N.;
"frazzled encodes a Drosoph
                                                                                                     Q94538
Q94538;
Q1-FEB-1997
Q1-FEB-1997
Q1-NOV-1999
FRAZZLED.
FRAZZLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 1375 AA; 151692
                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                       1017 MLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   628
                                                                                                                                                                                                                                          364 DVTVPNLKPLTVYCVKARAHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 MVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFEG
                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GKNLKS------PQKVEVDIIDDNFI-LRW------NRSDESVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - IRAEKENTSSWYE------
                                                                                                                                                                                                                                                                                                                                               PTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY-----
                                                                                                                                                                                                                                                                                                                                                                                        GRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYSPVHCIKTTVENELP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEWNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL-----TSWKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFTPFRKAQIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQK
                                                                                                                                                                                                                                                                                  SDSFHIYIGAPKQSGNTPVIQDYP-----LIYEIIFWENTSNAER-----KIIEKKT
                                                                                                                                                                                                                                                                                                        -HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSMSVLNSTYQNVPVTPP-----
                                                                                                                                                                                                                                                                                                                          CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                ------NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLGW
                                                                                                                                                                                                                                                              ---REVTVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 16.:
01; Conservative
                                                                                                                          7 (TrEMBLrel.
7 (TrEMBLrel.
9 (TrEMBLrel.
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              TYANMTFOVOWLHAFLKRN----
   Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%;
16.3%;
                                                                                                                        02, Created)
02, Last sequence update)
12, Last annotation updat
                    MITCHELL K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                       1037
                                                                                                                                                                                                                                           384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 123;
Pred. No. 0
                                                                                                                                                                    PRT;
   member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43806DBC CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PPEVHLE-AEDKAIVIHISPGTKDSVMWALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1526
  of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------PPENIEVSVONONYVLKW
  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .15;
                     GOODMAN C.S.,
                                                                                                                                                                    ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                          update)
  200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                  PGNHLYKWKQIPD
                     FRIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268;
                    ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507
                                                                                                                                                                                                                                                               1016
                                                                                                                                                                                                                                                                                                                            316
                                                                                                                                                                                                                                                                                                                                                                                                                                793
                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                        960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
  RRRCCOSETTAC
                                                                                                                                                                                     S
                                                                                                                                                                                                           밁
                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SO DR DR PR
                                                                                                                                                                   밁
```

```
Query Match

Best Local Similarity

Matches 101; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U71002; AAC47315.1; -
FLYBASE; FBG0011592; fra.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 1526 AA; 168787
                                                                                                    01-FEB-1997
01-FEB-1997
01-NOV-1999
                                                                                                                                               Q92859
Q92859;
                                                                                                                                                                                                                                      1168
                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                1111
                                                                                                                                                                                                                                                                                                                                                                                                                  1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfamily and is required Cell 87:197-204(1996).
               SEQUENCE FROM N.A.
                                                                                        NEOGENIN
                                                                                                                                                                                                                                                                                                                                                        1060
                                                                                                                                                                                                                                                                   364
                                                                                                                                                                                                                                                                                                                                                                                     257
                                                                                                                                                                                                                                                                                                                                                                                                                                             225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
                                                                                                                                                                                                                                                        DVTVPNLKPLTVYCVKARAHT
                                                                                                                                                                                                                                                                                             ---REVTYRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKNLKS-----POKVEVDIIDDNFI-LRW------NRSDESVG
                                                                                                                                                                                                                                      MLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                                                                                                                                                                                                                                               PTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEWNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL-----TSWKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQK
                                                                                                                                                                                                                                                                                                                           SDSFHIYIGAPKQSGNTPVIQDYP------LIYEIIFWENTSNAER-----KIIEKKT
                                                                                                                                                                                                                                                                                                                                                       -HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSWSVLNSTYQNVPVTPP------
                                                                                                                                                                                                                                                                                                                                                                                  CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -IRAEKENTSSWYE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101;
                                                                                                    (TremBLrel. 02, Created)
(TremBLrel. 02, Last seq
(TremBLrel. 12, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TYANMTFQVQWLHAFLKRN-----
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLGW
LOOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%;
16.3%;
A.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                      1188
                                                                                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW.
BIGNER S.H.,
                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 123;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F17B1EC9 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motor
                                             Vertebrata;
ae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
 FEARON
                                                                                                                                                              ₹
                                                                                                   on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  axon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184;
 E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ----PGNHLYKWKQIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  guidance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                        1111
                                                                                                                                                                                                                                                                                                                                                                                                               1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              658
                                                                                                                                                                                                                                                                                                 1167
                                                                                                                                                                                                                                                                                                                                                                                    316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
                                                                                                                                                                                                                                                                                                                           363
                                                                                                                                                                                                                                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225
```

```
밁
                                               ORDER PRODUCT OF STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SORDRORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                   日
                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 83
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 0:0-0(0).
EMBL; U61262; AAB17263.1; -
HSSP; P02751; ITTG.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII.
SEQUENCE 1461 AA; 159958
                                                         Genomics 41:414-421(1997).
EMBL; U72391; AAC51287.1; -.
HSSP; P02751; ITTG.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; ig; 4.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                     000340;
01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                 and
q23
                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                 SEQUENCE
                                                                                                                                                        MEDLINE; 97312699.
VIELMETTER J., CHENG X.N., MISKEVICH F.,
KORENBERG J.R., DREYER W.J.;
"Molecular characterization of human neoo
                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NEOGENIN
                                                                                                                                                                                                                                                                                                                                        000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
                                                                                                                                                                                                                                                                                                                                                                                                                          344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441
                                                                                                                                                                                                                                                                                                                                                                                                   776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 SPQKVEVDIIDDNFI-LRWN--RSDESVGNVTFSFDYQKTGM--DNWIKLSGCQNITSTK
                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                           the mapping of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTKEGIARERVENTSHPGEMQVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNLMPATYYIF-----RVMAQNKHGSG----ESSAPLRVET--QPEVQLPGPAPNLRAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVLKWD-----YTYANMT
                                                                                                                                                                                                                                                                                                                                                                                                   GI---
                                                                                                                                                                                                                                                                                                                                                                                                                         EIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPATDWLSAETFESDLDETRVPEVPSSLHVRPLVTSI-VVSWTPPENQNI-VVRGYAIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SFWSEEIKFDTEIQAFLLPPY---FNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYKIRYRKASRKSDVTETLVSGTQL-----SQLI--EGLDRGTEYNFRVAALTINGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - FQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VA--YNKHGPGVSTPDVAVRTLSDVPSAAPQNLSLEVRNSKSIMIHWQPPAPATQNGQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASPTSITYTWETPYSGNGEIQNYKLYYMEKGTDKEQDYDYSSHSYTINGLKKYTEYSFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 20.8
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 -GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                               1461 AA;
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FNTYPEIII.
                                                 FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.7%;
 20.5
                                                                                                                                            gene
 . 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 121; DB 4; Length 1461;
Pred. No. 0.24;
77; Mismatches 188; Indels 5
                                                  MW.
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                              (NEO1)
 Score
Pred.
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0AB7247E CRC32
                                                  9D5AE1C4 CRC32
 121;
No. (
                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                                         1461
                                                                                                                                                         neogenin,
                                                                                                                                               neogenin, a i
   0
  .24;
                                                                                                                                                                                 LANE
                                                                                                                                                                                                                                                                                                                                        ⋛
                                                                                                                                                                                                                                                                                         update)
            4.
                                                                                                                                                                                                                                                                                                                                                                                                     811
                                                                                                                                                                               R.P.,
               Length
                                                                                                                                            DCC-related protein,
l position 15q22.3-
                                                                                                                                                                                  YAMAKAWA
                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
```

```
RESULT PROJECT OF STATE OF STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                   Š
                                                                                                                                                             밁
                                                                                                                                                                                                            Š
Š
                                                    뮍
                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U10986; AAA70168.1;
HSSP; P56276; 1TLK.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 19; 4.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91562;
Q91562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Expression of a homologue of the deleted in colorectal of gene in the nervous system of developing Xenopus embryos. Dev. Biol. 166:654-665(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLLNE; 95113183.
PIERCEALL W.E., REALE M.A., CANDIA A.F.,
FEARON E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   550
                                                         484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344
                                                                                                                                                             431 APRDVVPVLVSSRFVRLSWRPPVESKGNIQTYTVYFSKQGVQRERAVNTSQPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        776 GI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                           64
                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L
u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASPTSITVTWETPVSGNGEIONYKLYYMEKGTDKEQDVDVSSHSYTINGLKKYTEYSFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTKEGIARERVENTSHPGEMQVTI 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPOKVEVDIIDDNFI-LRWN--RSDESVGNVTFSFDYQKTGM--DNWIKLSGCQNITSTK 60
                                                                                                                                                                                           SPQKVEVDIIDDNFI-LRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKCNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPATDWLSAETFESDLDETRVPEVPSSLHVRPLVTSI-VVSWTPPENQNI-VVRGYAIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYKIRYRKASRKSDVTETLVSGTQL------SQLI--EGLDRGTEYNFRVAALTINGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VA--YNKHGPGVSTPDVAVRTLSDVPSAAPQNLSLEVRNSKSIMIHWQPPAPATQNGQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVON-QNYVLKWD-----YTYANMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNLMPATVYIF ---- RVMAQNKHGSG ---- ESSAPLRVET -- QPEVQLPGPAPNLRAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 120
  KAIVIHISPGTKDSVMWALDGLSFT--
                                                                                                        SSLKLNV----YEEIKLRIRAEKENTSSWYEVDSFTPFR----KAQIGPPEVHLEAED
                                                       -SLQITYGNLTPEETYNFRVVAYNE---
                                                                                                                                                                                                                                                                   l Similarity
93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                                                                                                                                                                                                                                                                                                                                                                                  1427 AA; 156533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                            22.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                Score 117.5; D
Pred. No. 0.44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                       E50B7475
                                                         -WGPGESSQEVKVVTQPELQVPGPVENLQ---
     -YSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WRIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
                                                                                                                                                                                                                                                                                                                                                                                                       CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in colorectal cancer (DCC)
                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                      163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHO K.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230
           167
                                                                                                              113
                                                                                                                                                                                                                       63
                                                                                                                                                                  484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                           22;
```

```
RESULT RE
                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                ő
                                                                                                                                                                                                        문
                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
     멅
                                            Ş
                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   017859; Q20137;
017859; Q20137;
01-NOV-1996 (TrEMBLrel. 01
01-MAY-1999 (TREMBLrel. 10
01-NOV-1999 (TREMBLREL. 12
C09D8.1 PROTETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                          424
                                                                                                                                                                                                                                                                                                            380
                                                                                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          636
                                                                                                                                                                                                                                                          153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             745 WTPPLNPNI-VVRGYIIGYGV----GSPYAETVRVDSKQRYYSIENLEPSSHYVISLKA 798
                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Z46811; CAA86642.1; JOINED.; Z49938; CAA96842.1; JOINED.; Z49938; CAA96189.1; Z46811; CAA96189.1; JOINED.; P28827; IRPM.; FF00041; fn3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VVSTAP---TSVLISWDPPAYANGPVQGYRLFCAETFSGREQNIEVDGIVYRLEGLR
                                                                                                                                                                                                                                             RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEV-
                                                                                                                                                                                                                                                                                                       NRNPPKKSKISTADVY-----SAILHHAPGP-----LTHPISAALAKAKPTIGA
                                                                                                                                                                                                                                                                                                                                                                                                        TFEVNVRRAYLFKVAAATMKGIGPYSPVLTINPDPADLILDNNIEEEEGNQDPGEATMGE
VVSDLNAHKP--YAFCVLAVKNNRQGPCSDP---PTVLES--VTPTYMVQNLRVLWKTSN
                                               CVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSL----SD
                                                                                                                                                   SVONONYVLKWDYTYANM-TFQVQWLHAFLKRNPGNHL--YKWKQIP----DCENVKTTQ
                                                                                                                                                                                                                                                                                                                                                 SFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLKINVYEEIKLRIRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDVQYEVMKGKIVVSWRPPSEEKRNGNIT-SYKAILSAMD--ATADRYEQPVPAPSTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQKVEVDIIDDNFILRWNRSDESV--GNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAPKQSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEKGSQYSFQVAAMTVNGTGPSSDWYTAETPENDLDESQVPDQPSSLHVRPLTTSI-IMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRSIKVSW----LPPPPGTQNGFITGYK----IRHRKTTRRGELETLEPNNLWYLFTG
                                                                                                 ATSNSTAVVQWDFESQKADSFVVKYMH-----EPGNRMDTEKWKQLPVVSIDKENPKRFA
                                                                                                                                                                                                     PMPAPYTTTS----TPSTLFFQVTLPFMTTAWN-----RVTKLETLVGPPTNVRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -OKGI-YLLRVQASDGNNTSFWSEEIKFDT-----EIQAFLLPPVFNIRSLSDSFHIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMTFQVQWLHAFLKRNPGNHL-----YKWKQIPDCENVKTT-----QCVFPQNVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFTEYSIRVLA--YNRYGPGVSSEEHTVVTLSDVPSAMPQNVSLEVAN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOV-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.
178386 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 117.5; I
Pred. No. 0.51;
74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E403A8DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EKENTSSWYEV---D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                       423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227
                                                                                                                                                                                                     470
                                                                                                                                                                                                                                                                                                                                                                                                        379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     685
                                                  318
                                                                                                    525
                                                                                                                                                   264
                                                                                                                                                                                                                                                       212
                                                                                                                                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
```

```
THE THE THE TENT OF THE TENT O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q92673 PRELIMINARY;
Q92673; Q92856;
Q1-JUN-1998 (TIEMBLIE). 00
Q1-JUN-1998 (TIEMBLIE). 00
Q1-NOV-1999 (TIEMBLIE). 11
LOW-DENSITY LIPOPROTEIN R
                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Verence (Laria); Primates; Catarrhini; Hominidae;
                                                                                                                                                                               SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL RECEPTOR. B
MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA, AN
IT INTO CELLS BY ENDOCYTOSIS.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, LIVER, KIDNEY
WITH DETECTABLE LEVELS IN PLACENTA, LING AND HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JACOBSEN L., MADSEN P., MOESTRUP S.K., LUND A.H., TOMMERUP N., NYKJAER A., SOTTRUP-JENSEN L., GLIEBREN C.M.;
"MOLECULAR characterization of a novel human hybrid-type receptor binds the alpha2-macroglobulin receptor-associated protein.";
D. Biol. Chem. 271:31379-31383(1996).
                                                                                                                                                                                                                                                         PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JACOBSEN L., M. PETERSEN C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOERWALD S., YAMAZAKI H.,
MORISAKI N., NIMPF J., SCI
Arterioscler. Thromb. Vaso
                                                                                                                                                                                                                        Cholesterol
                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRPHMMYTIHVGVRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKPLTVYCVKARAHTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVQLTWEYNG-PRNVGFYVNHTGRKDY-VNHEL--QEKTMSTPGFGQDVDEKHREYLWTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFHI---YIGAPKOSG---NTPVIQDYPLIYEIIFWENTSNAE---RKIIEKKTDVTVPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97094912
                                                                                                                                                                                                                    Transmembrane; Signal; Repeat; Glycoprotein; ol metabolism; Lipid transport.
                                                           29
1076
1115
1156
1156
1197
1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MADSEN P.,
    2214
2135
1114
1155
1194
1226
1285
1317
1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vasc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1., BUJO H., KUSUNOKI J., KANAKI SCHNEIDER W.J., SAITO Y.; Vasc. Biol. 17:996-1092(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06, Created)
06, Last sequence update)
12, Last annotation update)
RECEPTOR-RELATED PROTEIN LR11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUND A.H., TOMMERUP N., GLIEMANN
EXTRACELLULAR.

LDL-RECEPTOR CLASS I

LDL-RECEPTOR CLASS I
                                                                                                                                                                                                 transport.
                                                                                                                                                                               LOW-DENSITY LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
    ~~~~~~
    87654321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIDNEY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia
                                                                                                                                                                                 RECEPTOR LR11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
.
                                                                                                                                                                                                                                         LDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDS LDL, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEIMIYA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369
```

```
Ş
                                                                  밁
                                                                                                          Ş
                                                                                                                                                        Query Match
Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                    1689
                                                                                                             88
                       86
RKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSL------LIWK 145
                                                                                          DYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPF 97
                                                                  EYSRSGSKMWASQRAASNFTEIK----NLLVNTLYTVRV-AAVTSRGIGNWSDSKSITTI 1743
                                                                                                                                                        75; Conservative
                                                                                                                                                                                                                                                                       10055
10085
10085
11127
11127
11125
11138
11138
11138
11144
11177
11177
11177
11177
11218
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
11332
1132
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
1132
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11322
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1417
1469
1556
1653
1653
1649
1749
1842
1933
2025
21933
                                                                                                                                                                                                                                                                   1417 1445

1469 1508

1512 1551

1556 1742

1749 1837

1842 1927

1842 1927

161 2214

63 265

1090 1090

1090 1112

1144

18 1170

6 1183

77 1192

99 1214

18 1234

18 1234

18 1234

18 1234

18 1234

18 1337

17 1193

18 1444

18 1234

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1337

18 1344

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403

18 1403
                                                                                                                                                                               5.5%;
                                                                                                                                                            68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDL-RECEPTOR CLASS A 9.
LDL-RECEPTOR CLASS A 10.
LDL-RECEPTOR CLASS A 11.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC.
CYTOPLASMIC.
CYTOPLASMIC.
CELL ATTACHMENT:
BY SIMILARITY.
                                                                                                                                                        Score 117.5;
Pred. No. 0.79
8; Mismatches
                                                                                                                                                                                                                                                                       POTENTIAL.
MW; EDF6608F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                  .79;
                                                                                                                                                                                                       DВ
                                                                                                                                                          130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                          indels
                                                                                                                                                          115;
                                                                                                                                                          Gaps
                                                                                                                                                            21;
```

```
밁
                                                                                                                                                  Ş
                                                                                                                                                                                   밁
                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                             g
                             Ş
                                                           밁
                                                                                       80
                                                                                                                                                                                                                                                1786
1977
                                                             1936
                                                                                                                                                                                    1838
                                                                                                                       1888 LTTSLHNKTV--IVSKD--EQYLFLVRVVVPYQGPSSDYVVVKMIPDSR-----LPP---
                                                                                                                                                                                                                                                                                                           1744 KGKVIPPPDIHIDS-------YGENYLSFTLTMESDIKVNGYVVNLFWA 1785
                             364 DVTVPNLKPLTVYCVKARAHTMDEKLNK 391
                                                                                          313
                                                                                                                                                    254
                                                                                                                                                                                                                 199
                                                                                                                                                                                 TRGVRPPAPSLKAKAINQTAV---ECTWTGPRNVVYGIFYATSFLDLYRNP-----KS
                                                                                                                                                                                                                                                                NSSGVEER----IENIYSRHKIYKLSPETTYCLKVKAALLTSW---KIGVYSPVHCIKTT : :| | : | :| :| :| | :|
DRS----YKVKSRNSTVEYTLNK 1995
                                                                                       IRSLSDSFHIYIGAPKQSGNTPVI------QDYPLIYEIIFWENTSNAERKIIEKKT 363
                                                                                                                                         VENELPPPENIEVSVQNQNYVLKWDYTYA---NMTFQVQWLHAFLK--RNPGNHLYKWKQ
                                                                                                                                                                                                                                                FDTHKQERRTLNFRGSILSHKVGNLTAHTSY-----EISAWAKTDLG-DSPLAFEHVM 1837
                                                             -----RHLHV---VHTGKTSVVIKWESPYDSPDQDLLYAIAV-----
                                                             -KDLIRKT
                                                                                                                                                                                                                                                                                198
                                                                                                                                                       312
                                                                                                                                                                                      1887
                                                                                                                          1936
                                                                                                                                                                                                                   253
```

Search completed: June 1, 2000, 04:38:06 Job time: 14298 sec

```
Resul:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
34
34
34
34
34
34
34
34
34
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n DB seq
                                                2313
2313
2313
2309
2309
2300
2206
2226
228.5
208.5
228.5
115.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
117.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
118.5
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 1000000
                                                                                                                                         11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
11000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-675-2
2313
1 MMYVLLGATTLVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_36: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June 1, 2000, 04:17:57; Search time 12.38 Seconds (without alignments) 834.180 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188963 segs, 23686106 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMVVLLGATTLYLVAVGPWV......KSSVFSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
489
1005
575
575
2214
2210
245
1728
1778
1910
2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB
                                                                               R24488
R226356
R426356
W21805
W21806
W21806
W21806
W21806
W31906
W79193
R71035
R71035
R71013
W97864
W97864
W97864
W97864
W97864
W97864
W97864
W97864
W97864
R70113
W97864
R70113
R714643
R714643
R146643
R166643
R1666
                              W42086
W26356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                         Gamma interferon r
Gamma interferon r
Extracellular doma
Plasmid pBABJUE hu
Rat receptor tyros
Interleukin-10 receptor
Mouse IL-10 receptor
Gamma interferon r
Soluble human inte
                                                                                                                                                                                                                                                                                                                                                                                                                                          IFN-gamma receptor
Human cytokine rec
Human cytokine rec
Gamma-IFN-R-GBP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zcytor7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRFB4 protein. New IFN-gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFN receptor extra Spliced-deleted in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembranal int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human interferon r
Human IFN receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete interfero 
Sequence of a soul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of a soul Human alpha-interf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soluble interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IFN-gamma ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spliced-deleted
   Human Down syndrom
Rabbit LDL recepto
EPH-like receptor
                                                                                        Deleted in Colorec
Human Down syndrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine r
```

В Š 맑 Š 밁 Š 밁 Š

181 181 121 121 61 61

240 180

240

TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180 Query Match
Best Local Similarity
Matches 436; Conserv

100.0%; nilarity 100.0%; Conservative 0

0

Score 2313; DB 1; Pred. No. 2.3e-203; ); Mismatches 0;

Length Indels

436; 0

Gaps

0

В δõ

301

S C C C C C C C C P P P P P P P P P P P	RESULT R14487 AC R AC R DT 1 DT 1 CONTROL R PN CONTROL R PR CONTROL R P CONTROL R P CONTROL R P	
Tove WPI; N-PS New beta apla clai The have rece are are rece See		60000044444 600000000000000000000000000
Tovey MG, Uze G; WPI; 91-319778/44. N-PSDB; 014239. New water-soluble pollybeta - used to treat eaplastic anaemia, dialiclaim 2; Page 45; 52pp The transmembrane and receptor. Potentially perivatives obtained lare also claimed as air eaceptor (or deriv.) 3 See also 014240. Sequence 436 AA;	- 1 1 m or c o 1 ··	107 107 107 105.5 105.5 105.5 104.5 104.5
UZe G; 14239. 14239. -soluble po ed to treat tanaemia, di. Page 45; 52; Page 45; 52; Meletted to Potentiall es obtained es obtained as (or deriv.) 014240. 436 AA;	standard; Prote 1992 (first en 1992 (first en 1991 ens 1990; 001298. 1990; 001298. 1990; BR-001298. LAB EURO BIOTE Gresser I, Lutf	444444444 000000000000
4G; Uze G; 1319778/44.  ; 01439.  used to treat e.g. lupus ic anaemia, diabetes mell.  ; page 45; 52pp; French.  ansmembrane and cytoplasm een deleted to obtain a sor.  Potentially immunogen tives obtained by substitted to obtain a social condition of corderiv.) and an imm so 014240.  ce 436 AA;	(first entry) (first entry) (first entry) unferon-alpha/beta une disease; graf  001298. FR-001298. ER-001298. EURO BIOTECHNO. er I, Lutfalla G,	426 1 427 1 753 1 1370 1 928 1 400 1 878 1 596 1 600 1 600 1
tide lup s me renc copla lin lin lin lin an lybri	436 } beta graf graf	
Tovey MG, Uze G; WPI; 91-319778/44. N-PSDB; 014239. N-PSDB; 014239. New water-soluble polypeptide(s) with affinity beta - used to treat e.g. lupus erythematosus, aplastic anaemia, diabetes mellitus, rheumatoiclaim 2; Page 45; 52pp; French. The transmembrane and cytoplasmic domains of the transmembrane and cytoplasmic domains of the transmembrane and cytoplasmic domains of the page 45; 52pp; French. The transmembrane and cytoplasmic domains of the page 45; 52pp; French. The transmembrane and cytoplasmic domains of the page 50 page 15 pag	436 AA.  Deta receptor.  graft rejection;  graft rejection;	W09822 W24973 W83927 W83927 R97853 R75203 R78616 R78616 R92526 R69633 ALIGNMENTS
Tovey MG, Uze G: WPI: 91-319778/44.  N-PSDB: Q14239.  N-PSDB: Q14239.  New water-soluble polypeptide(s) with affinity for IFN-alpha an beta - used to treat e.g. lupus erythematosus; Behcet's disease aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Claim 2; Page 45; 52pp; French.  The transmembrane and cytoplasmic domains of the native IFN recentable been deleted to obtain a soluble, circulating form of the receptor. Potentially immunogenic epitopes have thus been eliming the perivatives obtained by substitution or deletion of this sequent are also claimed as are hybrid molecules comprising the soluble receptor (or deriv.) and an immunoglobulin such as IgG1.  See also Q14240.  Sequence 436 AA;	on; histocompatibility Mogensen KE;	al.
peptide(s) with affinity for IFN-alpha and s.g. lupus erythematosus, Behcet's disease, etcs mellitus, rheumatoid arthritis, etc. p; French. cytoplasmic domains of the native IFN receptor cytoplasmic epitopes have thus been eliminated. Immunogenic epitopes have thus been eliminated by substitution or deletion of this sequence by substitution or deletion of the soluble and an immunoglobulin such as IgG1.	1b111ty.	Human interleukin- Human interleukin- Human 185 protein. Sequence encoded b Rat REK7 eph-relat Tyrosine IL-3 recept Expression vector Expression vector Fas antigen #1. Im Human interleukin-

```
RESULT
R28495
ID R28495
AC R28495
AC
                            밁
                                                                 Ş
                                                                                                                          밁
                                                                                                                                                              Ş
                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                             문
                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pr water soluble polypeptide(s) strongly bind interferon(s) alpha pr and beta - useful as immunosuppressants, for treating auto:immune pr diseases and transplant rejection

PT diseases and transplant rejection

CC Laim 2; Fig 1; 58pp; English.

CC DNA encoding the water-soluble polypeptide with a high affinity for CC IFN-alpha and -beta is isolated by PCR, using appropriate

CC digonucleotides as primers and cloned CDNA as template. For example, CC the IFN-alpha and -beta receptor (030531), was incubated with oligos CC the IFN-alpha and -beta receptor (030533), was incubated with oligos CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC lacks the transmembrane and cytoplasmic domains. Both forms bind CC treating autoimmune diseases and graft rejection. They lack the CC toxic side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                            301
                                                                        30.
                                                                                                                                                                           241
                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tovey M, Uze G; WPI; 92-382110/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-1991; WO-F00318.
(EUBI-) LAB EURO BIOTECHNOLOGIE.
E1d P, Gresser I, Lutfalla G, Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09218626-A.
29-OCT-1992.
17-APR-1991; F00318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; Q30532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1993 (first entry) (Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R28495;
31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R28495 standard; Protein; 436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
es 436; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>ب</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTP 360
                                                                                                NONYVLKWDYTYANWTFQVOWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                               ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELDPPENIEVSVO
                                                                                                                                                                                                                                                                                                ENIYSRHKIYKUSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                   FSFDYOKTGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYVLLGATTLYLYAYGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMVVLLGATTLVLVAVGFWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIYLLRYQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G, Meyer F, Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2313; DB 1;
Pred. No. 2.3e-203;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
Š
                               B
                                                  QY
                                                                                                                                                                                                                                                                                                                                                8
                                                                                             δÃ
                                                                                                                  멍
                                                                                                                                      Š
                                                                                                                                                              В
                                                                                                                                                                                 δÃ
                                                                                                                                                                                                        В
                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . B
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 436; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X 20-OCT-1989; F00758.

A (CNRS) CNRS CENT NAT RECH SCI.

MOGENSEN KE, UZE G, Lutfalla G, G,

N-ESD; 011701.

New human - 1
                                                                                                                                                                                                                                                                                                                                               New human alpha interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis Disclosure; fig 4; 30pp; French.

This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, between residues 479 and 480, are also useful.
          361
                               301
                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9105862-A.
02-MAY-1991.
19-OCT-1990;
20-OCT-1989;
                                                                         241
                                                                                              241
                                                                                                                    181
                                                                                                                                        181
                                                                                                                                                              121
                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human alpha-Interferon receptor protein.
Human alpha IFN; IFN agonists; antiviral; anti tumour agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R11958 standard;
R11958;
18-JUL-1991 (fir
                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 FSDAVCEKTKPGNTSK 436
VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                     GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                        GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIVIGAPKQSGNTP
                                                               NQNYVLKWDYTYANNTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                            NONYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                              TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                             MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNEILRWNRSDESVGNVT
                                                                                                                                                   TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                        MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            targetting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                              557 AA;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 557
                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                      Score 2313; DB 1;
Pred. No. 3.3e-203;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gresser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
                                                                                                                                                                                                                                                                                     ç
                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                diag-
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                   180
                      360
                                            360
                                                                300
                                                                                                          240
                                                                                                                               240
                                                                                                                                                                         180
                                                                                                                                                                                                120
                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                  0,:
```

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                      Ş
                                                                         밁
                                                                                                 Š
                                                                                                                             밁
                                                                                                                                                 Ş
                                                                                                                                                                              밁
                                                                                                                                                                                                     õ
                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                         S
Š
                          밁
                                               õ
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Sin
Matches 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EUBI-) LAB EURO BIOTECHNO.
Eld P, Gresser I, Lutfalla G
Tovey MG, Uze G;
WPI; 91-319778/44.
N-PSDB; Q14240.
                                                                                                                                                                                                                                                                                                                                                                                              New water-soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoli arthritis, etc.
Disclosure; Page 47; 52pp; French.
The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also 014239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R14488;
16-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete interferon-alpha/beta IFN; autoimmune disease: graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-1991.
05-FEB-1990; 001298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2657881-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                               121
  361
                          301
                                                                           241
                                                                                                     241
                                                                                                                              181
                                                                                                                                                     181
                                                                                                                                                                                                       121
                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSDAVCEKTKPGNTSK 436
                                                                                                                                                                              FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                             MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                       GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                             NONY VLKWDY TY ANM TFQ V QWLHAFLK RNPGNHLY KWKQ I PDC ENVKTTQC V FPQNV FQK
                                                                                       NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFFQNVFQK 300
                                                                                                                                         ENIYSRHKIYKLSPETTYCLKVKAALLISWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                          GIYLLRYQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                             ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label-
458. .55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 437. .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 457
                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1= transmembrane
.557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a/beta receptor.
graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ်ပ
                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ⋛
                                                                                                                                                                                                                                                                                                                                                 Score 2313; DB 1;
Pred. No. 3.3e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meyer
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   histocompatibility.
                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                  180
                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                     60
                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                       0
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                   밁
                                                                                                                              δõ
                                                                                                                                                             밁
                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                밁
                                            밁
                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      water soluble polypeptide(s) strongly bind interferon(s) alpha pri and beta - useful as immunosuppressants, for treating auto:immune pri diseases and transplant rejection Claim 3; Fig 2; S8pp; English.

CO DNA encoding the water-soluble polypeptide with a high affinity for DNA encoding the water-soluble polypeptide with a high affinity for CIFN-alpha and -beta is isolated by PCR, using appropriate coligonuclectides as primers and clonned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos C 16 che if Na 19h and -beta receptor (Q30533), was incubated with oligos C 16 che if Na 19h and cytoplasmic domains. Both forms bind C 16 che transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the C toxic side-effects of known immunosuppressants such as steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-1991; WO-F00318
(EUBI-) LAB EURO BIOTECHNOLOGIE.
Eld P, Gresser I, Lutfalla G, Me
TOVEY M, UZE G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09218626-A.
29-OCT-1992.
17-APR-1991; F00318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta. Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q30533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421
                361
                                            301
                                                                         301
                                                                                                      241
                                                                                                                                  241
                                                                                                                                                               181
                                                                                                                                                                                                                         121
                                                                                                                                                                                            181
                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                       FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSDAVCEKTKPGNTSK
VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                          NQNYVLKWDYTYANMTSQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                      TPFRKAOIGPPEVHLEAEDKAIVIHISPGTKDSVAWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                               FSFDYOKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92-382110/46.
                                                                                                                                                                                 ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                       TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                      NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
                                                                                                                                                                                                                                                                                                                                                                                                                         ).0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          557
                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                  Score 2313; DB 1;
Pred. No. 3.3e-203;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meyer F, Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              줌
                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                      120
                                                                              360
                                                                                                           300
                                                                                                                                      300
                                                                                                                                                                  240
                                                                                                                                                                                             240
                     420
                                                360
```

Ş 밁

```
RASOLT RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 436; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1992; 400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human interferon receptor.

Human interferon receptor.

IFN-R; extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia; fmmunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody to human interferon type-I receptor -
neutralising activity against human type I interferon, use
therapy and diagnosis
therapy and diagnosis
Disclosure; Fig 3; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Benoit P, Maguire D, WPI; 93-312951/40.
                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R42635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R42635 standard;
R42635;
      361
                                           361
                                                                                  301
                                                                                                                     301
                                                                                                                                                                                                  241
                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                    VIQDYPLIYEIIFWENTSNAERKIIEKKTDYTVPNLKPLTVYCVKARAHTKDEKLNKSSV
                                                                                                                                                  GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                            GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                               ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                   ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                                                                TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                           TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
  VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSDAVCEKTKPGNTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label-
/note- "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - extracellular_domain
"soluble, immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2313; DB 1;
Pred. No. 3.3e-203;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tovey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of IFN-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                having
ed for
                                     420
                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                    180
420
                                                                                                             360
                                                                                                                                                    300
                                                                                                                                                                                           300
                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                             δõ
                                                                                                             밁
                                                                                                                                              Š
                                                                                                                                                                                       밁
                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 435; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09507716-A.
23-MAR-1995.
16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE SI
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence of human interferon class I receptor is given in R73356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monocional antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IFN receptor.
IFN receptor; interinterieron-beta; mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful as immuno:modulator, eq
Disclosure; Fig.3A-2B; 105pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; 086458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                      421
                                                                                                             361
                                                                                                                                                361
                                                                                                                                                                                       301
                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R75356
                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ب
                                                                                                                                                                                                    GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKOSGNTP
                                                                                                                                                                                                                                                                                                                                        VIQDYPLIYEIIFWENTSNAERKIIEKKTDYTYPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                   GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                  NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTOCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                  TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                           TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYVLLGATTLYLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNEILRWNRSDESVGNYT
                                   FSDAVCEKTKPGNTSK
                                                                    FSDAVCEKTKPGNTSK 436
                                                                                                         VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                NONYVLKWDYTYANMTFQVQWLHAFFKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSDAVCEKTKPGNTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSDAVCEKTKPGNTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of monoclonal antibodies against interferon as immuno:modulator, eg. for treating AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon receptor; interferon-alpha;
a; monoclonal antibody; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .436
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , eg. ic.
np; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2309;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
.7e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

밁 Š

180

120

60 60

0,

180

420

360

360

300

240 240

300

ô 밁 Ş 밁 Š 용 S 밁 Š 밁 Š

밁

```
WASSULT TO CONCOCCO POTENTA PROPERTY OF THE PR
                                           Š
                                                                                               8
                                                                                                                                        Š
                                                                                                                                                                                           밁
                                                                                                                                                                                                                                       δõ
                                                                                                                                                                                                                                                                                             멼
                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU9475977-A.
11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Disclosure; Fig 7: 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804) includes a 21-amino acid transmembrane region. Novel, splice-deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W21804 standard; W21804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1997 (first entry)
Transmembranal interferon alpha-receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abramovich C, Ratovitski E, WPI; 95-200634/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interferon alpha-receptor; IFNAR.
                                                                                                                                                                                                                                                                                             241
                                                                                                                                               361
                                                                                                                                                                                                301
                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                   181
421
                                                421
                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                           VIQDYPLIYEIIFWENTSNAERKIIEKKTDYTYPNLKPLTYYCYKARAHTMDEKLNKSSV 420
                                                                                                                                                                                                                       GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                              TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                               VIQDYPLIYETIFWENTSNAERKITEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                           NQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                              FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                  NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
FSDAVCEKTKPGNTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              075977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Extracellular_domain
437. .457
/label= Transmembrane_domain
458. .557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2308; DB 1;
Pred. No. 9.5e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

RESULT W21805

OSWEDE

Homo

sapiens

W21805 standard; Protein; 434 AA.
W21805;
23-SEP-1997 (first entry)
Spliced-deleted interferon alpha-receptor
Interferon alpha-receptor; IFNAR.

```
RRESULT RRESULT RRESULT RRESULT RRESULT RRESULT RRESULT RESULT RE
                                        Ş
                                                                                           밁
                                                                                                                                         Š
                                                                                                                                                                                                     망
                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ᅜ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-SDB; Q86457.

Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS
Disclosure; Fig.2A-2B; 105pp; English.
Disclosure; Fig.2A-2B; 105pp; English.
A recombinant soluble form of the human interferon class I reprotein extracellular domain, given in R71723, was expressed either E. coli or COS cell hosts. The protein was used to raimmunomodulatory monoclonal antibodies.

Sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R71723 standa
R71723;
16-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1995.
16-SEP-1994;
17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1994; E03114.
17-SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO95077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFN receptor; interferon receptor; interferon-alpha;
interferon-beta; monoclonal antibody; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFN receptor extracellular domain.
IFN receptor; interferon receptor;
                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
421
                                             421
                                                                                                 361
                                                                                                                                                    361
                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                            VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPHLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                  NQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESFDYQKTGMDNWIKLSGCQNITSTKCNESSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                        FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                 VIQDYPLIYQIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCLKARAHTMDEKLNKSSV
FSDAVCEKTKPGNTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%;
436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2304; DB 1;
Pred. No. 1.5e-202;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                         420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                          360
                                                                                                                                                                                                                                                           360
```

```
RESULT
W21806
ID W2
                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                               ₽
                                                                                               Ş
                                                                                                               В
                                                                                                                                  ρy
                                                                                                                                                      밁
                                                                                                                                                                       Š
                                                                                                                                                                                           B
                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                              δô
                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                         inhibiting, modulating or modilying the activities of interferon(s) sexample 2; Fig 7; 46pp; English.

Novel splice-deleted interferon alpha-receptor (IFNAR) form 1

(W21805) is characterised by a new domain (S) which follows an end-deleted extracellular domain when compared to transmembranal in IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. From human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNS, either by acting as IFN antagonists or by regulating the activity of the multiple IFN modulate or modify the activities of IFNS alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sin
Matches 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abramovich C, Ratovitski E, Kever H,
Abramovich C, Ratovitski E, Kever H,
WPI; 95-200634/27.
WPI i 95-200634/27
New mammalian soluble interferon alpha-receptor forms
New mammalian soluble interferon alpha-receptor forms
 W21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO
(ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-1995.
20-OCT-1994; 075977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU9475977-A.
                                                              421
                                                                                 361
                                                                                                                    301
                                                                                                                                     301
                                                                                                                                                       241
                                              421
                                                                                                  361
                                                                                                                                                                         241
                                                                                                                                                                                           181
                                                                                                                                                                                                             181
                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                  121
                  11
                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                   FSDAVCE 427
                                                                                      VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                NONYVLKWDYTYANMTFOVOWLHAFLKRNPGNHLYKWKQIPDCENVKTTOCVFPONVFQK 300
                                                                                                                                                                                       TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                      TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                                                                                                                                                                                                                           FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF
                                                                               VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
standard;
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Extracellular_domain /note= "comprises amino acids 1-427 /note= managembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428. .434
/label= S_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .427
Protein;
                                                                                                                                                                                                                                                                                                                                                  97.78;
496
                                                                                                                                                                                                                                                                                                                                        Score 2260; D
Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                        0,
$
                                                                                                                                                                                                                                                                                                                                                 DB 1;
..6e-198;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - used for
interferon(s)
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                          240
                                                                                               420
                                                                                                                                   360
                                                                                                                                                                                         240
                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                        0
                   Š
                                        밁
                                                       δ
                                                                            밁
                                                                                          Qy
                                                                                                               g
                                                                                                                                δÃ
                                                                                                                                                   ₽
                                                                                                                                                                   Š
                                                                                                                                                                                       B
                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
                                                                            241
      361
                        361
                                         301
                                                          301
                                                                                                                 181
                                                                                                                                  181
                                                                                                                                                     121
                                                                                                                                                                      121
                                                                                              241
                                                                                                                                                                                        61
                                                                                                                                                                                                                           μ
                                                                                                                                                                                                                                             L
```

```
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2 (W21806) is characterised by a double deletion when compared to C transmembranal IFNAR (W21804). The extracellular domain is shortened by 6 amino acid residues and is followed by a truncated intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also T73521) obtd. C from human myeloma U266 cells. Soluble, non-membrane bound IFNAR C splice-deleted forms 1 (see also W21805) and 2 may regulate the response of human cells to IFNs, either by acting as IFN antagonists or by regulating IFN activities. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, corrected to the proposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-1994; 075977.
24-OCT-1993; IL-107378.
(YEDA ) YEDA RES & DEV CO LID.
(ABRA/) ABRAMOVICH C.
Abramovich C, Ratovitski E, Revel M;
WPI; 95-200534/27.
New mammalian soluble interferon alpha-receptor for inhibiting, modulating or modifying the activities Example 3; Fig 7; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w21806;
23-SEP-1997 (first entry)
Spliced-deleted interferon
Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
||||||||||||||||||
VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDE------
                                                                                    NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                         NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 95.5%;
al Similarity 97.9%;
418; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic purposes
ce 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- Extracellular_domain
/note- "comprises amino acid residues
422-427 of transmembranal IFNAR"
420. .496
/label- Intracellular_domain
/note- "comprises amino acids 481-557
transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-receptor IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2208; DB 1;
Pred. No. 1.1e-193;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forms
ies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used for interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                      360
                                                                                                                            360
                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
```

S

421 FSDAVCE

427

R75782 standard; Protein; R75782;

332

₹

13-NOV-1995 (first entry)

```
밁
                                                                                             ş
                                                                                                                                           밁
                                                                                                                                                                                ş
                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                              á
                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human CRFB4 sequence, DNA encoding it is used in the recombinant DNA (I) of the invention. (I) comprises a sequence (S1) cencoding the interleukin-10 (IL-10) receptor (ILION) and a sequence (S2) encoding CRFB4, both operably linked to expression control sequences. CC encoding CRFB4, both operably linked to expression control sequences. CC IL-10. Agonists are potentially useful, e.g. for preventing allograft rejection, as vaccine adjuvants, for treatment of photosensitivity. CC inflammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumpours, cc viruses, bacteria and parasites (especially intracellular pathogens) and CC for preventing organ rejection. A vector containing (I) is used to creatore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind IL-10 but not to transduce a signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit CC measure and localise CRBF4, for diagnosis of defective IL-10 activity in cells. Antibodies specific for CRFB4 are used to CC measure and localise CRBF4, for diagnosis of defective IL-10 activity. CC Tragments of (I) are used as primers or probes to assay CRFB4-specific CC RNA. Agonists/antagonists may be administered parenterally, orally or centally especially by intravenous injection or directly into a tumour or
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRFB4 protein.

CRFB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection; vaccine; photosensitivity; inflammation; autoimmune disease; septic shock; immune response; organ rejection; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page -; 79pp
This sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant DNA - comprises sequences encoding interleukin-10 and CRFB4 linked to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNE-) UNIV NEW JERS
Kotenko SV, Pestka S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W52296 standard; Protein; 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-1998
                                                            176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 -SDAVCE
                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-JAN-1998
                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                            w
ŭ
                                                                                                                                                                                                                                                                                                                                      WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD
                                                                                                                                                                                                                                                                                                          WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                                          EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP
                                                                                                 HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELP 230
                                                                                                                                                                                                                                                                NWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                  PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                                                           YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                                                           PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                                                                                                                                                                                                                                                          67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-683743.
NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79pp;
                                                                                                                                                                                                                                                                                                                                                                                                              9.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                        Score 228.5; DB 1;
; Pred. No. 5.1e-13;
42; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                          8
```

```
RESULT
W79159
                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTT SKKKKE DAC
                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AGUE/) AGUET M.
(BOEH/) BOEHNI R.
(HEMM/) HEMMI S.
Aguet M, Boehni R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage Claim 3; Fig.2A; 86pp; English.
The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived from mouse B-cells is given in R75782. Recombinant beta-subunit, pref. with the transmembrane anchoring domain deleted or inactivated and with the cytoplasmic domain deleted, may be used to treat pathological conditions associated with endogenous IFN-gamma production.
                                                          Zcytor? cytokine receptor polypeptide. Zcytor?; cytokine receptor; ligand-binding polypeptide; kidney; pancreas; type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue; type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue; agonist; cell proliferation; cell differentiation; renal disease; human; neural disease; pancreatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9516036-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFN-gamma receptor beta-subunit.
Interferon-gamma receptor beta s
                                              Homo sapiens
                                                                                                                                       20-NOV-1998 (first entry)
                                                                                                                                                                   W79159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q90808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aguet M, Boehni R
API; 95-224321/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interferon-gamma-antagonist
                                                                                                                                                                                                                                              185
                                                                                                                                                                                                                                                                                                         130
                                                                                                                                                                                                                                                                                                                                       123
                                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                                                                                                                71 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 LSAAAGG----KNIKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70
                                                                                                                                                                                                                                                              NIYSRHKIY--KLSPETTYCLKVKAAL-LISWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                              GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                       YENVTVGPPKNISVTPGKGSLVIHFSPPFD----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                  FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                     DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U14277.
US-164596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label-
267.
Location/Qualifiers 30..250 /note= "extracellula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Extracelular_domain 243 . . 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Sig_peptide
                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.8%; Score 203; DB 1;
30.1%; Pred. No. 1.1e-10;
tive 38; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemmi
 "extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane_anchoring_domain
                                                                                                                                                                       553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                     ጀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit; muIFN;
 (ligand-binding) domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                  69
```

13;

```
RESULT 15
R71035
ID R71035
AC R71035
                                                                                                                                                                                밁
                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PT Novel human Zcytor? DNA encodes a type 2 cytokine receptor - useful PT for treating renal, neural, pancreatic and prostatic diseases PS Claim 1; Pages 55-59; 72pp; English.

CC This represents the Zcytor? cytokine receptor. Zcytor? is a ligand-
CC binding receptor polypeptide and is a novel member of the type 2 cytokine receptor family (CRF2). An expression vector containing the Zcytor CC polynucleotide, operably linked to transcription promoter, a sequence CC encoding a transmembrane and intracellular domain, or both, and a CC transcriptional terminator can be used to transform host cells for the CC encoding a transmembrane and intracellular domain, or both, and a CC encoding a transmembrane and intracellular domain, or both, and a CC encoding a transmembrane and intracellular domain, or both, and a CC encoding a transmembrane and intracellular domain, or both, and a CC excombinant production of the polypeptide. The sequences can be used to Study the Zcytor? gene and to isolate ligands binding to it Zcytor? is combinant production of the polypeptide. The sequences can be used to Stimulate proliferation and CC differentiation of cell in these organs. The antagonists and agonists can also be used in the treatment of renal, neural, pancreatic and prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
R71035 standard; Protein; R71035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1998; U03029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
(ZYMO ) ZYMOGENETICS INC.
Addams RL, Farrah TM, Jelmberg AC, Kho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; V57515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 98-480798/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitmore TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9837193-A1.
27-AUG-199Я
                                                                                                           389
                                                                                                                                                392
                                                                                                                                                                                                                   340
                                                                                                                                                                                                                                                        290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                337
                                                                                                                                                                                                                                                                                            283
                                                                                                                                                                                                                                                                                                                                 252
                                                                                                                                                                                                                                                                                                                                                                   229
                                                                                                                                                                                                                                                                                                                                                                                                      196
                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                                                                                                                                                                                                                                                                                                   ERIENIYSRHKIYK--LSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENE------: : | | :| :
                                                                                                         SRTIPPDKTVIEY 401
                                                                                                                                          --TVPNLKPLTVY
                                                                                                                                                                           SSLND-----PQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESL
                                                                                                                                                                                                           RSLSDSFHIYIGAPKQSGNTFYIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV
                                                                                                                                                                                                                                                  ------LIYGNEFDKRFFV----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDV
                                                                                                                                                                                                                                                                                    CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEI---QAFLLPPVFNI 339
                                                                                                                                                                                                                                                                                                                         IFWYVLP----ISITV------FLFSVMGYSIYRYIHVGKEKHPANLI------
                                                                                                                                                                                                                                                                                                                                                            ----LPPPENIEVSVQNQNYVLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPD
                                                                                                                                                                                                                                                                                                                                                                                              QCVTN----HTLVLTWLEPHTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIGPPEVALTIDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPERKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-
                                                                                                                                            402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 198; DB 1
21.0%; Pred. No. 7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence claimed in claim .553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "intracellular domain"
                 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
                 ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CJ, Lok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195
                                                                                                                                                                                                               391
                                                                                                                                                                                                                                                                                                                                                                                                251
                                                                                                                                                                                                                                                  336
                                                                                                                                                                                                                                                                                                                           290
                                                                                                                                                                                                                                                                                                                                                               282
                                                                                                                                                                                                                                                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
```

```
밁
                                                                                               Ş
     밁
                                 δõ
                                                                                                                                밁
                                                                                                                                                              Ş
                                                                                                                                                                                              밁
                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                          SCCCCPTTRACTORS TO SCCCCO
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-1995.
22-AUG-1994, U09438.
20-AUG-1993; US-110119.
(UYNE-) UNIV NEW JERSEY.
COOK JR, Donnely RJ, Em
Pestka S, Schwartz B, So
                                                                                                                                                                                                                                                                                                                                                                                                                   Suppressing tumours in mammals with accessory factor 1 (AF-1) for interferon gamma, specifically induction of class I HLA antigens, including use of AF-1 DNA in gene therapy Disclosure; Fig 21A; 114pp; English.

The sequence is that of human interferon-gamma accessory factor-1. Incorporation of AF-1 into immune and tumour cells re-establishes normal function with elimination of malignant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 95-106679/14.
N-PSDB; Q84697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IFN-gamma accessory facto
Interferon-gamma; AF-1; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-1995 (first entry)
                                    219
                                                                  175
                                                                                                                             120 GALHSAWVIMPWFQHYRNVIVGPPE-NIEVIPGEGSLIIRFSSPFDIADISTAF----FC
                                                                                                                                                                                                69
                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                         12 VLVAVGPWVLSAAAGG---KNLKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFS 62
                                                                                                                                                                                                                                                               9
                              HCIKTTVENELPPPENIEVSV-------QNQNYVLKWDYTYANMTFQVQ 260
                                                               YYVHYWE--KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI
                                                                                             YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV 218
                                                                                                                                                                                           YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL
SCYETMADASTELQQVILISVGTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE
                                                                                                                                                                                                                           FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                         LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYQVQFK 68
                                                                                                                                                             ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT 164
                                                                                                                                                                                                                                                                                                                          67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          337 AA;
                                                                                                                                                                                                                                                                                                                                           6.7%;
22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soh J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emanuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor-1.
                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                        Score 155.5; DB 1;
Pred. No. 2.6e-06;
4; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kotenko S,
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ×
                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                       Gaps
                                                               232
                                                                                                                               174
                                                                                                                                                                                             119
```

14;

Search completed: June 1, 2000, 04:40:21 Job time: 1344 sec

```
Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2213
490.5
466.5
228.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*
1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 0
length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June 1, 2000, 04:35:21; Search time 12.75 Seconds
(without alignments)
493.702 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-240-675-2
2313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
100
100
97
21
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145308 segs, 14437401 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMYVLLGATTLVLVAVGPWV......KSSVFSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5COMB.pep:*
/cgn2_6/ptodata/1/1aa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
US-08-466-974-2
US-08-477-588-4
US-08-327-586-12
US-08-328-256-12
US-08-328-256-12
US-08-328-277-4
US-08-683-743-4
PCT-US94-14277-2
US-08-943-087-14
US-08-943-087-14
US-08-943-087-26
US-08-943-087-26
US-08-943-087-26
US-08-943-087-26
US-08-943-087-26
US-08-943-087-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-307-588-2
US-08-328-256-10
US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                        Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                   Sequence
Sequence
                                                                                                                       Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                         Sequence
     4, Appli
4, Appli
2, Appli
2, Appli
14, Appli
16, Appl
16, Appl
20, Appl
30, Appl
30
```

198 8.6 553 2 US-08-943-087-48 192 8.3 223 4 PCT-US94-14277-6 169.5 7.3 221 2 US-08-943-087-54 169.5 7.3 221 2 US-08-943-087-54 168.5 7.3 221 2 US-08-943-087-52 165.5 7.2 221 2 US-08-943-087-52 162.5 7.0 221 2 US-08-943-087-58 162.5 7.0 221 2 US-08-943-087-58 163.5 6.6 337 4 PCT-US94-14277-8 151 6.5 574 2 US-08-967-713-2 118 5.1 489 4 PCT-US93-11110-1 118 5.1 489 4 PCT-US93-11110-1 118 5.1 489 5 5221789-1 119 5.1 575 1 US-08-042-788-2 117.5 5.1 575 1 US-08-110-683-4	45	44	43	42	41	40	39	38	37	36	<u>ა</u>	ω <b>4</b>	<u>ω</u>	32	31	٥
553 2 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	117.5	117.5	118	118	118	151	153.5	162.5	165.5	167.5	168.5	169.5	174.5	192	198	TYO
1040000004040011	5.1	5 -	5 , 1	5.1	5.1	6.5	6.6	7.0	7.2	7.2	7.3	7.3	7.5	8	8.6	0.0
	575	575	1005	489	489	574	337	221	221	221	221	221	221	223	553	,
US-08-943-087-48 US-08-943-087-56 US-08-943-087-54 US-08-943-087-52 US-08-943-087-52 US-08-943-087-52 US-08-943-087-52 US-08-943-087-58 US-08-943-087-58 US-08-943-087-58 US-08-943-107-8 US-08-943-11110-1 5221789-1 5221789-1 5221789-1 5221789-1 52-08-424-788-2 US-08-424-788-2	Ь	ب	N	v	4	N	4	N	N	N	N	N	N	4	N	١
	US-08-110-683-4	US-08-424-788-2	US-08-469-537A-103	5221789-1	PCT-US93-11110-1	US-08-906-713-2	PCT-US94-14277-8	US-08-943-087-58	US-08-943-087-60	US-08-943-087-52	US-08-943-087-50	US-08-943-087-54	US-08-943-087-56	PCT-US94-14277-6	US-08-943-087-48	00 00 040 007 40
	4, Appii	2, Appli	103, App	5221789	1, Appli	2, Appli	B, Appli					54, Appl		6, Appii	48, Appi	•

## ALIGNMENTS

RESULT 1 US-08-307-588-2

Sequence 2, Apprair No. 5919453

Application US/08307588

GENERAL INFORMATION:
APPLICANT: BENOIT,
APPLICANT: MEYER,
APPLICANT: MAGUIRE

APPLICANT:

BENOIT, Patrick
MEYER, Francois
MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.

```
APPLICANT: TOVEY, MICHAEL G.
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
TITLE OF INVENTION: INTERFERON
NUMBER OF SEQUENCES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

STATE: D.C.
ZIF: 2007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TIBM PC COMPARTS
COMPUTER TIBM PC COMPARTS
COMPUTER PAPLICATION DATA:
APPLICATION NUMBER: US/08/307.588
FILING DATE: DATA:
APPLICATION NUMBER: US/08/307.588
FILING DATE: 05-DEC-1994
FILING DATE: 05-DEC-1994
FILING DATE: 05-DEC-1994
FILING DATE: 01-DATA:
APPLICATION NUMBER: EP 2400902.0
FILING DATE: 31-MAR-1993
FILING DATE: 31-MAR-1993
FILING DATE: 31-MAR-1993
ATTORAPPLICATION NUMBER: 28.665
REFERENCE/DOCKET NUMBER: 17283/117/GUPL
TELEPHONE: 5AXE, BETCHARION:
TELEPHONE: 610-5300
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: Linear
US-08-307-589-2

Query Match
Best Local Similarity 100.0%: Score 2313: DB 2: Length 436;
Best Local Similarity 100.0%: Pred. No. 1.8e-230;
```

Gaps

0

```
US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08328256 Patent No. 5643749
                                                                  APPLICATION NUMBER: US/08/328,256
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                   STREET: 419 Seven:
CITY: Washington
STATE: D.C.
                       TELEFAX:
                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIQDYPLIYEIIFWENTSNAERKIIEKKTDYTVPNLKPLTVYCYKARAHTMDEKLNKSSV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NONYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436;
                                                                                                                                                                                                                                                                                                             E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                              USA
          SEQ ID NO:
          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                              Version
                                                                                                                                                                                                                                                                                                               Suite 300
                                                                                                                                                                                                #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                            ITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MIECULE TYPE: protein
US-08-328-256-10
                                                                                                                                                                                                                                                                                                                    US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08471454 Patent No. 5731169
                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georg
APPLICANT: GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                           TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                        421
                                                                                                                                                                                                                                                                                                                                                                                   421 FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                               361 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                      COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                            ADDRESSEE: NIXON & VANDERHYE F
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPOKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ىر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                          GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                 VANDERHYE P.C.
                                                                                                                                                                                                                                         Georges
US/08/471,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2313; DB 1;
Pred. No. 2.7e-230;
Mismatches 0;
                      #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557;
```

420 420

360

240 240 120 120 60 60

FOR

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

FR 89/13770 US 07/900,642 DATE:

06-JUN-1995

PREPARATION OF

THE CORRESPONDING

PROTEIN

```
õ
                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                            US-08-466-974-2
                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/900, FILLING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/1377
FILLING DATE: 20-OCT-1989
FILLING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32.205
REFERENCE/DOCKET NUMBER: 960-7
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: 200797 NIXN UR 7
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                      Sequence 2, Application Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E. APPLICANT: UZE, Gilles APPLICANT: LUTFALLA, GEOGGES APPLICANT: GRESSER, ION TITLE OF INVENTION: CDNA FRAGM TITLE OF INVENTION: THE ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                            241 NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 100.0%; Score 2313; DB 1; Local Similarity 100.0%; Pred. No. 2.7e-230; nes 436; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                                                                                                                                                                                                                 FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                        GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSFDYOKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                         GIYLLRYQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                FSDAVCEKTKPGNTSK 436
                                                                                                                                          Application US/08466974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
 CDNA FRAGMENT CODING THE ALPHA INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960-7
 FOR THE GENE
RECEPTOR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
     PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
     FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
       THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

```
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-466-974-2
                             Ş
                                                            멂
                                                                                        δÃ
                                                                                                                         뮍
                                                                                                                                                       Š
                                                                                                                                                                                        밁
                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                   멎
                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 2313; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-230; Matches 436; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/466,974
FILING DATE: 06-JUN-1995
CCLASSIFICATION: 435
CRASSIFICATION DATA:
APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: US 07/900,642
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E. 20-OCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PHONOMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
                               361
                                                              301
                                                                                            301
                                                                                                                           241
                                                                                                                                                          241
                                                                                                                                                                                        181
                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                  ...
                                                                                                                                                                                                                                                                                                                                                                               MMYVLLGATTLYLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                           FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                           VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                           NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                          NONYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFFQNVFQK 300
                                                                                                                                                                                        ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                        ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ 240
                                                                                                                                                                                                                                                      TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                     TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                          180
                                                                                             360
      420
                                  420
                                                                 360
                                                                                                                              300
                                                                                                                                                                                           240
```

FSDAVCEKTKPGNTSK 436

```
Ş
                                                                                                밁
                                                                                                                                         ş
                                                                                                                                                                                                                           ş
                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                   ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IELEFAX: (703) 816-4000
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amin
                                                                                                                                                                                                                                                              Query Match 100.0%; Score 2313; DB 2; Best Local Similarity 100.0%; Pred. No. 2.7e-230; Matches 436; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,453
FILING DATE: 06-TUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-TUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 15-TUN-1992
APPLICATION NUMBER: PR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGITERATION NUMBER: ER 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
REGITERATION NUMBER: BR 89/13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08471453
Patent No. 5886153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Gec
APPLICANT: GRESSER, ION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR THE TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
                                         121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NORT
CITY: ARLINGTON
STATE: VIRGINIA
             121
                                                                                                  61
                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 557 amino acids
                                                                                                                                                                         ADDRESSEE:
                                                                                                           FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                    FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOGENSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knud E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960-7
                                                                                                                                                                                                                                                                                                         Length 557;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                0
```

```
; MOLECULE TYPE: US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                              TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Patent No. "
                                                                                                                                  REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                               FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 1
FILING DATE: 30-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TOVEY, Michael G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3000 K ST
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 NONYVLKWDYTYANMTFOVOWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPONVFQK 300
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                591945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08307588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Foley & Lardner
3000 K Street; N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAGUIRE, Deborah
PLAVEC, Ivan
TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEYER, Francois
               protein
                                                                                                                                                                                                                                                                                                   30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patrick
                                                                                                                                                                                                                                                                   EP 92400902.0
                                                                                                                                                                                                                                                                                                                      PCT/EP93/00770
                                                                                                                                                                                           28,665
                                                                                                                                                                        17283/117/GUPL
                                                                                                                                                                                                                                                                                                                                                                                                             (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360
```

Query Match Best Local Similarity

100.0%;

Score 2313; DB 2; Pred. No. 2.7e-230;

Length 557;

0;

Indels

0

```
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08328256 Patent No. 5643749
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                 FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                     STREET: 419 Seven CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ب
                                                               NAME: BROWDY, Roger L.
REGISTRATION NUMBER: REVEL-13
REFERENCE/DOCKET NUMBER: 25,618
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIODYPLIYEIIFWENTSNAERKIIEKKTDYTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENIYSRHKIYKLSPETTYCLKYKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIQDYPLIYETIFWENTSNAERKTIEKKTOVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                            20004
              248633
FOR SEQ ID NO:
                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                               419 Seventh
                                                                                                                                                                                                                                                                                                                                                                                           ABRAMOVICH, Carolii
RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      REVEL, Michel
                                                                                                                                                                                                                                                                                                               BROWDY AND NEIMARK
9 Seventh Street, N.W.,
                                                                                                                                                                     US/08/328,256
                                                                                                                                                                                                                                                                                                                                                                                                          Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                 Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
```

```
; MOLECULE TYPE: protein US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŠÕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 427; Conserv
                                                                                                                                                                                                                                                       Sequence 12, Application US/08328256
Patent No. 5643749
GENERAL INFORMATION:
APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
           ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/08/328,256

FILING DATE: 24-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                            APPLICANT: ABRAMOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                 421 FSDAVCE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                            421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT
                                                                                                                                                                                                                                                                                                                                                                                                                            FSDAVCE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2265; DB 1;
; Pred. No. 1.6e-225;
0; Mismatches 0;
                                                                                                                                                                             Suite 300
                                                       #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
```

360

420

360

420

240

240 180 180 60 60

APPLICATION NUMBER:

```
RESULT 9
PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-328-256-12
                                                                                                                                                                                       Sequence 3, Application PC/TUS9414277 GENERAL INFORMATION:
               APPLICANT: BODNI, Ruth
APPLICANT: Hemmi, Silvio
TITLE OF INVENTION: Receptor Subunit
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        APPLICANT: Aguet, Michel
                                                                                                                                                                                                                                                                                     414 -SDAVCE 419
                                                                                                                                                                                                                                                                                                                                             361 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                     421 FSDAVCE 427
                                                                                                                                                                                                                                                                                                                                                            361 VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTNDEKLNKSSV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: REVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 NONYVIKWDYTYANMTFQVQWLHAFIKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MYVYLLGATTLVLVAVGPWVLSAAAGGKNLKSDQKVEVDIIDDNFILRWNRSDESVGNVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                         GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                                                                                                                                                                                                                                                                                            GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKOIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELEPPENIEVSVQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVT 60
94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                имыек: IL 107378
24-ост-1993
                                                                                                                    Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.7%; Score 2213; DB 1;
98.1%; Pred. No. 4.7e-220;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
                                                                                                                                                                                                                                                                                                                                                                                                         맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
```

```
PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                        TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 antino acids
TYPE: amtino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/164
FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
181 PSLKKHSNYSTXQCISTTVANK 202
                                                                                                     147 SPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14277
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                     207 LTSWKIGVYSPVHCIKTTVENE 228
                                                                                                                                           61 EFSLLDTNXYIKTQFRVRAEEGNSTSSWNEVDPFIPFYTAHMSPPEVRLEREDKAILVHI 120
                                                                                                                                                                               88 NFSSIKLNYYEEIKLRIRAEKEN-TSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHI 146
                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible operating system: pc-Dos/MS-Dos SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                   SPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTINSTYYVEKIPELLPETTYCLEXKAIH 180
                                                                                                                                                                                                                                                                                                     ch 21.2%; Score 490.5; DB 4 1 Similarity 48.5%; Pred. No. 7.4e-43; 98; Conservative 34; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              866PCT
                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                   69; Indels
                                                                                                                                                                                                                                                                                                                                       Length 202;
                                                                                                                                                                                                                                                                                                 1;
```

Gaps

1;

60 87

RESULT 10 PCT-US94-14277-4 Sequence 4, Application PC/TUS9414277 GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb fl.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/1427
FILING DATE: 07-DEC-1994 APPLICANT: 1
APPLICANT: 1 TITLE OF INVENTION: Receptor Subunit Polypeptides NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California ADDRESSEE: 94080 USA Aguet, Michel Bohni, Ruth Hemmi, Silvio Genentech, 360 Kb floppy disk

CLASSIFICATION: IOR APPLICATION DATA:

APPLICATION NUMBER:

08/164596

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
"---hes 93; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICATION NUMBER: US/08/683, FILING DATE: 17-JUL-1996 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: DAVID A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,6
                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pestka, Sidney
APPLICANT: Kotenko, Sergu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 LPPPENIEVSVQNQNYVLKWDY-TYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 V-LFRALLNKTSNFSEKLCEKTRPGSFS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 IYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKAR 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 TTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFH 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPVPGNLQVDAQGKSYVLKWDYIASADVLFRAQWLPGYSKSSSGSHSDKWKPIPTCANVQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LICANT: KOtenko, Sergue1

LE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHTMDEKLNKSSVFSDAVCEKTKPGNTS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYXNCQDSTCD-----GLNYEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQAR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTHCVFSQDTXYTGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPPPPVITVTAMSDTLL 120
                                                                                                                                                                                                                                                                                   07601
                                                                                                                                                                                                                                                                                                                                               Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 200 amino acids, amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08683743
                                                                                                                                                                                                                                                                                                                           New Jersey
                                                                                                                                                                                                                                                                                                                                                                                          411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.2%; Score 466.5; DB 4
44.7%; Pred. No. 2.2e-40;
                                                                                                                               US/08/683,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866PCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 200;
```

```
Д
О
                                Š
                                                                       밁
                                                                                                         Š
                                                                                                                                              밁
                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                       ; HYPOTHETICAL: ; FRAGMENT TYPE: US-08-683-743-4
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                         131 PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
176 EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP 219
                                187 HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELP 230
                                                                                                                                                                                                                                                                                       Jocal Similarity 29.9%;
nes 67; Conserva++...
                                                                                                                                            59 YRIFQDKCMNTTLIECDESS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP 115
                                                                                                                                                                                 72 WWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                          19 WYLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                     3 WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                                                     PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                               ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                  Score 228.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                  1.8e-15
                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                Indels 19;
```

Gaps

PCT-US94-14277-2 Sequence 2, Application: INFORMATION FOR CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC:
FILING DATE: 07-DEC-199 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION: ATTORNEY/AGENT INFORMATION: NAME: Love, Richard B. PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 09-DEC-: CORRESPONDENCE ADDRESS FITTLE OF INVENTION: Receptor Subunit Polypeptides NUMBER OF SEQUENCES:  $\theta$ COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) TELEX: REGISTRATION NUMBER: CLASSIFICATION: COUNTRY: TELEFAX: TELEPHONE: SSEE: Genentech, Inc.
T: 460 Point San Bruno
South San Francisco
California 94080 Application PC/TUS9414277 910/371-7168 FOR SEQ ID NO: USA Hemmi, Silvio Aguet, Michel Bohni, Ruth 09-DEC-1993 07-DEC-1994 08/164596 PCT/US94/14277 34,659 866PCT

DB 2;

Length 553;

90;

Gaps

17;

```
RESULT 13
US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                NFORMATION FOR SEQ ID NO:
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
                                                                                                                                               REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION: 206-442-6627
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1. Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT 233
                                                                                                                                                                                                                                      TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 YENVTVGPPKNISVTPGKGSLVIHFSPPFD----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 D-NWIKL--SGCQNITSTKCNF$S---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF------ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSAAAGG----KNLKSPOKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70

    Application US/08943087
    5945511

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    emino acids
                                                                                                                                   206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lok, Si
Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZymoGenetics, Inc.
01 Eastlake Avenue East
                                                                                                                                                                                                                         Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 203; DB 4
30.1%; Pred. No. 8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theodore E.
                                                                                              <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                                                                                                                                      96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: FRAGMENT TYPE: US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, App.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. GENERAL IN
                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 SRTIPPDKTVIEY 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 -- TVPNLKPLTVY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 RSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEI---QAFLLPPVFNI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 -----LPPPENIEVSVQNQNYVLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 QCVTN----HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 ERIENIYSRHKIYK--LSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 IFWYVLP----ISITV------FLFSVMGYSIYRYIHVGKEKHPANLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 QIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                     COMPUTER: IBM CONTOPERATING SYSTEM:
                                                     APPLICATION NUMBER: US/08/943,087 FILING DATE:
                                     CLASSIFICATION:
                                                                                                                                                                                                 ZIP: 98102
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                                                                                                                                                                                          E OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSLND------PQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LIYGNEFDKRFFV----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                 Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 8.6%;
Similarity 21.0%;
                                                                                                                                                                                                                                                                                                                                   : Farrah, Theresa M.
INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                  ₩Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08943087
                                                                                                                                                                                                                                                                      1201
                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                        Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                          Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                     Jelmberg, Anna C.
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                    ZymoGenetics,
                                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                    Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
internal
                                                                                                                                                                                                                                                                                                                                                                      Theodore E.
08/803,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 198; DB 2
Pred. No. 6e-12;
```

- IFWENTSNAERKI IEKKTDV

391 336 290

```
; TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                         GENERAL INFORMATION:
APPLICANT: Lok, S1
APPLICANT: Kho, Choon J.
APPLICANT: Yelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 8.6%; Score 198; DB 2; Length 553
Best Local Similarity 21.0%; Pred. No. 6e-12;
Matches 91; Conservative 79; Mismatches 173; Indels
                                                                                                                                                                                                                                                         Sequence 16, Application US/08943087 Patent No. 5945511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340
                                                                                                                                                                                                                                                                                                                                                                                     389 SRTIPPDKTVIEY 401
                                                                                                                                                                                                                                                                                                                                                                                                                            392 -- TVPNLKPLTVY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEI --- QAFLLPPVFNI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 QCVTN----HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 QIGPPEVALTTDEKSISVYLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKYKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                        DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLND------PQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------LIYGNEFDKRFFV----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFWYVLP----ISITV-----FLFSVMGYSIYRYIHVGKEKHPANLI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LPPPENIEVSVQNQNYVLKWDYTYANMTFQV-QWLHAFLKRNPGNHLYKWKQIPD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERIENIYSRHKIYK--LSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENE------
2: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                       Ş
                                                                                                                                                 밁
                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                           밁
```

```
US-08-943-087-16
                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 QIGPPEVALITDEKSISYVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWS 195
                                                                                     337
                                                                                                                                                                      340 RSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEI-----IFWENTSNAERKIIEKKTDV 391
                                                                                                                                                                                                                                                                           290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 ERIENIYSRHKIYK--LSPETTYCLKYKAALLTSWKIGVYSPVHCIKTTVENE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 QIGPPEVHLEAEDKAIVIHISPGTK------DSVMWALDGLSFTYSLLIWKNSSGVE 177
392 -- TVPNLKPLTVY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TENGTH: 555 L. TENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LVLVAVGPW--VLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVG-NVTFSFDYQK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 206-442-66
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/803,305 FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/943,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 YGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 TGMDNWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRA-EKENTSSWYEVDSFTPFRKA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LLLLLAAPWGRAVPCVSGG--LPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYFI 75
                                                                                                                                                                                                                                                                                                                                                       CENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEI---QAFLLPPVFNI 339
                                                                                          SSLND--
                                                                                                                                                                                                                                                                      -----LIYGNEFDKRFFY----PAEKIVINFITLNISDDSKISHQDMSLLGKSSDV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFWYVLP----ISITV------FLFSVMGYSIYRYIHVGKEKHPANLI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LPPPENIEVSVQNQNYVLKWDYTYANWTFQV-QWLHAFLKRNPGNHLYKWKQIPD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCVTN----HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                     -----PQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSFTQQESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.6%; Score 198; DB 2
21.0%; Pred. No. 6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
```

Gaps

17;

389 SRTIPPDKTVIEY 403

388

229

Search completed: June 1, 2000, 05:52:41 Job time: 4640 sec

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0% Listing first 45.summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                       1507
1069
233.5
228.5
221.5
221.5
221.5
115.5
129
129
119
119
118
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
117.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
65.2
46.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June .1, 2000, 04:36:46 ; Search time 16.46 Seconds (without alignments) 1553.011 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-2
2313
    168808 seqs, 58629743 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMVVLLGATTLVLVAVGPWV......KSSVFSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
    DB
  1450600
1436080
1436080
1431555
15516080
1431555
15916080
1591607
1191669
1191669
1191669
1191669
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
119169
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A32694
S27387
A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168808
                                                                                                                                                                                                                                                                              interferon recepto
interferon gamma r
interferon gamma r
interferon gamma r
frazzled gene prot
frazzled gene prot
neogenin chicken
190K protein chicken
190K protein hum
insulin receptor p
interferon gamma r
receptor tyrosine
                                                                                                                                 protein-tyrosine-p
hypothetical prote
165K myofibrillar
                                                                                                                                                                                                interleukin-10 rec
tumor suppressor -
probable protein-t
titin, muscle - ch
                                   protein-tyrosine-p
protein-tyrosine-p
leukocyte antigen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine receptor cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
hypothetical prote
twitchin - Caenorh
                                                                                                titin, cardiac mus
protein-tyrosine k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interferon alpha/b
interferon alpha r
interferon alpha/b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 2 2 2 L
```

Result No.

Searched:

104.5	105	105	105.5	105.5	105.5	106.5	108	108.5	108.5	108.5	109	109	111.5	113
	5	4.5	4.6	0	6	0	4.7	4.7	4.7	4.7	4.7	4.7	8	4.9
662	13055	56	1825	893	878	898	991	2215	2033	1028	1372	416	1896	7160
2	N	N	N	Ν	μ	N	N	N	N	N	2	N	N	N
137892	T16580	S41602	T32828	S51603	A40091	S47489	178843	T00348	T09123	I58164	A34157	T25036	T08851	T27935
IL12 receptor comp	hypothetical prote	interferon alpha r	hypothetical prote	receptor-like tyro	interleukin-3 rece	receptor tyrosine	receptor protein-t	LR11 protein - mou	hybrid receptor So	BIG-1 protein - ra	insulin receptor p	hypothetical prote	Down syndrome cell	hypothetical prote

οy	D	Que Bes Mat Qy Db	0 0 2 1 X 1 X 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A; Moj A; Res A; Crr A; Cut R; Lut Subm A; Des A; Rej A; Re A; Acr C; Ger	RESUI A326S inter C;Spe C;Dat C;Acc C;Acc Cell A;Tit A;Rei		
Oy 181 ENIYSRHKIYKLSPETTYCLKVKAALLISWKIGVYSPVHCIKTTVENELPPPENIEVSV	61 FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKEN;	Query Match 100.0%; Score 2313; DB 2; Lengt Best Local Similarity 100.0%; Pred. No. 3.2e-165; Matches 436; Conservative 0; Mismatches 0; Indel 1 MAVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWN 1	Gene: GDB:IFNAR1; IFNAR; IFRC Cross-references: GDB:120078; OMIM:107450  Map position: 21922.1-21922.1  Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 3  Keywords: cytokine receptor; glycoprotein; transmembrane  1-21/Domain: transmembrane #status predicted <trn1> 437-455/Domain: transmembrane #status predicted <trn2> 437-455/Domain: transmembrane #status predicted <trn2></trn2></trn2></trn1>	A; Molecule type: mRNA A; Residues: 1-557 <uze> A; Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; A; Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; A; Cross-references: GB:J03171; NID:g184645; PIDN:AAA52730.1; A; Description: The structuree of the human interferon alpha/b A; Reference number: S17112 A; Accession: S17112 A; Accession: S17112 A; Molecule type: DNA A; Residues: 1-16, 'A', 18-329, 'V', 343-557 <lut> A; Cross-references: EMBL:X80459; NID:g32671 C:Genetics:</lut></uze>	eceptor precursor - human (man) juence_revision 22-Jun-1990 #text_cha 7112 ; Gresser, I. er of a functional human interferon a	ALIGNMENTS	34 109 4.7 1372 2 A34157 B1 35 108.5 4.7 2033 2 T09132 h3 36 108.5 4.7 2033 2 T09133 h3 37 108.5 4.7 2215 2 T00348 LE 38 108 4.7 991 2 178843 re 39 106.5 4.6 898 2 S47489 re 40 105.5 4.6 898 1 A40091 in 41 105.5 4.6 893 2 S51603 h3 42 105.5 4.6 1825 2 T32828 h3 43 105.5 4.6 1825 2 T32828 h7 44 105.5 4.6 1825 2 T32828 h7 45 104.5 4.5 13055 2 T16580 h7 47 105 4.5 13055 2 T16580 h7 48 104.5 4.5 13055 2 T16580 h7 49 104.5 4.5 13055 2 T16580 h7
PPENIEVSVQ 240	TSSWYEVDSF 120	.h 557; .s 0; Gaps 0; .RSDESVGNVT 60 .	881/3; 432/1; 480/3 protein sinding site: carbohydr	PID:g306914 beta receptor gene.	nge 22-Oct-1999 Lpha receptor into mo		insulin receptor p BIG-1 protein - ra hybrid receptor So LR11 protein - mou receptor tyrosine interleukin-3 rece receptor-like tyro hypothetical prote interferon alpha r hypothetical prote interferon appa r

```
C:Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S27387; S33770
R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
                                                                                                                                                                                                                                    Š
                                                                                                                    멍
                                                                                                                                                          Ş
                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                     ᄝ
                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Experimental source: lung
C;Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-421,'V',423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha
A;Reference number: S33770; MUID:93305725
A;Recession: S33770
A;Recession: S33770
A;Status: preliminary; nucleic acid sequence not shown
Ş
                                        용
                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-560 <MOU>
A; Cross-references: EMBL: X68443; NID: g431; PIDN: CAA48484.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Specific antiviral activities of A; Reference number: S27387; MUID:93076908 A; Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Lim, J.K.; Langer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: MDBK cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon alpha receptor type 1 precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24/Domain: signal sequence *status predicted <SIG> redicted interferon alpha receptor type 1 *status predicted
    299
                                          239
                                                                                                                        179
                                                                                                                                                                179
                                                                                                                                                                                                      119
                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hes 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                     \boldsymbol{\mu}
                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                  FTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGTKDSVMWALDGLSFTYSLLIWKNSSGVEE 178
                                                                                                                                                                                                                                                                                   QKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLS-DSFHIYIGAPKQSG
                                                               VQNQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVF
                                                                                                                    RTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPVYCINTTERHKVPSPENIQIN
                                                                                                                                             RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVS
                                                                                                                                                                                                                                                                                                                                                                                                       MVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                   MLALLGATTLMLVA-GRWVLPAASGEANLK-PENVEIHIIDDNFFLKWNSSSESVKNVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NONYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1507; DB 2;
Pred. No. 5.2e-105;
55; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferons are determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID: 9432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMAT
                                                                                                                                                            238
                                                                                                                      238
                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
  357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lutfalla, G.; Uze, G.

Gene 148, 343-346, 1994
A;Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high A;Reference number: 148423; MUID:95047447
A;Accession: 148423
                                 A;Gene: IFNAR
A;Introns: 177/3;
C;Keywords: cytok
                                                                                                                                     A;Status: preliminar
A;Molecule type: DNA
A;Residues: 473-590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A45289; 148423; I48424; I48425; I48426; I48427; I48428; I48429
R;Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A;Title: Behavior of a cloned murine interferon alpha/beta receptor expressions.
                                                                                               A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 426-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                    A; Accession: I48429
                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                              A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                      A; Cross-references:
A; Accession: I48428
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 397-424 < RE5>
                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; A;Accession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 265-375 < RE4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; A;Accession: 148426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; A;Accession: I48425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: I48424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 118-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: sequence extracted R; Lutfalla, G.; Uze, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; A;Note: sequence extracted from NCBI backbone (NCBIN:102354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A45283; A; Accession: A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMSVNQLYPLIYEVIFWENTSNAERKVLEKKTNFIFPDLKPLTVYCVKARALIENDRRNK 418
                                                                                                                                                                           preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSVFSDAVCEKTKPGNTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNK 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRGIXYVRVRASNGNGTSFWSEEKEFNTEMKTIIFPPVISVKSVTDDSLHVSVGASEESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha/beta receptor - mouse
                                      cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-590 <UZE>
                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                         EMBL: U06241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <RES>
EMBL:U06237; NID:g497103; FIDN:AAA65003.1;
                                                                                                                  EMBL:U06244;
                                                                                                                                         <RE7>
                                                                                                                                                                                                                 EMBL: U06242; NID: g497112; PIDN: AAA65007.1; PID: g755813
                                                                                                                                                                                                                                             <RE6>
                                                                                                                                                                             translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUID:92262522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437
                                                                                                                  NID: g497114; PIDN: AAA65008.1;
                                                                                                                                                                                                                                                                                                                       NID: 9497110; PIDN: AAA65006.1;
                                                                                                                                                                                                                                                                                 from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                    from
                                                                                                                                                                                                                                                                                                                                                                                    GB/EMBL/DDBJ
```

PID: g194112 NCBIP: 102357)

expressed

ä

×

PID:g510265

PID:g755812

PID:g510262

PID:g510261

PID:g755811

PID: 9755810

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                               Š
                                                                      밁
                                                                                                    Ş
                                                                                                                                           멼
                                                                                                                                                                           á
                                                                                                                                                                                                                                                                                                      A;Gene: GDB:CRFB4; CRF2-4
A;Cross-references: GDB:138168; OMIM:123889
A;Map postition: 21922.1-21922.2
A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: G01418
R;Lutialla, G.
submitted to the EMBL Data Library,
A;Reference number: G06935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine receptor family II, member 4 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
 밁
                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-273 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U08988; NID:g571295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reference number:
Accession: G01418
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                             Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
 116
                                     131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 NFSEKLCEKTRPGSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 VFSDAVCEKTKPGNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SAEYRTKDEAKWLKVPECQHTTTTKCEFSLLDTNVYIKTQFRVRAEEGNSTSSWNEVDPF
                                                                      59
                                                                                                        72
                                                                                                                                                                             19 WYLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
                                                                                                                                                                                                                  Local Similarity
les 67; Conserv
                                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 MYVLLGATTLVLVAVGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNYTF
|: ::|| ||||| |||| :||||:||| ||: ::| |||||: |:|: ||:|:|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NQNYVLKWDY-TYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKSYVLKWDYIASADVLFRAQWLPGYSKSSSGSHSDKWKPIPTCANVQTTHCVFSQDTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSTYTYEKIPELLPETTYCLEVKAIHPSLKKHSNYSTVQCISTTVANKMPVPGNLQVDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLAVVGAAALVLVAGAPWVLPSAAGGENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTF
 PGMQVEVLDDSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                 PEVHLEAEDKAIVIH-ISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                     YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
                                                                                                      NWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                           WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GLNYEIIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQARV-LFRALLNKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPPPPVITVTAMSDTLLVYVNCQDSTCD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPTYTAHMSPPEVRLEAEDKALLVHISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKEN-TSSWYEVDSF 120
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%; Score 1069; DB 2; 48.6%; Pred. No. 2.9e-72;
                                                                                                                                                                                                                             10.1%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435
                                                                                                                                                                                                                  44;
                                                                                                                                                                                                             Score 233.5; DB 2;
Pred. No. 2.6e-10;
""" tches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                              PID: g571296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 590;
                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                      273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
175
                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                æ
```

```
C;Accession: A47003
R;Lutfâlla, G.; Gardiner, K.; Uze, G.
Genomics 16, 366-373, 1993
A;Title: A new member of the cytokine receptor gene
A;Reference number: A47003; MUID:93300510
A;Accession: A47003
                                                                                                                                                                                                                               A; Reference number: JC6311
A; Accession: JC6311
A; Status: preliminary
                                                                                                                                                                                                                                                                                  C; Accession: JC6311
R; G1bbs, V.C.; Pennica, D.
Gene 186, 97-101, 1997
A; Title: CRF2-4:isolation
                                                                                                                                                                                                                                                                                                                                               interferon receptor-class II cytokine receptor -
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 21q
C; Keywords: transmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine receptor family class II protein CRF2-4 precursor C; Species: Homo sapiens (man)
C; Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
S
                                 Вp
                                                             Š
                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-349 <GIB>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:Z17227; NID:g393378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                   Matches
                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD 71
   74
                                                              16 VGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ--KTGMDNW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 NWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVLRNLEPWITYCVQVRGFLPDRNKAGEWSEPVCEQTIHDETVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP
   IKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGPPE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                 LGGFLLVPALG--MIPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQYESYRSFQDH- 66
                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 29.9
67; Conservative
                                                                                                 Conservative
                                                                                                                                                                                    GB:U53696
                                                                                                              9.6%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.98;
                                                                                                                                                                                                                                                                                     of cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                               Score 221.5;
Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 228.5; DB 2
Pred. No. 7.8e-10;
                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                    16-Jul-1999
                                                                                                                                                                                                                                                                                     encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID: g393379
                                                                                                                   .9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                      mouse
                                                                                                                                                                                                                                                                                     the
                                                                                                   86;
                                                                                                                                                                                                                                                                                                                                                    #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 10-sep-1997
                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family maps
                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                 Length 349;
                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                   29;
                                                                                                                                                                                                                                                                                       mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
```

67;

Gaps

14;

62

119

174

8

```
A; Note:
C; Keywor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon gamma receptor beta subunit - mouse

N.Alternate names: IFN-gamma R beta chain; IFN-gamma R species-specific cofactor;

C;Species: Mus musculus (house mouse)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: A49947

R;Hemmi, S.; Bohni, R.; Stark, G.; Di Marco, F.; Aguet, M.

Cell 76, 803-810, 1994

A;Title: A novel member of the interferon receptor family complements functionality

A;Reference number: A49947; MUID:94170381
                                                                                                                                                                         interferon gamma receptor accessory factor-1 precursor - human C;Speciaes: Homo sapiens (man)
C;Date: 16:Feb-1996 *sequence_revision 16:Feb-1996 *text_change C;Accession: I38500; I38501
R;Soh, J.; Donnelly, R.J.; Kotenko, S.; Mariano, T.M.; Cook, J. cell 76, 793-802, 1994
A;Title: Identification and sequence of an accessory factor req A;Reference number: A49946; MUID:94170380
A;Accession: I38500
A; Acteur type: mRNA
A; Residues: 1-63,'0',65-337 <RE2>
A; Residues: EMBL: U05877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ş
                                                                             A; Experimental A; Accession: I:
                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-337 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:S69336; NID:g545841; PIDN:AAB30165.1; PID:g545842
A;Experimental source: early B-cell line Y16
A;Note: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-332 <HEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Reference number: A49947;
A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                               A;Cross-references: EMBL:U05875; NID:g463549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-WWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIYSRHKIY--KLSPETTYCLKVKAAL-LTSWKI---GVYSPVHCIKTT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM
                                                                                                                                                                                                                                                                                                                                                                                                                                              GPFKSNSIVLGNLKPYRVYCLQTEAQLILKNKKIRPHGLLSNVSCHETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YENVTVGPPKNISVTPGKGSLVIHFSPPFD----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDSEVLRNLEPWTTYCIQVQGFLLDQNRTGEWSEPIC-ERTGNDEITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MQIESLAESLELRFSAPQIENEPET-----WTLKNIYDSWAYRVQYWKNGTNEKFQVVSP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine receptor
                                                                             al source: clone pSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CKRTASTQCDFS--HLSKYGDYTVRVRAELADEHSEWVNV-TFCPVEDTIIGPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8%;
                                                                                                                                                                                                   sequence of an accessory factor required for activation of MUID:94170380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PGTKDSVMWALDGL--SFTYSLLIWKNSSGVEERIENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
               NID: g463551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 203; DB
Pred. No. 6.5e-
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor family complements functionality
                                                                                                                 PIDN: AAA16955.1;
            PIDN: AAA16956.1;
                                                                                                                                                                                                                                                          T.M.; Cook, J.R.; Wang, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .98;
                                                                                                                                                                                                                                                                                                   #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219
                                                                                                                                                                                                                                                                                                                                                                                                                                                 233
            PID:g463552
                                                                                                               PID:g463550
                                                                                                                                                                                                                                                                                                   05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                          Emanuel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
                                                                                                                                                                                                                                                            ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 *sequence_revision 20-
C;Accession: T13822
R;Kolodziej, P.A.; Timpe, L.; Mitchell, K.
Cell 87, 197-204, 1996
A;Title: Frazzled encodes a Drosophila mer
A;Reference number: Z17780
A;Accession: T13822
A;Accession: T13822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone | C; Genetics:
A; Map position: 21
C; Keywords: cytokine receptor
                                                                    ő
                                                                                                             밁
                                                                                                                                                 Š
                                                                                                                                                                                              밁
                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1375 < KOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frazzled gene protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          皮
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.3
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                               Matches 102;
                                                                                                                                                        104
                                                                                                                                                                                                                                                                                  447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GALHSAWVTMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FC
                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                      26 GGKNLKS------PQKVEVDIIDDNFI-LRW------
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 VLVAVGPWVLSAAAGG---KNLKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                frazzled
                                                                                                                                                        --IRAEKENTSSWYE----
                                                                                                                                                                                                                                     GNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCIKTTVENELPPPENIEVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YYVHYWE---KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDYQKTGMDNWIKLS-----GCQNITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFK
                                ISVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQI
                                                                           DSFTPFRKAQIG----
                                                                                                               GYARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYV
                                                                                                                                                                                              KMVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFE 566
                                                                                                                                                                                                                                                                                GGKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQ 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCYETMADASTELQQVILISVGTESLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTDSK-----WFTADIMSIGVNCTQITATECDFTAASPSAGFPMDFNV----TLRLRAEL
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function in vivo as a receptor or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL:U71001;
                                                                                                                                                                                                                                                                                                                                                                                  16.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%; Score 155.5; DB 2; 22.3%; Pred. No. 0.00023; tive 54; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pJS3
                                                                                                                                                                                                                                                                                                                                                               ;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g1621114; PID:g1621115;
                                                                                                                                                                                                                                                                                                                                                                                  Score 129; DB Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                             Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.J.; Goodman, C.S.; Fried,
                                                                        PPEVHLE-AEDKAIVIHISPGTKDSVMWAL
                                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QNQNYVLKWDYTYANMTFQVQ
                                                                                                                                                                                                                                                                                                                                                                                                        Length 1375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                      -----NRSDESV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN: AAC47314.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337;
                                                                                                                                                                                                                                                                                                                                                               268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a
```

20-Sep-1999

260

292

232

S.; Jan,

L.Y.;

subfamily

----V 117

989

158 626 receptor mediat

Gaps

22;

Ouery Match  5.6%; Score 129; DB 2; Length 1526;  Best Local Similarity 16.4%; Pred. No. 0.18;  Matches 102; Conservative 68; Mismatches 184; Indels 268; Gaps 22;  Qy 26 GGKNLKS	nogaster nce_revision 20-Sep-1999 #text_cl L.; Mitchell, K.J.; Goodman, C.S. a Drosophila member of the DCC in nslated from GB/EMBL/DDBJ 71002; NID:g1621116; PID:g1621117	Qy 342 LSDSFHIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKK 388  Db 960REVTVRLDENNPTVIQWIPPKHTLGQITGYNIYYTDTTKRDRDWSVEAFAGEE 1015  Qy 389 TDVTVPNLKPLTVYCVKARAHIT 410    : :	93 WGRGIPDENTIELKETERYHILKNLESNM 93 WGRGIPDENTIELKETERYHILKNLESNM 51	159 DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKI
OP 416 LAPATTOPLPTAPRDVVATLVSTREIRLTWRTPVSDPOGDNLTYSIFYTKEGINRE 471  OY 78 GCQNITSTKCNESSLKLNYYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEA 137	J. Cell Biol. 127, 2009-2020, 1994 A;Title: Neogenin, an avian cell surface protein expressed during terminal neuron A;Reference number: A55193; MUID:95105243 A;Accession: I50600 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1443 <vie> A;Cross-references: EMBL:U07644; NID:g641965; PID:g641966 A;Cross-references: EMBL:U07644; NID:g641965; DB 2; Length 1443; Best Local Similarity 22.2%; Pred. No. 0.21; Matches 92; Conservative 61; Mismatches 201; Indels 61; Gaps 19; Matches 92; Conservative 61; Mismatches 201; Indels 61; Gaps 19; YEADAAGKNLKSPQKVEVDIDDNEI-LEWNRSDESVGNVTFSEDYOKTGMDNWIKLS 77</vie>	Qy 389 TDVTVPNLKPLTVYCVKARAHT 410   : :                         Db 1167 TMLMLPNLKPYTTYYFKVQART 1188  RESULT 11 150600 neogenin - chicken (fragment) C:Species: Gallus gallus (chicken) C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996 C:Accession: I50600 R:Violimetter: J: Kayvem. J.F.: Roman. J.M.: Draver. W.J.	APTPLEVPYGLRAIIMSSSSIVVYMIDTMLNKNQHYTDNRHYTVSYGITGSNRYRY  DCENVKTTQCVFPONVFQKGIYLLRVOASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSMSVLNSTYQNVPVTPP  LSDSFHIYIGAPKQSGNTPVIQDYPLIVEIIFWENTSNAERKIIEKK  :	213 GVYSPVHCIKTTVENELP

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Vinkemeier, U.; Obermann, W.; Weber, K.; Fuerst, D.O. J. Cell Sci. 106, 319-330, 1993
A;Title: The globular head domain of titin extends into the A;Reference number: S42166; MUID:94095665
A;Accession: S42167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                     Mol. Endocrinol. 4, 235-244, 1990
A;Title: The rat insulin receptor: primary structure
A;Reference number: A36080; MUID:90231337
A;Accession: A36080
                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-1451 <VIN>
A;Cross-references: EMBL:X69090; NID:g407098; PIDN:CAA48833.1;
A;Cross-references: GB:M29014; NID:g204953; PIDN:AAA41441.1; C;Superfamily: insulin receptor; protein kinase homology
                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1383 <GOL>
                                                                                                                                                                                                                                             insulin receptor precursor - rat
C.Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: skelemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 19.8
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S42167
                                                                                                                                                                                  Accession: A36080
Goldstein, B.J.; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388
                                                                                                                                                                                                                                                                                                                                                                        762 A-YKISNLKENMVYQFQVAAMNMAGLGAPSAVSECFKCEE 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLIEGRSYIFRVRAVNKMGIGFPSRVSEAVAALDPAEKARLKSP---LSTLDWTVIVTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KL-----RIRAEKENTSSW-----YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYIIISWKQPAVDGGSPILGYFIDKCEVGTDSW------SQCNDTPVKFARFPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEI
                                                                                                                                                                                                                                                                                                                                                                                                              TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDITCLESFRDSMVLGWKQPDKTGGAEITGYYVNYREVIDGVPGKWR----EANVKAVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --VFNIRSLSDSFHIYIGAPKQSGNTPVIQDYPLIYEII-----FWENTSNAERKIIEKK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TCHGLVTGQS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSRNTDTSV-----VVSWEESKDAKELVGYYIEANVAGSGKWEPC--NNNPVKTHRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPENIEVSVQNQNYVLKWD------YTYANMTFQVQWLHAFLKRNP-GNHLYKWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVKSPRFALFDLAEGKSYCFRVRC----SNSAGVGEPSEATEVTVVGDKLDIPKAPGKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPSEGIVPGPPTDLSVTEATRSYVVLSWKPPGQRGHEGIMYFVEKCEAGTENWQRVNTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGTKDSVMWALDGLSFT----YSLLIWK----NSSGVEERIENIYS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTV-----ENELP
                                                                                                                                                                                    Dudley, A.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.3%;
19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----YIFRVRAVNAAGLSEYSQDSE-AIEVKAAIAPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 123.5; D
Pred. No. 0.42;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181;
                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1451;
                                                                                                                                              conservation of tissue-specifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            center
                         PID:g204954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: g407099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sarcomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            z
```

```
C;Keywords: ATP; autophosphorylation; hormone receptor; phosphoprotein; transmembra F;1022-1298/Domain: protein kinase homology <KIN>F;1030-1038/Region: protein kinase ATP-binding motif
                                                      밁
                                                                                     Š
                                                                                                                           밁
                                                                                                                                                            Š
                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                      805
                                                                                          388 KTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKP
                                                                                                                             747 TSSGNGAEDTRPSRKRRSLEEVGNVTATTPTLPDFPNISSTI--APTSHEEHRPFEKVVN
                                                                                                                                                                                                                                                                              650 NGNIT--
                                                                                                                                                                                                                                                                                                               252 YANMTFQVQWLHAFLKRNPGNHLYKW-KQIPDCENVKTTQCVFPQNVFQKGIYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                             567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 VTEFDGQDAC-----IDPPQ---RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 NDIALKTNGDQASCENELLKFSFIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQN 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 DNFILRWNRSDESVGNVTFSFDYQKTGMDN-------WIKLSGCQN 81
14
                                                      KESLVISGLRHFTGYRIELQACNQDSPEERSGV-AAYVSARTMP
                                                                                                                                                                                                     PPFESDDSQKHNQSEYDDSASECCSCPKTDSQILKELEESSFR-KTFEDYLHNVVFVPRK
                                                                                                                                                                                                                                      --LRVQASDGNNTSFWSEEI-----KFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQ
                                                                                                                                                                                                                                                                                                                                                    YAIFVKTLVTFSDERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDP
                                                                                                                                                                                                                                                                                                                                                                                     YCLKYKAALLTSWK---IGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKW---DYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IT----STKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.18;
                                                                                                                                                                                                                                                                            -HYLVYWERQAEDSELFELDYCL-----KGLKLPSRTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 119;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                -TPVIQDYPLIYEIIFWENTSNAERKIIEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1383
                                                      847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 172;
                                                                                                                                                                                                                                                                                                                                                                                                                           ----LKPWTQ 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                    649
                                                                                                                                                                388
                                                                                                                                                                                                     746
                                                                                                                                                                                                                                                                            687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       566
                                                                                                                                                                                                                                         355
                                                                                                                                                                                                                                                                                                                 305
                                                                                                                                                                                                                                                                                                                                                                                         251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
```

```
A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
A;Map position: 6q23-6q24
C;Superfamily: interferon gamma receptor
C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                          R:Aguet, M.: Dembic, Z.; Merlin, Cell 55, 273-280, 1988
A:Title: Molecular cloning and e A:Reference number: A31555; MUID A:Accession: A31555
Ş
                                          В
                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-489 < AGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interferon gamma receptor precursor - )
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision
                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:J03143; NID:g184650;
                                                                                                                             Query Match
Best Local S
Matches 50
                                          27
NVKTTQCVFPQNVFQKGIYL-LRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS--
                                          SSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVE-----VKNYGVKNSEW--IDACI 78
                                                                                NELPPPENIEVSVQNQNYVLKWDYTYANM--TFQVQWLHAFLKRNPGNHLYKWKQIPDCE 284
                                                                                                                             l Similarity
50; Conserv
                                                                                                                             5.1%; Score 118; DB 2; Ilarity 22.2%; Pred. No. 0.25; Conservative 39; Mismatches 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     and expression; MUID:89003065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-Feb-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                    PIDN: AAA52731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                               102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
                                                                                                                                                                      Length 489;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interferon-gamma receptor
                                                                                                                                                                                                                                                                                                                                                                  PID: g306915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-Jul-1999
                                                                                                                             Gaps
      342
                                                                                                                                  10;
```

```
RESULT
S51604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase fam A;Reference number: $49015; MUID:94067777
A;Accession: $51604
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor-like tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:S68029
A;Cross-references: EMBL:S68029
A;Cross-references: EMBL:S68029
A;Cross-references: EMBL:S68029
A;Cross-references: EMBL:S68029
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-translated, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; transmembrane protein
C;Keywords: ATP; transmembrane protein
F;651-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif
                                                      S
                                                                                                                   멇
                                                                                                                                                                   Ş
                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 5.1%; Score 118; DB 2; Length 981; Best Local Similarity 20.1%; Pred. No. 0.64; Matches 92; Conservative 51; Mismatches 165; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
Residues: 1-981 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 QCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFNSSI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 --- VTVPNLKPLTVYCVKARA--HTMDEKLNKS----- SVFSDAV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 KQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEI 198
                                       374 WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT 410
                                                                                                                      449
                                                                                                                                                                                                                                      416
                                                                                                                                                                                                                                                                                             279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GFFKASPHSQTCSKCPP------HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 GRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG---- 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 ---LSDSFH--IYIGAPKQSGN-TPVIQDYPLIYEIIFWENTSNAERKIIEKKTD-----
                                                                                                                                                                         360 PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR--- 416
                                                                                                                                                                                                                                                                                                                                                                                                       232 ---PENIEVSVQNQNYVLKW-------DYTYANMTFQVQWLHAFLKRNPGNHLYKWK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH------CIKTTVENELPP------ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 DPPKMHCSAEGEWLV----PIGKCMC-------KAGYEEKNGTCQVCRP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ----ACIALVSVRVYYKKCPSVVRHLAVFPD-----TITGADSSQLLEVSGSCVNHSVTD 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 NISHHYCNISDHYGDPSNSLWYRYKARYGQKESAYAKSEEFAYCRDGKIGPPKLDIRKEE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 GKNLKSPQKVEVDII--DDNF------ILRWNRSDESVGNVT---FSFDYQKTGMDNW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
FEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART 546
                                                                                                                   VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY 508
                                                                                                                                                                                                                                                                                             QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKLSGCQNITST-----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI 128
                                                                                                                                                                                                                                   ---YLPQQIGLKNTSVMMADPLAHTNYTF-----EIEA-----VNG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391
```

Search completed: June

۲,

2000, 05:53:08

Job time: 4582 sec

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched
          Pred. No. is the number of results predicted by chance to hav score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
          2313
1503
11069
2218:5.5
1123.5
1123.5
1139
1111
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
1111.5
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         June 1, 2000, 04:40:22; Search time 28.35 Seconds (without alignments) 468.373 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-240-675-2
2313
1 MMYVLLGATTLVLVAVGPWV.....KSSVFSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83857 seqs, 30454973 residues
       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
       13431
13431
13433
10489
10595
11912
11912
11912
11912
11037
11037
11037
11037
11037
11037
11037
11037
11037
11037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
B
INR1_HUMAN
INR1_SHEEP
INR1_MOUSE
CRF4_HUMAN
INGS_HUMAN
INGS_HUMAN
INGR_HUMAN

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ltd.
                                                                        1 drosophila
6 homo saplen
6 nicotiana t
9 homo saplen
1 mus musculu
5 homo saplen
1 mus musculu
5 homo saplen
3 spinacia ol
6 arabidopisi
1 haemophilus
                                                                                                                                                                                                                                                                                                                           1 mus musculu
8 mus musculu
6 homo sapien
2 homo sapien
4 mus musculu
1 homo sapien
6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 mus musculu
4 homo sapien
4 homo sapien
6 homo sapien
7 rattus norv
7 mus musculu
8 homo sapien
8 gallus gall
6 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 homo sapien
0 bos taurus
9 ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      printed,
```

EMBL; J03171; AAA52730.1; -.
EMBL; X60459; CAA42992.1; -.
PIR; A32694; A32694.
PIR; S17112; S17112.
MIM; 107450; -.

388	88	888	323	388	388	388	388	388	2 2 2	323	2 Z Z	공 공 공	R R	RR	g R R	222	R R	2008	0 G G		S A C	i R							
			T'E	:			-	<u> </u>	Mol	3 K C	MEI	_ ; [3]:	"Lut	MEC	Cel	1 7 G G		But	UF N	101- 101-	P17	SULT R1_HUM		444	42	40 41	38 39	36	ม ภ
send an e	anoi	pear	.s SWISS-I	SIMILARI	PIM: PHO	TISSUE	SUBUNITS	I IFNS 1	the type	lersman :	SPHORYLAS	Biol. Che	falla G., le structi	UENCE FRO	1 60:225	netic tra	INE	heria; Pr	AR1 OR IN	AUG-1990 FEB-2000 ERFERON-#	181; AUG-1990	1 LAN LHUMAN		6.9	٠, ١		7.		0
quires	1-prof	Bioi	ROT e	TY: BI	SPHOR	SPECIF	THEM	RIGGE	I into	)., Yai	110N B	m. 26	re of	M N.A	234 (19	nsfer	M N.A	Metazoa Metazoa	NAR.	(Rel. (Rel. (Rel.	RA	STA							
a lice	it ins	format	ntry is	LONGS	CLATED	CITY:	SELVES	SPTOR I	erferor	tte M.	7 TYK2	7:2802	the h			i i i	<b>.</b>	~~~				NDARD;		517 515	1256	1091 1162	578 306	1345	1 2 2 3
nse	nent	ics	8	9,	385	IFN	, ,	OR SIN	3-81	Kr		280	man P		ď	9 5 8		dat		CEP	Ď T								
(See n	ong as its oved. Usage	There are	yright. It is produced	THE CLASS II CYTOKINE FAN	MOST IFN-RESISTANT CELLS TYROSINE RESIDUES BY TYK!	RECEPTORS ARE PRESENT II	ADE I MEMBRANE DECLEIN	₽⋗∑	ceptor by pl35tyk2 tyrosi42(1994).	ishnan K., Krolewski J.;		92).	on D., Vielh E., rferon alpha/beta	:		1.;   Interferong	•	a; Craniata; Vertebrata; ini; Hominidae; Homo.		sequence update) annotation update) TOR ALPHA CHAIN PRECURSOF	P.C.	·• ຫ	ALIGNMENTS	TR7_YEAST INR2_HUMAN	FINC_CHICK	CIC2_HUMAN LEPR_MOUSE	I10R_HUMAN KI28_YEAST	YHOO_YEAST RRPO_TMV	0
		ָר ל ה	through a collaborat	RECEPTORS.	2 TYROSINE KINASE.	N ALL TISSUES AND	,	OF PROTEINS	e kinase.";	מולנות שלווס		,	3.; eptor gene."	'		277		Mammalia;						524	22	56 mus	51 hoπ 42 sac	00 saccharomy 86 tobacco mo	la homo canto
	entities requires a license agreement (see http://www.j or send an email to license@isb-sib.ch).	use by non-profit institutions as long as its contemporal modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.ior send an email to license@isb-sib.ch).	between the swiss institute of bioinformatics and the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/annour or send an email to license@isb-sib.ch).	This SWISS-PROT entry is copyright. It is produced throbetween the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no ruse by non-profit institutions as long as its contempolified and this statement is not removed. Usage by entities requires a license agreement (See http://www.jor send an email to license@isb-sib.ch).	INTERPRETE CONTRING & FIDEWARD IN THE STATE OF THE CLASS II CYTOKINE FAMILY This SWISS-PROT entry is copyright. It is produced through the European Bioinformatics Institute of Bioinformatics and the the European Bioinformatics Institute. There are no ruse by non-profit institutions as long as its contemporal modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.ior send an email to license@isb-sib.ch).	-!- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYKE TY -!- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYKE TO -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DO -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY This SWISS-PROT entry is copyright. It is produced thro between the Swiss Institute of Bioinformatics and the the European Bioinformatics institute. There are no I use by non-profit institutions as long as its conte modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.jor.send.an.email to license@isb-sib.ch).	-I TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALEVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS!- PYM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TY -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DO -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY This SWISS-PROT entry is copyright. It is produced throbetween the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no represent the Swiss Institutions as long as its contemporal modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.jors.end.agreement (See http://www.jors.end.agr	SUBULTS THEMSELVES.	-I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. I ITNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBE INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHY SUBURITS THEMSELVES	of the type I interferon receptor by p135tyk2 tyrosine plane	Mullersman J., Witte M., Krishaan K., Krolewski J.;  **Pirect binding to and tyrosine phosphorylation of the of the type I interferon receptor by p135tyk2 tyrosine of the type I interferon receptor by p135tyk2 tyrosine Mol. Cell. Biol. 14:8133-8142(1994).  -i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. I INTERFERONS ALPHA AND BETA. I INTERFERONS ALPHA AND IFN-R ALPHA INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA SUBUNITS THEMSELVES.  -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEINi- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALPHA SUBUNITS THEMSELVES OF MOST IFN-RESISTANT CELLSi- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TY-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILYi- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  This SWISS-PROT entry is copyright. It is produced through by non-profit institute of Bioinformatics and the the European Bioinformatics Institute. There are no is modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.ionresides.comes.)	MEDLINE: 95059042.  MEDLINE: 95059042.  MEDLINE: 95059042.  MILLERMANDICOLO, Yan H., Domanski P., Handa R., Smalley E Colamonicolo, Yan H., Domanski P., Krolewski J., Millersman J., Witte M., Krishnan K., Krolewski J., "Direct binding to and tyrosine phosphorylation of the of the type I interferon receptor by p135tyk2 tyrosine of the type I interferon receptor by p135tyk2 tyrosine Mol. Cell. Biol. 14:8133-8142(1994).  1. FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. I IENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBE INCLUDING JAKS, TYK2, STAT PROTEINS AND IEN-R ALPHA SUBUNITS THEMSELVES.  1. SUBCELIULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALPHA SUBCELIULAR LOCATION: TYPE I MEMBRANE PRESENT IN ALPHA SUBCELIULAR LOCATION TYPE III-LES DISTRIBUTED ON TYROSINE RESIDUES BY TYK2 TYK1.  1. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DO SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY THIS SWISS-PROT entry is copyright. It is produced throuse by non-profit institute of Bioinformatics and the the European Bioinformatics institute. There are no use by non-profit institutes of Bioinformatics and the modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.ior.send.)	J. Biol. Chem. 267:2802-2809(1992).  [3]  PHOSPHORYLATION BY TYK2.  MEDLINE; 95059042.  Colamonici O., Yan H., Domanski P., Handa R., Smalley E Colamonici O., Yan H., Domanski P., Handa R., Smalley E Millersman J., Witte M., Krishnan K., Krolewski J.;  Millersman J., Witte M., Krishnan K., Krolewski J.;  Millersman J., Witte M., Krishnan K., Krolewski J.;  Plirect binding to and tyrosine phosphorylation of the of the type I interferon receptor by pl35tyk2 tyrosine of the type I interferon FOR INTERFERONS ALPHA AND BETA.  I IFNS TRIGGERS TYROSINE PROTEINS AND IFN-R ALPHA INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA SUBUNITS THEMSELVES.  FUNCTION: RECEPTOR FOR INTERFERON PROTEIN.  TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALEVEN ON THE SUBRACE OF MOST IFN-RESISTANT CELLS.  PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TY-  SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  This SWISS-PROT entry is copyright. It is produced through by non-profit institute of Bioinformatics and the the European Bioinformatics Institute. There are no incompleted and this statement is not removed. Usage by entities requires a license agreement (See http://www.ionresection.com.)	Luttaila G., Gardiner K., Proudnon D., Vielh E., Uze G. The structure of the human interferon alpha/beta recep J. Biol. Chem. 267:2802-2809(1992).  [3] PHOSPHORYLATION BY TYK2.  MEDLINE; 95059042.  MEDLINE; 95059042.  MEDLINE; 95059042.  MILLERSMAN J., Witte M., Domanski P., Handa R., Smalley E Mullersman J., Witte M., Krishnan K., Krolewski J.;  "Direct binding to and tyrosine phosphorylation of the of the type I interferon receptor by pl35tyk2 tyrosine Mol. Cell. Biol. 14:8133-8142(1994).  "I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND IN-R ALPHA SUBUNITS THAUSELVES.  "I FUNCTION: RECEPTOR FOR INTERFERONS AND IN-R ALPHA SUBUNITS THAUSELVES.  "I SUBCELLULAR LOCATION: TYPE I MEMBRANE PRESENT IN AI EVEN ON THE SUBRACE OF MOST IN-RESISTANT CELLS.  "I FIM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TY  "I SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FEMILY.  "I SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FEMILY.  "This SWISS-PROT entry is copyright. It is produced through by non-profit institute of Bioinformatics and the the European Bioinformatics Institute. There are no use by non-profit institute. There are no use by non-profit institute of Bioinformatics and the modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.iorr.)  or send an email to license@isb-sib.ch).	SEQUENCE FROM N.A.  MEDLINE; 92129376.  Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.  The structure of the human interferon alpha/beta recep  J. Biol. Chem. 267:2802-2809(1992).  [3]  PHOSPHORYLATION BY TYK2.  MEDLINE; 95059042.  COLAMONICIO., Yan H., Domanski P., Handa R., Smalley E.  MILIETSMAN J., Witte M., Krishnan K., Krolewski J.;  "Direct binding to and tyrosine phosphorylation of the  of the type I interferon receptor by p135tyk2 tyrosine  of the type I interferon receptor by p135tyk2 tyrosine  for the type I interferon receptor by p135tyk2 tyrosine  p1 IFNS TRIGGERS TYROSINE PROTEINS ALPHA AND BETA.  I IFNS TRIGGERS TYROSINE PROTEINS AND IFN-R ALPHA  FINCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA  SUBUNITS THEMSELVES.  FUNCTION: TYPE I MEMBRANE PROTEIN.  TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN AL  EVEN ON THE SUBRACE OF MOST IFN-RESISTANT CELLS.  PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TY  SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY  This SWISS-PROT entry is copyright. It is produced through by non-profit institute of Bioinformatics and the  the European Bioinformatics Institute. There are no  use by non-profit institute. There are no  use by non-profit institute. See http://www.io  or send an email to license@isb-sib.ch).	Cell 60:225-234(1990).  [2]  SEQUENCE FROM N.A.  MEDLINE; 92129376.  Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.  "The Structure of the human interferon alpha/beta recep."  "The STRUCTURE of the human interferon alpha/beta recep."  "The STRUCTURE of the human interferon alpha/beta recep."  J. Biol. Chem. 267:2802-2809(1992).  [3]  PHOSPHORYLATION BY TYK2.  MEDLINE; 95059042.  Colamonici O., Yan H., Domanski P., Handa R., Smalley E.  MILLERSTAND J., Witte M., Krishnan K., Krolewski J.;  PHOSPHORYLATION BY TYK2.  MILLERSTAND STRIGGERS TYROSINE phosphorylation of the of the type I interferon receptor by pl35tyk2 tyrosine wol. Cell. Biol. 14.8133-8142(1994).  I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBE OF THE SUBJULIAR LOCATION: TYPE I MEMBRANE PROTEIN ALPHA SUBJULIAR LOCATION: TYPE I MEMBRANE PROTEIN N. SUBJULIAR LOCATION: TYPE I MEMBRANE PRESENT IN ALEVEN ON THE SUBRACE OF MOST IEN-RESISTANT CELLS.  -I- PIM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYPE: SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE DO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY.  -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE	"Genetic transfer of a functional human interferon alphinto mouse cells: cloning and expression of its cDNA.";  [2] [2] [2] [2] [2] [2] [2] [2] [2] [2]	MEDLINE; 90124632.  Uze G., Lutfalla G., Gresser I.;  "Genetic transfer of a functional human interferon alph into mouse cells: cloning and expression of its cDNA.";  Cell 60:225-234(1990).  [2]  [2]  [2]  [2]  [3]  [4]  MEDLINE; 92129376.  Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G. The structure of the human interferon alpha/beta recep The structure of the human interferon alpha/beta recep J. Biol. Chem. 267:2802-2809(1992).  [3]  [3]  [3]  [4]  MEDLINE; 95059042.  [5]  [6]  MEDLINE; 95059042.  [7]  MEDLINE; 95059042.  [8]  [9]  MEDLINE; 95059042.  [9]  Colamonici O., Yan H., Domanski P., Handa R., Smalley E MILIETSMAN J., Witte M., Krishnan K., Krolewski J.,  "Direct binding to and tyrosine phosphorylation of the of the type I interferon receptor by p135tyk2 tyrosine MOL Cell. Biol. 14:18133-8142(1994).  [1]  MEDLINE; 95059042.  [1]  Colamonici O., Yan H., Domanski P., Handa R., Smalley E MILIETSMAN J., Witte M., Krishnan K., Krolewski J.,  "Direct binding to and tyrosine phosphorylation of the of the type I interferon receptor by p135tyk2 tyrosine MOL Cell. Biol. 14:18133-8142(1994).  [1]  MEDLINE; 95059042.  [2]  Colamonici O., Yan H., Domanski P., Handa R., Smalley E MILIETSMAN J., Witte M., Krishnan K., Krolewski J.,  "Direct binding to and tyrosine phosphorylation of the of the type I interferon receptor by p135tyk2 tyrosine MOL Cell. Biol. 14:1813-8142(1994).  [3]  MEDLINE; 95059042.  [4]  MEDLINE; 95059042.  [5]  MEDLINE; 95059042.  [6]  MEDLINE; 95059042.  [6]  MEDLINE; 95059042.  [7]  MEDLINE; 95059042.  [8]  MEDLINE; 95059042.  [8]  MEDLINE; 95059042.  [9]  MEDLINE; 950	Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Man Butheria; Metazoa; Chordata; Craniata; Vertebrata; Man Butheria; Metazoa; Catarrhini; Hominidae; Homo. SEQUENCE FROM N.A. MEDLINE; 90124632. Uze G., Lutfalla G., Gresser I.; "Genetic transfer of a functional human interferon alph Into mouse cells: cloning and expression of its cDNA."; Cell 60:225-234(1990). [2] [2] [2] [2] [2] [2] [2] [2]	IFNARI OR IFNAR. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Man Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Man Eutheria; Primates; Catarrhini; Hominidae; Homo.  [1] SEQUENCE FROM N.A. MEDLINE; 90124632.  (2] Gell 60:225-234(1990). [2] SEQUENCE FROM N.A. MEDLINE; 92129376. Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G. The structure of the human interferon alph- form 267:2802-2809(1992). [2] PHOSPHORYLATION BY TYK2. MEDLINE; 95059042. Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G. The structure of the human interferon alpha/beta recep J. Biol. Chem. 267:2802-2809(1992).  [3] PHOSPHORYLATION BY TYK2. MEDLINE; 95059042.  Colamonicol O., Yan H., Domanski P., Handa R., Smalley I MILIERS PRINCETON TECEPTOR DATA FOR INTERPERONS ALPHA AND BETA. I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBE INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA SUBUNITS THEMSELVESI- FUNCTION: TYPE I MEMBRANE PROTEINI- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN AL EVEN ON THE SURRACE OF MOST IFN-RESIDUES BY TYK2 TY -I- SUBCLIULAR LOCATION: TYPE I MEMBRANE PROTEINI- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN AL EVEN ON THE SURRACE OF MOST IFN-RESIDUES BY TYK2 TY -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY -I- SIMILARITY: GONTAINS 2 FIBRONECTIN TYPE III-LIKE DC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY -I- SIMILARITY: GONTAINS 2 FIBRONECTIN TYPE III-LIKE DC -I- SIMILARITY: GONTAINS 2 FIBRONECTIN TYPE III-LIKE DC -I- SIMILARITY: GONTAIN THE	OI-AUG-1990 (Rel. 15, Last sequence update) 15-FEB-2000 (Rel. 39, Last sequence update) 11-EREPERON ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (I 1FNAR1 OR IFNAR.  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Man Eutheria; primates; Catarrhini; Hominidae; Homo.  1) 200ENCE FROM N.A. MEDLINE; 90124632.  Uze G., Lutfalla G., Gresser I.; Uze G., Lutfalla G., Gresser I.; Cell 60:225-234(1990).  [2] 10	01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 115-FEB-2000 (Rel. 39, Last sequence update) 115-FEB-2000 (Rel. 39, Last sequence update) 11FARG. 1991 (Rel. 39, Last sequence update) 11FARG. 1992 (Rel. 39, Last sequence update) 11FARG. 1992 (Rel. 39, Last sequence update) 11FARG. 1992 (Rel. 39, Last sequence update) 11FARG. 1994 (Rel. 39, Last sequence	JRSOR (I JRSOR (I JRSOR (I JRSOR (I JRSOR II) NAME I ROBETA A NUMBE A NUMBELLS IT KELLS IT KELLS IT KELLS IT KELLS IT I A I TELLS IT I A I I TELLS I A I TELLS I TELLS I A	LUT 1  INGL. HUMAN STANDARD; PRT; 557 AA.  17181;  01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) 15-FEB-2000 (Rel. 39, Last sequence update) 11 FNAR1 OR IFWAR.  Ewkaryota; Metazoa; Chordata; Craniata; Vertebrata; Man Eukaryota; Man Interferon alpha (Lastial) 1. Cacil 60:225-234(1990).  2. Glenetic transfer of a functional human interferon alpha/Deta receptions; 92129376.  2. Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G. The structure of the human interferon alpha/Deta receptions; 92129376.  2. Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G. The structure of the human interferon alpha/Deta receptions; 92129376.  2. Biol. Chem. 267:2802-2809(1992).  2. Biol. Chem. 267:2802-2809(1992).  3. Biol. Chem. 267:2802-2809(1992).  3. Biol. Chem. 267:2802-2809(1992).  4. PHOSPHORYLATION BY TYK2.  MEDLINE; 95059042.  Colamonici O., Van H., Domanski P., Handa R., Smalley E., Medliner S., Medliner	A4 97 4.2 515 1 INR2_HUMAN  PHUMAN  INTAL HUMAN  INTAL HUMAN  INTERFERON.ALPHA, DETA RECEPTOR ALPHA CHAIN PRECURSOR (INTERFERON.ALPHA, DETA RECEPTOR ALPHA CHAIN PROTEINS AND INTERFERON PROTEINS AN	A2 97.5 4.2 1256 1 FIN_CHICK 43 97.5 4.2 3134 1 KTR7_TEART 44 97 4.2 517 1 KTR7_TEART 44 97 4.2 517 1 KTR7_TEART 45 96.5 4.2 515 1 INR2_HUMAN  ALIGNMENTS  ALIGNMENT  ALIGNMENTS  ALIGNMENTS  ALIGNMENT  ALIGNME	40 97.5 4.2 1091 CIC2_HUMAN 41 97.5 4.2 1162 I LERR_MOUSE 42 97.5 4.2 1126 I FINC_CHICK 43 97.5 4.2 3124 I CAIC_CHICK 44 97 4.2 517 I KTR_CHICK 45 96.5 4.2 518 I INRZ_HUMAN  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  INAL_HUMAN  STANDARD; PRT; 557 AA.  P17181.  15-FEB-2000 (Rel. 15, Last sequence update) 15-FEB-2000 (Rel. 15, Last sequence update) 11-FEBR-2000 (Rel. 15, Last annoctation update) 15-FEB-2000 (Rel. 15, Last annoctation update) 11-FEBR-2000 (Rel. 15, Last annoctation up	99 97.5 4.2 306 1 KIRE_VENAN 99.5 4.2 1091 1 CIC2_HUMAN 41 97.5 4.2 11021 1 CIC2_HUMAN 41 97.5 4.2 11021 1 CIC2_HUMAN 42 97.5 4.2 1126 1 LER_MOUSE 43 97.5 4.2 1126 1 LER_MOUSE 44 97.4 2 512 1 LER_MOUSE 44 97.4 2 512 1 LER_MOUSE 44 97.5 4.2 1126 1 LER_CHICK 44 97.4 2 512 1 LER_CHICK 44 97.5 4.2 1126 1 CAIC_CHICK 44 97.5 4.2 512 1 LER_CHICK 45 98.5 4.2 515 1 LINE_CHICK 46 97.5 4.2 517 1 KER_CENT 47 1 LINEAL HUMAN 48 98.5 4.2 515 1 LINE_CHICK 49 98.5 4.2 515 1 LINE_CHICK 40 97.5 4.2 515 1 LINE_CHICK 41 97.5 4.2 515 1 LINE_CHICK 42 97.5 4.2 515 1 LINE_CHICK 43 97.5 4.2 515 1 LINE_CHICK 44 97.6 4.2 515 1 LINE_CHICK 45 98.5 4.2 515 1 LINE_CHICK 46 97.6 4.2 515 1 LINE_CHICK 47.6 4.2 515 1 LINE_CHICK 48 97.5 4.2 515 1 LINE_CHICK 49.7 4.2 515 1 LINE_CHICK 40 97.6 4.2 515 1 LINE_CHICK 40 97.6 4.2 515 1 LINE_CHICK 41 11 LINE_CHIC	98.5 4.3 1345 1 THOO_TENTS 37 98.5 4.3 1615 1 RRPO_THW 38 99.5 4.2 1991 1 CEC2_HUMAN 41 97.5 4.2 1991 1 CEC2_HUMAN 41 97.5 4.2 1962 1 LEPR_MOUSE 42 97.5 4.2 1256 1 EINC_CHICK 43 97.5 4.2 1256 1 EINC_CHICK 43 97.5 4.2 1256 1 CALC_CHICK 44 97.5 4.2 1256 1 EINC_CHICK 45 97.5 4.2 1256 1 EINC_CHICK 46 97.5 4.2 1256 1 EINC_CHICK 47 97.5 4.2 1256 1 EINC_CHICK 48 97.5 4.2 1256 1 EINC_CHICK 49 97.5 4.2 1256 1 EINC_CHICK 40 97.5 4.2 1257 1 KTRZ_MUMAN 41 97.5 4.2 1256 1 EINC_CHICK 42 97.5 4.2 1256 1 EINC_CHICK 43 97.5 4.2 1256 1 EINC_CHICK 44 97.5 4.2 125 1 INRZ_HUMAN 41 97.5 4.2 1256 1 EINC_CHICK 42 97.5 4.2 1256 1 EINC_CHICK 43 97.5 4.2 1256 1 EINC_CHICK 44 97.5 4.2 1256 1 EINC_CHICK 45 97.5 4.2 1256 1 EINC_CHICK 46 97.5 4.2 125 1 INRZ_HUMAN 41 97.5 4.2 1 INRZ_HUMAN 41 97.5 4.2 125 1 INRZ_HUMAN 41 97.5 4.2 1 INRZ_HUMAN 41 11

```
RESULT 2
INR1_BOVIN
                                                                     Ş
                                                                                    밁
                                                                                                δÃ
                                                                                                                 밁
                                                                                                                           δδ
                                                                                                                                            밁
                                                                                                                                                        δõ
                                                                                                                                                                        밁
                                                                                                                                                                                    Š
                                                                                                                                                                                                     밁
                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                무
                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                             3385
                                                                                                                                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 436; Conservative
INRI_BOVIN
Q04790;
Q1-OCT-1993
Q1-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Tra
Phosphorylati
SIGNAL
                                                                                                                                                                                                                                                                                                                             CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                       421
                                                                                     361
                                                                                                   361
                                                                                                                 301
                                                                                                                               301
                                                                                                                                            241
                                                                                                                                                           241
                                                                                                                                                                         181
                                                                                                                                                                                       181
                                                                                                                                                                                                     121
                                                         421
                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                            TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMMALDGLSFTYSLLIWKNSSGVEERI 180
                                                                                    VIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSV 420
                                                                                                                GIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTP 360
                                                                                                                                                   NQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFFQNVFQK 300
                                                                                                                                                                                ENIYSRHKIYKLSPETTYCLKVKAALLISWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                FSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNYYEEIKLRIRAEKENTSSWYEVDSF 120
                                                                 FSDAVCEKTKPGNTSK 436
                                                        FSDAVCEKTKPGNTSK
                                                                                                                                            NONYVEKWDYTYANMTFQVQWEHAFEKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK
                                                                                                                                                                         ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
(Rel. 27, Created)
(Rel. 28, Last seq
                                                                                                                                                                                                                                                                                                                                                 28
437
458
79
199
1199
481
50
58
81
1100
1172
2254
416
3313
3113
3114
4133
                                                                                                                                                                                                                                                                                                                             ξ,
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                 17
63525
                                                         436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal; Polymorphism
                                                                                                                                                                                                                                                                                                                             ¥.
sequence update)
                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

L -> V.
/FTId-VAR_002717.

G -> A (IN REF. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION PHOSPHORYLATION POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                        Score 2313;
Pred. No. 4.4
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                     PRT;
                                                                                                                                                                                                                                                                                                                             -> A (IN REF. 2).
OF6744C8A1ADBE73 CRC64;
                     560
                                                                                                                                                                                                                                                                                                4.4e-166;
                     ጀ
                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
YB)
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYK2)
                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROBABLE).
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                            300
                                                                                                                                                                                       240
                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                        0
Š
              밁
                         δõ
```

62 بر

65;

6,

Gaps

6,

58 61

SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKL-NVYEEIKLRIRAEK-ENTSSWYEVDS

```
Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lim J.-K., Langer J.A.;
Lim J.-K., Langer J.A.;
"Cloning and characterization of a bovine alpha interferon receptor.";
"Cloning and characterization of a bovine alpha interferon receptor.";
"I characterization of a limit alpha and beta. Binding to type in irus tricgers tyrosine phosphorylation of a number of proteins including jaks, tyk2, Stat proteins and ifu-r alpha-and beta-subunits themselves.

-i- Subunits themselves.
-i- Subcellular location: type I membrane protein.
-i- Similarity: Compains 2 fibronectin type III-Like Domains.
-i- Similarity: Belongs to the Class II Cytokine family of receptors.
                                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93076908.

Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;

"Specific antiviral activities of the human alpha interferons
determined at the level of receptor (IFNAR) structure.";
                                                                                                                                                                                                                                                                                                                      EMBL; X68443; CAA48484.1; -.
EMBL; L06320; AAA02571.1; -.
PIR; S33770; S33770.
PIR; S27387; S27387.
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOY-1997 (Rel. 35, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                   SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 93305725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett.
[2]
                                                                                                                                                                                                                                                                                                           Receptor;
 Local Similarity
nes 285; Conserv
                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313:255-259(1992).
                                                                            438
438
459
199
199
109
172
172
172
173
131
313
                                                                                                                                                                                                                                                                                 25
                                                                            437
458
840
220
220
220
254
254
254
254
254
254
254
254
254
                                                                                                                                                                                                                                                                                   560
                                                                63818
          64.98;
                                                                                                                                                                                                                                                                                               Glycoprotein; Signal.
BY SIMILARITY.
                                                                ¥.
                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
Score 1507; D
Pred. No. 1.1e
55; Mismatches
                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                           'n
                                                               POTENTIAL.
F -> V (IN REF. 2).
66D76B72861E1D11
                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                   INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pecora; Bovoidea; Bovidae;
; DB 1;
1.1e-105;
hes 83;
                                                                CRC64;
                      Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                .ch/announce/
```

Ş

밁 S 믕

Š 밁 Ş 밁 Š 8

밁 Š 밁

s as long of removed.

as Usage its content

and d for

'n

commercial

```
Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;

"Molecular cloning of ovine and bowine type I interferon receptor

graphics from uter1, and endometrial expression of messenger

ribonucleic acid for ovine receptors during the estrous cycle and

pregnancy.";

Lendocrinology 118:4757-4767(1997).

C.-I-FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE

I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS

C.-I-FUNDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-

SUBUNITS THEMSELVES.

C.-I-SUBCLIDLAR LOCATION: TYPE I MEMBRANE PROTEIN.

C.-I-SUBLIDLARITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT

C.-I-SUMLARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

C.-I-SUMLARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             028589; Q95206; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-FEB-2000 (Rel. 39, Last annotation update) INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN: (INTERFERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                    Kaluz S., Fisher P.A.,
"Structure of an ovine
endometrium.";
J: Mol. Endocrinol. 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; F
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                          TISSUE-ENDOMETRIUM;
MEDLINE; 97135690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHEEP
                                                                                                                                                                                                                                                               MEDLINE; 98006426
                                                                                                                                                                                                                                                                            TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSSFSDTVCEKTKPGNTSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSVFSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMSVNQLYPLIYEVIFWENTSNAERKVLEKRINFIFPDLKPLIVYCVKARALIENDRRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRGIYYVRVRASNGNGTSFWSEEKEFNTEMKTIIFPPVISVKSVTDDSLHVSVGASEESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADNQIYVLKWDYPYENATFQAQWLRAFFKKIPGNHSDKWKQIPNCENVTSTHCVFPREVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQNQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPVYCINTTERHKVPSPENIQIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                      17:207-215(1996).
                                                                                                                                                                                                                                                                                                                                              Kaluzova M., Sheldrick E.L.;
interferon receptor and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRECURSOR (IFN-ALPHA-REC)
                                                                                                                                                                                                                                                                                                                                                expression
                                                                                                                                                                                                                                                                                                                                                           Flint
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
idea; Bovidae;
                                                                                                                             TO TYPE
TO BETA-
                                                                                                                                                                                                                                                                                                                                                             A.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298
RESULT 4
INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                             Ş
                                                                                                          밁
                                                                                                                                    Š
                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                               Š
                                                      맑
                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                       239
                                                                                                                                                                                                                                                 239
                                                        419
                                                                                418
                                                                                                            359
                                                                                                                                       358
                                                                                                                                                                 299
                                                                                                                                                                                           299
                                                                                                                                                                                                                                                                             179
                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                 \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
```

```
Query Match
Best Local Similarity
Matches 283; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X95939; CAA65183.1; -. EMBL; U65978; AAB84231.1; -. PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as lone modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVS
                                                                                                                                                                     VQNQNYVLKWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVF
                                                                                                                                                                                                                                                                                                                                                                    HISTIGATTIMIVA-GRWYLPAASGEANIKS-ENVEIHIIDDNEFIKWNSSSESVRNVTF
                                                                                                                                                                                                                                                                                                                                                                                             MYVLLGATTLYLVAYGFWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
GSSYSDTVCEKTKPGNTSK
                       SSVFSDAVCEKTKPGNTSK 436
                                                                NTPVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHTMDEKLNK
                                                                                                                                                       VDNQAYVLKWDYPYESTTFQAQWLRAFLKKIPGKHSNKWKQIPNCENVTTTHCVFPRDIF
                                                                                                                                                                                                          RTETVYPEDKIYKLSPEITYCLKVKAELRLQSRVGCYSPVYCINTTERHKVPSPENVQIN
                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522
313
313
352
352
352
352
352
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63918
                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1503; I
Pred. No. 2.2e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERFERON-ALPHA/BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
2.2e-105;
les 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                  118
                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                61
                                                     418
                                                                            417
                                                                                                                                                                                 298
                                                                                                                                                                                                            238
                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                                                178
                                                                                                      358
                                                                                                                               357
                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                         6
```

```
밁
                                                Š
                                                                        В
                                                                                                 8
                                                                                                                           밁
                                                                                                                                                 Š
  õ
                                                                                                                                                                          Query Match
Best Local Similarity
Matches 212; Conser
                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
IFNARI OR IFNAR OR IFAR.
                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28,
01-FEB-1994 (Rel. 28,
15-FEB-2000 (Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INR1_MOUSE P33896;
                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jze G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
   181
                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Behavior of a cloned
                                                    121
                                                                            61
                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e G., Luttalla G., Bandu M.T., Proudhon D., Mogensen K.E.; ehavior of a cloned muritme interferon alpha/peta receptor homospecific or heterospecific background."; oc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).

OC. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).

FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDI I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND
                                                                                                                           ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: COUTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:107658;
                                                                      TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERI
                                                                                                                                       MVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTF
ENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQ
                                                                                                                         MLAVVGAAALVLVAGAPWVLPSAAGGENLKPPENIDVYIIDDNYTLKWSSHGESMGSVTF
                       IPFYTAHMSPPEVRLEAEDKAILVHISPPGQDGNMWALEKPSFSYTIRIWQKSSSDKKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M89641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                         27
430
450
78
199
43
109
181
214
370
409
413
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA37890.1;
                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFNAR
                                                                                                                                                                                                                                                                  220
43
109
181
214
314
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                         65776
                                                                                                                                                                                      46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal.
POTENTIAL.
                                                                                                                                                                                                                                         ₩;
                                                                                                                                                                          Score 1069; DB 1;
Pred. No. 7.9e-73;
7; Mismatches 137
                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                        POTENTIAL.
7EC6DFF370185D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                              INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⋧
                                                                                                                                                                           137;
                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA. BINDING TO TYPE NUMBER OF PROTEINS ALPHA-AND BETA-
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia
                                                                                                                                                                                                   590;
                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed
                                                                                                                                                                         Gaps
                        180
                                                180
                                                                         120
                                                                                                  120
                                                                                                                                                  61
240
                                                                                                                         60
                                                                                                                                                                          4
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
 DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         "A new member of the cytokine recep 21 at less than 35 kb from IFNAR."; Genomics 16:366-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-FEB-1995 (Rel. 31, Createu, Ol-FEB-1995 (Rel. 31, Last sequence update) Ol-OCT-1996 (Rel. 34, Last annotation update) Or-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 96054036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                         PIR; A47003; A47003
HSSP; P13726; 1DAN:
                                                                                                                                                    EMBL; Z17227; CAA78933.1; -. EMBL; U08988; AAA86872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 93300510.
Lutfalla G., Gardiner K.,
                                                                       CHAIN
                                                                                  SIGNAL
                                                                                                               MIM; 123889
                                                                                                                                                                                                                                                                                                  -i- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                         J. Mol. Evol. 41:338-344(1995)
                                                                                                                                                                                                                                                                                                                                                                        neighbor.
                                                                                                                                                                                                                                                                                                                                                                                                 Lutfalla G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q08334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                   'Structure of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-FETAL BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 NFSEKLCEKTRPGSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 VFSDAVCEKTKPGNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVIQDYPLIYEIIFWENTSNAERKIIEKKTDVTVPNIKPLTVYCVKARAHTMDEKLNKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTFFLHVQASEGNHTSFWSEEKFIDSQKHILPPPPVITVTAMSDTLLVYVNCQDSTCD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGIYLLRYQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKSYVLKWDYIASADVLFRAQWLPGYSKSSSGSHSDKWKPIPTCANVQTTHCVFSQDTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONYVLKWDY-TYANWTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSTYYVEKIPELLPETTYCLEVKAIHPSLKKHSNYSTVQCISTTVANKMPVPGNLQVDAQ
                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GLNYELIFWENTSNTKISMEKDGPEFTLKNLQPLTVYCVQARV-LFRALLNKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                 McInnis M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
  325
220
220
325
325
749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435
                                                                                                                                                                                                                                                                                                                                                                                     CRFB4
                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                Antonarakis
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                  POTENTIAL.
CYTOKINE RECEPTOR CLASS-II CRF2-4.
                                                                                                                                                                                                                                                                                                                                                                                     gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor gene family maps on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                   comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325
                                                                                                                                                                                                                                                                                                                                                                                                ß
                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         = = :: - - ::
                                                                                                                                                                                                                                                                                                                                                                                     Uze G.;
on with
                                                                                                                                                                                                                                                                                                                                                                                     its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
```

```
RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                    MEDLINE: 94170380.

Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R.,
Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
"Identification and sequence of an accessory factor required for
activation of the human interferon gamma receptor.";
Cell 76:793-802(1994).
Cell 76:793-807(1994).
THE IRN-GAMMA SIGNAL THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF
INTERACT WITH GAF, JAKI, AND/OR JAKE.

INTERACT WITH GAF, JAKI, AND/OR JAKE.

INTERACT WITH GAF, JAKI, AND/OR JAKE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
         EMBL; U05875; AAA16955
EMBL; U05877; AAA16956
MIM; 147569; -
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation PRECURSOR (INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA TRANSDUCER-1).
RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFNGR2 OR IFNGT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P38484;
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LUNG FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRIFQDKCMNTTLTECDFSS--LSKYGDHTLRVRAEFADEHSDWVNI-TFCPVDDTIIGP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVLSAAAGGKNLKS-----PQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQKTGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEVHLEA-EDKAIVIHISPGTKDSV-MWALDGL--SFTYSLLIWKNSSGVEERIENIYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWIKLSGCONITSTKCNFSSLKLNVYEEIKLRIRAE-KENTSSWYEVDSFTPFRKAQIGP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQY----LS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVLRNLEPWTTYCVQVRGFLPDRNKAGEWSEPVCEQTTHDETVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49
68
102
161
124
269
274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                          AAA16955.1;
AAA16956.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
102
161
161
124
273
37011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
A -> D (IN REF. 2).
FLGHP -> VGRME (IN REF. 2).
MISSING (IN REF. 2).
MG 66706C79F8514B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 228.5;
Pred. No. 3.5e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     œ
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                         _HUMAN _HUMAN STANDARD; PRT; 1451 AA.
PS2179;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-UT-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
MYOMESIN 1 (190 KD TITIN-ASSOCIATED PROTEIN) (190 KD CONNECTIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor;
SIGNAL
                                                                            Vinkemeler U., Obermann W., Weber K., Fuerst D.O.;
"The globular head domain of titin extends into the center of t sarcomeric M band. cDNA cloning, epitope mapping and immunoelec microscopy of two titin-associated proteins.";
J. Cell Sci. 106:319-330(1993).
-i- FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS
                         DEPENDENT.
-!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN-
-!- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                TISSUE-SKELETAL MUSCLE; MEDLINE; 94095665.
                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                   TWOAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165
                                                                                                                                                                                                                                                                                                                                                                                                233
                                                                                                                                                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                                                                                                                                                                              175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 VLVAVGPWVLSAAAGG---KNLKSPQKVEVDIIDDNFILRW-----NRSDESVGNVTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                SCYETMADASTELQQVILISVGTFSLLSVLAGACFFLVLKYRGLIKYWFHTPPSIPLQIE
                                                                                                                                                                                                                                                                                                                                                                                                                      HCIKTTVENELPPPENIEVSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSLLIWKNSSGVEERIENIYSRHKIY--KLSPETTYCLKVKAALLTS----WKIGVYSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALHSAWVIMPWFQHYRNVTVGPPE-NIEVTPGEGSLIIRFSSPFDIADTSTAF----FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENT-SSWYEVDSFTPFRKAQIGPPEVHLE---AEDKAIVIHISPGTKDSVMWALDGLSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIDSK----WETADIMSIGVNCTQITATECDFTAASPSAGFPMDENV----TLRLRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDYOKTGMDNWIKLS-----GCONITSTKCNFSS-----LKLNVYEEIKLRIRAEK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLLLGVFAAAAAAPPDPLSQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRPVVYRVQFK
                                                                                                                                                                                                                                                                                                                                                                                                                                              YYVHYWE---KGGIQQVKGPFRSNSISLDNLKPSRVYCLQVQAQLLWNKSNIFRVGHLSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
248
269
269
2110
2110
2110
2110
2110
                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
337
247
268
337
337
110
110
1137
219
231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 155.5; I
Pred. No. 0.000
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
R -> Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R -> Q.
/FTId-VAR_002718.
18C61B10AD90E509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERFERON-GAMMA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                      -QNQNYVLKWDYTYANMTFQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                immunoelectron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA CHAIN
                                                         DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67;
                                                                                                                                            the
                                                                                 DOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                       260
                                                                                                                                                                                                                                                                                                                                                                                                                                               232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
```

between the the European

the

Swiss Institute Bioinformatics 1

of.

Bioinformatics

s and t

the

restrictions

outstation

```
RESULT 8
INSR_RAT
ID INSR_RAT
                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
REPEAT
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 603508; -
PEAM; PE00041; fn3; 5.
PEAM; PE00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X69090; CAA48833.1; MIM; 603508; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                  762
                                                                                                                                                                                                                                                                                                                                660
                                                                                                                                                                                                                                                                                                                                                                              279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 DNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEI
                                                                                                                                                                           TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KL-----RIRAEKENTSSW-----YEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS
                                                                                                                           A-YKISNLKENMVYQFQVAAMNMAGLGAPSAVSECFKCEE
                                                                                                                                                                                                                                                                     --VFNIRSLSDSFHTYIGAPKQSGNTPVIQDYPLIYEII-----FWENTSNAERKIIEKK
                                                                                                                                                                                                                                                                                                                                                                       QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVKSPRFALFDLAEGKSYCFRVRC----SNSAGVGEPSEATEVTVVGDKLDIPKAPGKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLIEGRSYIFRVRAVNKMGIGFPSRVSEAVAALDPAEKARLKSP---LSTLDWTVIVTEE
                                                                                                                                                                                                                            CDITCLESFRDSMVLGWKQPDKTGGAEITGYYVNYREVIDGVPGKWR----EANVKAVREE
                                                                                                                                                                                                                                                                                                                         ---TCHGLVTGQS-----YIFRVRAVNAAGLSEYSQDSE-AIEVKAAIAPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                       PSRNTDTSV----VVSWEESKDAKELVGYYIEANVAGSGKWEPC--NNNPVKTHRF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPENIEVSVQNQNYVLKWD------YTYANMTFQVQWLHAFLKRNP-GNHLYKWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPSEGIVPGPPTDLSVTEATRSYVVLSWKPPGQRGHEGIMYFVEKCEAGTENWQRVNTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGTKDSVMWALDGLSFT----YSLLIWK-----NSSGVEERIENIYS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYIIISWKQPAVDGGSPILGYFIDKCEVGTDSW------SQCNDTPVKFARFPVT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTV-----ENELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46
52
58
64
70
70
156
290
385
512
512
613
712
817
918
1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
57
63
69
75
81
289
289
384
511
612
711
816
816
917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYPE-III.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE TII.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 123.5; Description of the Pred. No. 0.19; Type of the Prediction of the Predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.
FIBRONECTIN TYPE-III.
TTRRONECTIN TYPE-III.
       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Thick filament; Repeat.
5 X 6 AA TANDEM REPEATS.
       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181;
                                                                                                                             800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278
                                                                                                                                                                                                                                                                        388
                                                                                                                                                                                                                                                                                                                                                                                                                          660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493
                                                                                                                                                                                                                                                                                                                         704
                                                                                                                                                                                                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
     A TO COOR RESERVABING ON THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M29014; AAA41441.1; -.
EMBL; AF005777; AAB61415.1; -.
EMBL; AF005777; AAB61415.1; -.
EMBL; U80633; AAB38746.1; -.
EMBL; U80632; AAB38968.1; -OINED
EMBL; U80631; AAB38967.1; -.
EMBL; U80630; AAB38967.1; -.
EMBL; U80630; AAB38967.1; -.
                                                                                                                                                         PROSITE: PSOULL,

PFAM: PF00041; fn3; 1.

PFAM: PF00069; pkinase; 1.

PFAM: PF00757; Furin-like; 1.

PFAM: PF00757; Furin-like; 1.

PFAM; PF01030; Recep_L_domain; 1.

PFAM; PF01030; Recep_L_domain; 1.

"ransferase; Tyrosine-protein kinase; Receptor; Tran-
"ransferase; Tyrosine-hinding; Phosphorylation; Signal;

"ransferase; Tyrosine-hinding; Phosphorylation; Signal;
TRANSMEM
DOMAIN
DOMAIN
                                                                       CHAIN
PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.

PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed; entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN TYROSINE PHOSPHATE.
-1- ENZYME REGULATION: AUTOPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldstein B.J., Dudley A.L.;
"The rat insulin receptor: primary structure and conservation tissue-specific alternative messenger RNA splicing.";
Mol. Endocrinol. 4:235-244(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P15127; P97681;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A36080;
HSSP; P06213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
MEDLINE: 90231337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu Y., Tam J.W.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVITY

ACTIVITY

ACTIVITY

SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBLIARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
     761
761
764
764
958
979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB38746.1; -.
AAB38968.1; -.
AAB38968.1; JOINED
  26
760
763
1383
1383
957
978
1383
1383
                                                                  INSULIN RECEPTOR, ALPHA-SU
REMOVED IN MATURE FORM.
INSULIN RECEPTOR, BETA-SUB
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                    Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ong as its content is in
                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                              BETA-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP
                                                                                                                                                                                                Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
```

```
RESULT 9
INGR_HUMAN
ID INGR_H
AC P15260
DT 01-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                             Ş
                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
BINDING
INGR_HUMAN STANDARD;
P15260;
O1-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                   805
                                                                                                                                                 388
                                                                                                                                                                                                                                                                                                          650
                                                                                                                                                                                                                                                                                                                                                                        590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                747
                                                                                                                                                                                                                                                                            305
                                                                                                                                                                                                                                                                                                                                                                                                                                    567
                                                                                                                                                                                                                                                                                                                                                                                                       198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNFILRWNRSDESVGNVTFSFDYQKTGMDN-----------WIKLSGCQN
                                                                                                                                               KTDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKP
                                                                                                                                                                                                                                                                                                                                    YANMTFQVQWLHAFLKRNPGNHLYKW-KQIPDCENVKTTQCVFPQNVFQKGIYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDIALKINGDQASCENELLKFSFIRTSFDKILLRWEPYWPPDFRDLLGFMLFYKEAPYQN 540
                                                                                                                                                                                                                                                                      --LRVQASDGNNTSFWSEEI-----KFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQ
                                                                                                                                                                                                                                                                                                          NGNIT --
                                                                                                                                                                                                                                                                                                                                                                                                  YCLKYKAALLTSWK---IGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKW---DYT
                                                                                                                                                                                                                                                                                                                                                                                                                                    NDPKSQTPSHPG-----WLMRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTEFDGQDAC-----IDPPQ---RS
                                                                                                                KESLVISGLRHFTGYRIELQACNQDSPEERSGV-AAYVSARTMP
                                                                                                                                                                              TSSGNGAEDTRPSRKRRSLEEVGNVTATTPTLPDFPNISSTI--APTSHEEHRPFEKVVN
                                                                                                                                                                                                                                            PPFESDDSQKHNQSEYDDSASECCSCPKTDSQILKELEESSFR-KTFEDYLHNVVFVPRK
                                                                                                                                                                                                                                                                                                                                                                    YAIFVKTLVTFSDERRTYGAKSDIIYVQTDATNPSVPLDPISVSNSSSQIILKWKPPSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IT----STKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1119
AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11299
11299
11058
11058
11050
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
100000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
100000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
100000
10000
10000
10000
10000
10000
10000
10000
10000
10000
100000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10000
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156756
                                                                                                                                                                                                                                                                                                          ----HYLVYWERQAEDSELFELDYCL-----KGLKLPSRTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 119; DB
Pred. No. 0.38
52; Mismatches
                                                                                                                                                                                                           ----TPVIQDYPLIYEIIFWENTSNAERKIIEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (AUTO-).
IMPORTANT FOR BIOLOGICAL ACTIVITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      > M (IN REF. 2).
4B919566902A944A CRC64;
                                     489
                                     À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1383;
                                                                                                                                                 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LKPWTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                              804
                                                                                                                                                                                                             388
                                                                                                                                                                                                                                            746
                                                                                                                                                                                                                                                                                                        687
                                                                                                                                                                                                                                                                                                                                       305
                                                                                                                                                                                                                                                                                                                                                                    649
                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                                                                                                                                                                                                                                                  589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
      DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A., Winkler F.K., Robinson J.A.;
"Neutralizing epitopes on the extracellular interferon gamma receptor (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex.";

J. Mol. Biol. 273:882-897(1997).

-!- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERFERON-GAMMA DIMER.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walter M.R., Windsor W.T., Nagabhushan T
Zauodny P.J., Narula S.K.;
"Crystal structure of a complex between
soluble high-affinity receptor.";
Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo Sapiens (Human).
Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR
                                                                                                TRANSMEM
                                                                                                              DOMAIN
                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                         EMBL; J03143; AAA52731.1;
                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon gamma receptor and investigation of their role
biological activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stueber D., Friedlein A., Four Palignment of disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.";
Cell 55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89003065.
Aguet M., Dembic Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                            Immunoglobulin
                                                                                                                                                                            Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning
receptor.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iochemistry 32:2423-2430(1993).
                                                                                                                                                                                                             1JRH; 25
107470;
                                                                                                                                                                                                                                            A31555;
                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98035727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E BONDS,
93183911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95342235
                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                            25-MAR-98
                                                                                                                                                                                                                                            A31555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     z
P
                                                                                                                                                    domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
    245
245
245
266
489
489
200
200
235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merlin
                                                                                                                                                              3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression
                                                                                                                                                                           Glycoprotein; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fountoulakis M., Lahm H. onds of the extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ဂ
    POTENTIAL
                                                                               POTENTIAL.
CYTOPLASMIC
                                                                                                              INTERFERON-GAMMA RECEPTOR ALPHA CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ဋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                    There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.L., Lundell D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon-gamma
                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-122 COMPLEX WITH ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lahm H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CDW119).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -W., Garotta
domain of t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.A.,
```

the European Bioinformatics Institute.

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTT
                                 A LASSMANN H., Steck A.J.;

A LASSMANN H., Steck A.J.;

T Expression and developmental regulation of Ehk-1, a neuronal T Elk-like receptor tyrosine kinase in brain.";

L Neuroscience 63:163-178(1994).

C -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A1, -A2, -A3, -A4 AND -A5.

C -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A1, -A2, -A3, -A4 AND -A5.

C -!- FUNCTION: TYPOSINE PROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PRODUCED BY ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

C -!- ALTERNATIVE SPLICING.

C -!- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVO SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.

C -!- SIMILARITY: TO OTHER PROTEIN TYPOSINE KINASES IN THE CATALYTI DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

C -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPA5_RAT P54757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1).
                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE; 95206467.
Taylor V., Pfarr S., Miescher G.C., Honegger P.,
                                                                                                                                                                                                                                                                                                                                                                "Eak-1 and Eak-2: two novel members of the Eph receptor-like tyrosin kinase family with distinctive structures and neuronal expression."; Oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE; 94067777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHA5 OR EKH1 OR EHK-1
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 NELPPPENIEVSVQNQNYVLKWDYTYANM--TFQVQWLHAFLKRNPGNHLYKWKQIPDCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
              SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFNSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VTVPNLKPLTVYCVKARA--HTMDEKLNKS-----SVFSDAV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LSDSFH--IYIGAPKQSGN-TPVIQDYPLIYEIIFWENTSNAERKIIEKKTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGKIGPPKLDIRKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVKTTQCVFPQNVFQKGIYL-LRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVE-----VKNYGVKNSEW--IDACI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
86
179
240
489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
54404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
86
179
 Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                              ta N.X., Yancopoulos G.D.;
members of the Eph receptor-like tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
CF9E574D8F47400 C
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1005
               It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
            produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 489
                                                                                                                                                                                                                                                                                         Breitschopf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                              FAMILY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
Rattus.
                                                                                                     IN THE NERVOUS
EMBL outstation
                                                                         CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                              TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
```

```
S
                                                      Š
                                                                                      В
                                                                                                               Š
                                                                                                                                               밁
                                                                                                                                                                          Š
                             밁
                                                                                                                                                                                                        Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P00523; 2P
PRINTS; PR00014;
PRINTS; PR00109;
                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS00107; PROTEIN_KINASE_ATP; FAI
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00101; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE: PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00069; pkinase; 1.
PFAM; PF01404; EPH_lbd; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X78689;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
 188
                                                                                                                                                 165
                                                                                                                   74
                                                                                                                                                                             27
 KIYKLSPETTYCLKVKAALLTSWKIGVYSPVH----
                                                                                                                                                 GRNIKDNOYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG----
                             DPPKMHCSAEGEWLV----PIGKCMC-----
                                                         GPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIENI-YSRH
                                                                                                                                                                           GKNLKSPQKVEVDII--DDNF-----ILRWNRSDESVGNVT---FSFDYQKTGMDNW
                                                                                        ----ACIALVSVRVYYKKCPSVVRHLAVFPD----TITGADSSQLLEVSGSCVNHSVTD
                                                                                                                  IKLSGCQNITST-----KCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQI 128
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                               170
566
578
708
979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       576
577
583
709
802
266
425
438
438
100
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA55357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FNTYPEIII.
                                                                                                                                                                                                                                                                                 Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1005
575
1005
1005
1005
1005
338
691
709
802
802
301
371
                                                                                                                                                                                                                                                                                                 170
566
578
669
708
979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463
                                                                                                                                                                                                                        5.1%;
20.1%;
                                                                                                                                                                                                                                                                                   111007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal; Alternative
                                                                                                                                                                                                          51,
                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                             SPLICED 1 (C -> A (C) (C) (C))))))))))))))))
                                                                                                                                                                                                                        Score 118;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR RESDPPTMACTR -> G (IN SPLICED FORMS). RPPSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                     SGSCCECGCGRASSLCAVAHPSLIW ->
                                                                                                                                                                                                                                                                                                                                                                                                                     SPLICED FORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                  TFEIEAVNGVSDLSPGTRQYVSVNVTTNQAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                KCNSHAGVCEECGGHVRYLPQQIGLKNTSVMMADPLAHTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPLICED FORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRRRTQGRGGG ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHRIN TYPE-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                             ICED FORMS).

> E (IN REF. 2).

> A (IN REF. 2).

> A (IN REF. 2).

> A (IN REF. 2).

> I (IN REF. 2).

> I (IN REF. 2).
                                                                                                                                                                                                                                                                                    1AED42C99693C574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ng as its content is in
                                                                                                                                                                                                                        DB
. 29;
 ----CIKTTVENELPP---
                             -----KAGYEEKNGTCOVCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR 5
                                                                                                                                                                                                          165;
                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DADGPRAQASWCHARR (IN
                                                                                                                                                                                                                                       Length 1005;
                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                        Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                     Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splicing.
                                                                                                                                                                                                          Gaps
                                                          187
                                                                                                                                                 221
                                                                                                                                                                           73
 232
                              309
                                                                                      271
                                                                                                                                                                                                          21;
```

```
IIOR_MOUSE
ID IIOR_MOUSE
ID IOR_MOUSE
ID IOR_MOUSE
ID IOR_MOUSE
ID INTERL
INTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                      Ş
                                                                       Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I10R_MOUSE
Q61727;
                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.; **RA receptor for interleukin 10 is related to interferon receptors."; **Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
-i- FUNCTION: RECEPTOR FOR.IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6 X AJ F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL10RA OR IL10R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).
                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L12120; AAA16156.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
13 LVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRW----NRSDESVGNVTFSFDYQKT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFFKASPHSQTCSKCPP-----HSYTHEEASTSCVCEKDYFRRESDPPTMACTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:96538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEKDQETSYTIIKSKETTITAEGLKPASVYVFQIRART 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WENTSNAERKIIE-KKTDVTVPNLKPLTVYCVKARAHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QIPDCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCKKCN-SHAGVCEECGGHVR--- 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PENIEVSVONONYVLKW------DYTYANMTFQVQWLHAFLKRNPGNHLYKWK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSDLSPGTRQYVSVNVTTNQAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKY 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRSLSDSFHIYIG---APKQSGNTPVIQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94068585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                              242
263
204
50
66
113
182
238
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---YLPQQIGLKNTSVMMADPLAHTNYTF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL10RA
                                                                                                                                                                                                                       575
241
262
575
225
225
113
113
113
238
                                                                                                                                                                                                   64248 MW;
                                                                                             5.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HEMATOPOIETIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal
                                                                         47;
                                                                       Score 117.5; I
Pred. No. 0.15;
47; Mismatches
                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                POTENTIAL. 820B9CD576F686B7 CRC64;
                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERLEUKIN-10 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                             117.5;
No. 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₿
                                                                                                  .15;
                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410
                                                                            138;
                                                                            Indels
                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EIEA----VNG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DYP----LIYEIIF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                            125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
                                                                            16;
```

```
RESULT 12
PTPD_HUMAN
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 95204468.

Pulldo R., Krueger N.X., Serra-Pages C., Salto H., Streuli M.;

"Molecular characterization of the human transmembrane
protein-tyrosine phosphatase delta. Evidence for tissue-specific
expression of alternative human transmembrane protein-tyrosine
phosphatase delta isoforms.";
J. Biol. Chem. 270:6722-6728(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTPD_HUMAN P23468;
                                                                                                                                                                                                                                                                 - i - C
                                                                                                                                                                                                                                                                              MEDLINE; 91006018.

Krueger N.X., Streuli M., Saito H.;

"Structural diversity and evolution of human receptor-like protein
"Structural diversity";
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELTA).
                                                                                                                                         ÷
                                                                                                                                                                                                            ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTPRD
                                                                                                                                                                           ÷
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 390-1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 DSVLHGSTDSGFGSGKPSLQTEESQFLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263
                                                                                                                                                                                                                                                                                                                                                                         ISSUE-PLACENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
TISSUES DUE TO ALTERNATIVE SPLICING.
PIM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
FROM THE TRANSMEMBRANE SEGMENT.
SIMILARITY: EXTRACELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
LIKE DOMAINS FOLLOWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
AND A CYTOPLASMIC REGION COMPOSED OF TWO PTPASE DOMAINS.
                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + PROTEIN TYROSINE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQCLLITTEQY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNSTWNDIHICRKAQALSCDLTTFTLDLYHRSYGYRARVRAVDNSQYSNWTTTETRFT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQASDGNNTS-FWSEEIKFDTEIQAFLLP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFKDLRVYKISIRKFSELKNATKRVKQETFTLTVPIGVRKFCVKVLPRLESRINKAEWSE 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMDNWIKLSGCONITSTKCNFSSLKLNVYEE---IKLRIRA-EKENTSSWYEVDS-FTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVTISSLSLEFIAYGTELPSPSYVWFEARFFQHILHWKPIPNQSESTYYEVAL----KQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYSRHKIYKLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKAQIGPPEVHLEAEDKAIVIHISPGTKDSV-MWALDGLSFTYSLLIWKNSSGVEERIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---YIRHPG-----KLPTVLVFKKPHDFFPANPLCPETPDAIHIVDLEVFPKVSLELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VDEVIL-----TVDSVTLKAMDGIIYGTIHPPRPTITPAGDEYEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---PET-----TYCLKVKAALLTSWKIGVYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FTVTNLSILVISMLLFCGILVCLVLQW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1912 AA
         ormatics and the EMBL outstation
There are no restrictions on it
ing as its content is in no we
                                                                                                                                                                                                              FOUND IN DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VFQKGIYLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -OWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
```

non-profit and this s

statement is not removed.

Usage

ý

and for

in no way commercial

```
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L38929; AAC41749.1; -.
EMBL; X54133; CAA38068.1; -.
PIR; S12052; S12052.
HSSP; P18052; 1YFO.
MIM; 601598; -.
PRINTS; PR00014; FNTYPPIII.
PRINTS; PR00700; PRTYPHPHTASE.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
VARSPLIC
VARSPLIC
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
ACT_SITE
ACT_SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00047; ig; 3. PFAM; PF00102; Y_phosphatase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                     403
                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                           171 KNSSGVEERIENI-YSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunoglobulin
                                                                                                                                                                                                                                                P--PPENIEVSVQNQNYVL-KWDYTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENV 286
                                                                                                                                                                                                                                                                                                      KNSEELYKEIDGVATTRYSVAGLSPYSDYEFRVVAVN----NIGRGPPSEPVLTQTSEQA 416
                                                                                                                                                                            KTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSF 346
                                                                                                                                                                                                                    PSSAPRDVQARMLSSTTILVQWKEP-EEPNGQIQGYRVYYTMDPTQHVNNWMK----HNV
                                                          ILLSWTPPRS-----DTIANYELVYKDGEHGEEQRITIEPGTSYRLQGLKPNSLYYFR
                                                                                                HIYIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKI-IEKKTDVTVPNLKPLTVY---
                                                                                                                                         ADSQITTIGNLVPQKTYSVKVLAFTSIGDGPLSSDIQVITQTGVPGQPLNFKAEPESETS
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain;
1 20
1 1912
21 1912
21 1265
21 1290
11912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 822
916
1017
1137
1618
1912
                                                                                                                                                                                                                                                                                                                                                                                                         5.0%;
21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; Transmembrane; Duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRONECTIN TYPE-III.
PROTEIN-TYROSINE PHOSPHATASE.
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹.
                                                                                                                                                                                                                                                                                                                                                                                                           Score 116;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN KIDNEY ISOFORM).
MISSING (IN KIDNEY ISOFORM).
MISSING (IN KIDNEY ISOFORM).
MISSING (IN FETAL BRAIN ISOFORM).
R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
M; JAEBCBCD32182E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN-TYROSINE PHOSPHATASE DELTA
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                        136;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1912;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                          584
                                                                                                403
                                                                                                                                         531
                                                                                                                                                                                                                                                                                                                                               229
                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                         RESULT 13

RESULT 13

RMPSF_CHECK
ID MPSST_CHECK
ID MPSST_CHECK
AC Q02173

DT 01-JUN
RA NOGUCH
RX MEDLIN
RA Tanaka
RT TANAKA
ST CCC
-!- IT
CCC
CC This ST
CCC
DOT Sen
CCC
USet EU
CCC
OF Sen
CCC
OF Sen
CCC
OF Sen
CCC
OF Sen
CCC
DRALIN
FT DOMAIN
FT DOM
                                Ş
                                                                         밁
                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                        Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
Muscle p
DOMAIN
                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPSF_CHICK
Q02173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION:
                                                                           366
                                  78
```

S 밁 δÃ 밁 Ş 밁 Š

26;

밁

```
EMBL; D11474; BAA02033.1; -
PIR; A44027; A44027.
HSSP; P56276; 1TLK.
PFAM; PF00041; fn3; 5.
PFAM; PF00047; 1g; 3.
PFAM; PF00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
M-PROTEIN, STRIATED MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pectoralis M-protein.
J. Biol. Chem. 267:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93015907
Noguchi J., Yanag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanaka T., Masaki T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-EMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Complete primary structure and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               585 LAARSPQGLGASTAEISARTMQSK--PSAPPQDISC--TSPSSTS 625
                                                                  21 LSAAAGGKNLKSPQKVEV-DIIDDNFILRWNRSDESVGN--VTFSFDYQKTGMDNWIKLS
GCQNITSTKCNFSSLKLNVYEEIKL-----RIRAEKENTSSWYEVDSFTPFRKAQIG 129
                                          LIAGAPG----APMDVKCHDANRDYVIVTWKPPNTTSQNPVIGYFVDKCEVGLENWV--- 419
                                                                                                                                               Similarity
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yanagisawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS A STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267:20302-20310(1992)
                                                                                                                                                                                                                                    Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PECTORALIS MUSCLE;
                                                                                                                                             5.0%;
                                                                                                                                                                                                                                    163400
                                                                                                                                                                                                                                               t; Immunoglobulin domain.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

IFIBRONECTIN TYPE-III.

IFIBRONECTIN TYPE-III.

IG-LIKE C2-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.
                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Imamura
                                                                                                                                                                                                                                    MW;
                                                                                                                         Score 115; DB
Pred. No. 0.8;
63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONSTITUENT OF MYOFIBRILLAR M-BAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                    E313C7D39FE6CAC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1450 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kasuya Y.,
                                                                                                                                               . 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                   Length 1450
                                                                                                                                                                                                                                 CRC64;
                                                                                                                              Indels
                                                                                                                              136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ħ
                                                                                    77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
```

Glycoprotein;

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
EMBL; D37880; BAA07119.1; -.
HSSP; P11362; 1FG1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PFAM; PF00047; 19; 2.
PFAM; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P55146;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                            Ohashi K., Honda S., Ichinomiya N., Nakamura T., Mizuno K.;
"Molecular cloning and in situ localization in the brain of rat sky
receptor tyrosine kinase.";
J. Blochem. 117:1267-1275(1995).
-!- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
IN THE CENTRAL NERWOUS SYSTEM.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
OTHER TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridaė; Murinae;
                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96104999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYRO3 OR SKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYO3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                SIMILARITY:
                                                                                                                                                                                                                                                                                    SIMILARITY:
                                                                                                                                                                                                                                                                                                     DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIQDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPEVHLEAED--KAIVIHISPG-----TKDSVMWALDG------LSFTYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIWKN-----RHKIYKLSPETTYCLKVKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNAVGFSENSQESEAIK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASDG---NNTSFWSEEIKFDTEIQAFLLPPVF--NIRSLS-DSFHIYIG---APKOSGNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIDYSVVGSNQW-----EPÄNH----KPI----NYNR----FVVHGLETGEQYIFRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTYANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQKG-IYLLRVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LSANKHGISDPSEITEPIQPQDIVVVPSAPGRVVATRNTKTSVVVQWDKPKHEENLYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLTSWKIGVYSPVHCIKTTVENEL---PPPENIEVSVQN--QNYVLKWD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSWDPPVPRGREPLTYFIEKSMYGSGSWQRVNAQVAVKSPRYAVFDLAEGKPYVFRV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPVAALDPVDLERTQTVHVDEGRKIVISKDD----LEGDIQIPGPPTNVHASEISKTYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD
                                                                                                                                                                                                                                                                  CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                    ō
                                                                                                                                                                                                                                                                                                                  OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

    VQAALTCPSYPHGITLLNCDGHSMTLGWKAPKYSGGSP

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      088
                                                                                                                                                           (See
                                                      ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                           http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                                                                                                                                             ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250
```

```
RESULT 15
  RRRROCOGEPPPACE
                                                                                                                                                                                       õ
                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                             δ.
                                                                                                                                                                                                          В
                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                             DCC_MOUSE
P70211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
MEDLINE; 96112625.
                                                                                  01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUL-1999 (Rel.
                                    Eutheria;
                                              Mus musculus (Mouse
Eukaryota; Metazoa;
                                                                          TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunog Lobu J
                                                                                                                                                                                        273
                                                                                                                                                                                                          214
                                                                                                                                                                                                                             220
                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                 160
                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                       108
                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                              3 VVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKV-----EVDIIDDNFILRWN
                                                                                                                                                                      --- EWEALAVVVPVPPFTCLL-RNLAPATNYSLRVRCANALGPSPYGDWVPFQTK
                                                                                                                                                                                       HLYKWKOIPDCENVKTTOCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTE
                                                                                                                                                                                                                                                        GLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVH
                                                                                                                                                                                                                                              GPASSPSVL---NVTGVTQRTEFSCEAHNIKGLATSRPAIIRLQA-------
                                                                                                                                                                                                                                                                                                                       KDGAVVQNASQVSISISEQ-----NWIGLLSLKSAERSDAGLYWCQVKDGEETKI----
                                                                                                                                                                                                                                                                                                                                                            LLLAGLASLLLPG-----SAAAGLKLMGAPVKMTVSQGQPVKLNCSVEGMDDPDI-HWM
                                                                                                                                                                                                                            CIKTTVENELPP--PENIEV-SVQNQNYVLKW----DYTYANMTFQVQWLHAFLKRNPGN
                                                                                                                                                                                                                                                                                    -- SQSVWLTVEGVPFFTVEPKDLAVPPNVPFQLSCEA----VGPPEPVTIFWWRGPTKVG
                                                                                                                                                                                                                                                                                                     KENTSSWYEVDS----FTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMW-----ALD
                                                                                                                                                                                                                                                                                                                                          RSDESVGN----VTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAE
                                                                                                                                                                                                                                                                                                                                                                                                  79; Conser
                                      Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
214
508
514
540
676
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                       (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /coprotein; Tyrosine-protein kinase;
Phosphorylation; Transmembrane; Sign
                                                                                                                                                                                                          -PPAAPFNITVTTISSSNASVAWVPGADGLALLHSCTVQVAHA-----PG-
                                                                                                                                                                                                                                                                                                                                                                                                                                               ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 doma:
                                                                                                                        STANDARD;
                                                                         . 35, Created)
. 35, Last sequence upd
. 38, Last annotation u
PROTEIN DCC PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                               95918
                                                                                                                                                                                                                                                                                                                                                                                                          4.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WW.
                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                               Score 113.5; DE 
Pred. No. 0.54; 
53; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE DOMAIN.
IG-LIKE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR POTENTIAL.
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
C3751E86AAE5FA5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINE-PROTEIN KINASE RECEPTOR TYRO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-)
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY). (BY SIMILARITY).
                                                                                             update)
                                                                                                                        1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINASE.
                                                                                 update)
                                                                                                                        ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                  132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding nal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                               Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                    680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                        327
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                    159
                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                           107
                                                                                                                                                                                                                                                                 219
                                                                                                                                                                                                                             272
                                                                                                                                                                                                                                               214
                                                                                                                                                                                                                                                                                    171
                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                                  17;
```

29;

```
EMBL; X85788; CAA59786.1; -. HSSP; P56276; ITLK.
MGD; MGI:94869; DCC.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 1g; 4.
PRINTS; PR00014; FNTYPEIII.
       DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.; "Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo."; Oncogene 11:2243-2254(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooper H.M.
                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE SPLICING. THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGHLY EXPRESSED IN DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN LEVELS FOUND IN TESTIS, HEART AND THYMUS. BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS. DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION AND REMAIN AT THIS LEVEL IN THE ADULT.

SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitted (JUN-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Transmembrane; Signal;
; Alternative initiation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
       ξ
                                                                                                                                                                                                                                                                                                                       816
940
1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1097
1122
1447
                              299
318
478
628
702
838
                                                                                                                                                                                                                                                                                                                                                                                              124
219
317
407
522
618
716
       158298
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
MISSING (IN EMBRYONIC ISOFORM).
MW; OD1F1097C2ZD5B9F CRC64;
                                                                                                POTENTIAL.
POTENTIAL.
                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR SUPPRESSOR PROTEIN DCC, LONG FORM.
                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III
                                                                                                                                                                                                                        C SIMILARITY.
C SIMILARITY.
C SIMILARITY.
C SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THIRD
```

Query Match Best Local Similarity

4.8%; 21.4%;

Score 111.5; Pred. No. 1.5;

DB 1;

Length 1447;

```
밁
                                                      밁
                                                                                Ş
                                                                                                         .명
                                                                                                                                     δ
                                                                                                                                                                        B
                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                 766
                                                                                                                                            311
                                                                                                                                                                                                                                                            594
                                                                                                                                                                                                                                                                                                        483 GSLQLTVGNLKPEAMYTFRVVAYN--EWGPGESSQPİKVATQPELQVPGPVENLHA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 APRDVLPVLVSSRFVRLSWRPPAEAKGNIQTFTVFFSREGDNRERALNTTQP-----
 VSWADNSVPKNQKTSD
                           AHTMDEKLNKSSVFSD 423
                                                        RSITDPTDPVDYYPLLDDF----PTSG---
                                                                                   PVIQD-----YPLIYEIIFWENTSNAERKIIEKKTDVTVPNLKPLTVYCV-----KAR
                                                                                                              ----SPYAETVRVDSKQR-----YYSIERLESSSHYVISLKAFNNAGEGVPLYESATT
                                                                                                                                         DGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYI-----GAP-KQSGNT
                                                                                                                                                                      ---YTAETPENDLDE-SQVPDQPSSLHVRPQTNCIIMSWTPPLNPNIVVRG-YIIGYGVG
                                                                                                                                                                                                   LHAFLKRNPGNHLYKWKQIPDCENV----KTTQCVFPQ-----NVFQKGIYLLRVQAS
                                                                                                                                                                                                                                NGFITGYKIRHRKTTRRGEMETLEPNNLW-YLFTGLEKGSQYSFQVSAMTVNGTGPPSNW
                                                                                                                                                                                                                                                                                        YTLRFLA--YNRYGPGVSTDDITVVTLSDVPSAPPQNISLEVVNSRSIKVSWLPPPSGTQ
                                                                                                                                                                                                                                                                                                                                              --VSTSP-TSILITWEPPAYANGPVQGYRLECTEVSTGKEQNIEVDGLSYKLEGLKKFTE
                                                                                                                                                                                                                                                                                                                                                                           IVIHISPGTKDSVMWA----LDGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETT
                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLKL---NVYEEIKLRIRAEKENTSSWYEVDSFTPFRKA-----QIGPPEVHLEAEDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPOKVEVDIIDDNFI-LRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKCNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                        -PDVSTPMLPPVGVQAVALTHEAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                            -----QW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                   ó
                                                                                   407
                                                                                                                                                                                                                                                                                                                                                593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                        861
                                                                                                                                           359
                                                                                                                                                                                                    310
                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                                                                                         651
                                                                                                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                        537
                                                                                                                                                                                                                                                                                                                                                                                                                                      141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483
                                                                                                                814
                                                                                                                                                                        765
                                                                                                                                                                                                                                                                                                                    242
```

Search completed: June 1, 2000, 10:24:04 Job time: 20622 sec

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein -
                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                 Post-processing:
                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 131
130
129
129
127.5
127.5
127.5
117.5
117.5
117.5
117.5
117.5
                                                                                                                                              686.5
222.5
                                                                                                                       203
189.5
138.5
                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                length: 0 length: 1000000
                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                             10:
11:
12:
13:
                                                                                                                                                                                                                                                                                                                                                           SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                         Minimum Match
Listing first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               June
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-2
2313
                                                                                                                                                                                                                                                                                                                                                                                                                                        225878 seqs, 69334122 residues
  ຆຆຆຆຆຆຆຆຆຆຆຆຆຆຆຆຆ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMYVLLGATTLVLVAVGPWV.....KSSVFSDAVCEKTKPGNTSK 436
                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
    sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                 sp_archea:*
                                                                                                                                                                                                                                                                                                   sp_mhc:*
                                                                                                                                                                                                                                                                                                                           sp_human:*
                                                                                                                                                                                                                                                                                                                                          sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                   sp_fung1:*
                                                                                                                                                                                                                                                                                                            sp_mammal:*
                                                                                                                                                                                                                                                                                                                  sp_invertebrate:*
                                                                                                                                                                                                                                             sp_unclassified: *
                                                                                                                                                                                                                                                                         sp_plant:*
                                                                                                                                                                      Length DB

    2000, 04:38:55; Search time 17.42 Seconds
(without alignments)
1735.343 Million cell updates/sec

  1461
1427
1585
2214
484
817
1264
658
                                                                1443
873
1461
                                                                                        332
341
918
508
1493
1375
1526
                                                                                                                                              569
349
                                                                                       5 5 1 1 3
                                                                                                                                                                                                                                                                                                                                                                           4 9
5
 Q94537
Q94538
Q946510
Q98949
Q98859
Q92859
Q92859
Q17859
Q17859
Q1797784
P91767
                                                                                                                                                                       ä
                                                                                                       Q9YHW0
Q61190
Q63953
Q9YGC8
Q9W6U9
Q9YHV9
Q9YHV9
                                                                                                                                                                                                                                                                                                                                                                           summaries
                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                         225878
092859 homo sapien
000340 homo sapien
091562 xenopus lae
Q17859 caenorhabdi
092673 homo sapien
Q14936 homo sapien
007784 gallus gall
p91767 manduca sex
Q09946 caenorhabdi
                                                                                                      O9yhw0 gallus gall
Q61190 mus musculu
Q63953 mus musculu
Q63953 mus musculu
Q9ygc8 gallus gall
Q9y6u9 gallus gall
Q9yhv9 gallus gall
P97798 mus musculu
                                                                                        Q94537 drosophila
Q94538 drosophila
                                                                                                                                                                      Description
                                                                       Q90610 gallus
Q98949 gallus
                                                                       gall
gall
                                                                                                                                                                                                                                                                                                                                  RESULT
Q9YHW0
                                 밁
                                               δ.
                                                                В
                                                                               Š
                                                                                                              Š
                                                                                                                                                                       SO RETT
                Ş
                                                                                               밁
                 179
                                  128
                                                 121
                                                                 89
                                                                                67
                                                                                               9
                                                                                                               7
```

5	44	43	42	41	40	39	ა 8	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	
104	105	105	105	105.5	106.5	107	108.5	108.5	108.5	109	109	110	111.5	111.5	111.5	112	113	113	113	113	113	113.5	115	115.5	
4.5	51	5	4.5	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.8	4. 8	4.8	4.8	4.8	4.9	4.9	4.9	4.9	4.9	4.9	5.0	5.0	
1239	13055	1948	777	1825	1894	1651	2215	2033	1028	427	416	2213	1896	1571	1445	572	7160	6831	6048	1898	1767	1040	26926	1377	
U	Ģ	4	4	ហ	11	4		H		4	رب ر	თ	4	4		σ								11	
061541	Q09165	Q13332	Q9Y2H6	061210	Q64487	Q9Y6N7	088307	054711	Q62682	095646	018094	Q95209	060468	060469	Q63155	Q29117	Q23551	Q23550	Q23020	Q64604	Q24495	Q9W675	Q10466	P97603	
O61541 drosophila	Q09165 caenorhabd1	homo	Q9y2h6 homo sapien	O61210 caenorhabdi	Q64487 mus musculu	homo	. 088307 mus musculu	O54711 mus musculu	Q62682 rattus norv	095646 homo sapien		Q95209 oryctolagus		O60469 homo sapien	. Q63155 rattus norv	Q29117 sus scrofa		Q23550 caenorhabd1	Q23020 caenorhabd1		Q24495 drosophila		Q10466 homo sapien	P97603 rattus norv	

## ALIGNMENTS

```
밁
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9YHWO PRELIMINAKX; Q9YHWO; Q9YHWO; Q9YHWO; Q9YHWO; Q9YHWO; Q1-MAY-1999 (TrEMBLrel. 10, Created) Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update) Q1-MAY-1999 (TrEMBLrel. 10, Last annotation update) INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of receptor gene cluster.";
Genome Res. 0:0-0(1999).
EMBL; AF082664; AAD13669.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REBOUL J., GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
186
                                                                                             TPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSV--MWALDGLSFTYSLLIWKNSSGVEE 178
                                                                                                                                                      KVRSILPIDVINDLAPETTYCLKVQATVPLEDKGGLFSPIHCIKTTRKVNDLLCPTNVRV
                                  RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVE-NELPPPENIEV 237
                                                                         GRLAAVLLCVLVVVSRCCAGQTNLKSPQDIQVYAVNTNFTLMWNYTGDGT-NVTFSAQYQ 67
                                                                                                                                                                                                                                                                      GATTLYLYAYGPWYLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDESVGNVTFSFDYQ 66
                                                                                                                                                                                                                                                                                                                                                                                                            569 AA;
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            64055 MW;
                                                                                                                                                                                                                                                                                                                                 29.78;
                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                             Score 686.5; DB 13;
Pred. No. 8.5e-47;
B; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                            F99BC099 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UZE G., LUTFALLA G.; interferon/interleukin-10
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                   Length 569;
                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                               12;
```

```
RESULT OCCUPANT OF SERVICE SER
RESULT
Q63953
ID Q6
AC Q6
DT 01
DT 01
DT 01
DE 11
GN III
                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 용
                                                                                                                                                                                                                                                                                  맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 56
                  Q63953 PRELIMINARY;
Q63953;
Q1-NOV-1996 (TrEMBLrel. 01, CI
Q1-NOV-1996 (TrEMBLrel. 01, La
Q1-NOV-1999 (TrEMBLrel. 12, La
INTERFERON GAMMA RECEPTOR 2 (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CRE2-4: isolation of cDN proteins."; Gene 186:97:101(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 97199375. GIBBS V.C., PENNICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILIORB OR CRFB4 OR CRF2-4.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 186:97-101(1997).

EMBL; U53696; AAC53062.1; -.

MGD; MGI:109380; I110rb.

PFAM; PF00041; fn3; 1.

SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                                                                     00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 26.2 nes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                             TVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGN 433
                                                                                                                                                                                                                                                                               TTYCIQVQGFLLDQ--NRTGEWSEPICERT--GN 214
                                                                                                                                                                                                                                                                                                                                                                                   SLHLRFSAP-QIENEPETWTLKNIYDSWAYRVQYWKNGTNEKFQVVSPYDSEVLRNLEPW
                                                                                                                                                                                                                                                                                                                                                                                                              SFHIXIGAPKQSGNTPVIQDYPLIXE-----IIFWENTSNAERKIIEKKTDVTVPNLKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTASTQCDF-SHLSKYGDYTVRVRAELADEHSEW-VNVTFCPVEDTIIGPPEMQIESLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPPPEKVRMNSVNFKNILQWEVPAFPKTNLTFTAQY------ESYRSFQDHCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTMDEKLNKSSVFSDAVCEKTKPG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APKQSGNTPVIQDYPLIYEIIFWENTSNAERKIIEKKTD---VTVPNLKPLTVYCVKARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKPTS----ASYYFRVQAMNEYSKSCLSKDVEVDPPVTNEIGPPDVKVDISDVLLHIKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FALNMKFYLLWDNHYNEHVTYTVQYLTGYLKNLYDDYSSKWQKVSGCENITSMKCNLSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVQNQNYVLKWDYTY-ANMTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --FSEAYNKSSDFSREECIGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPGGPGNKIMSDLYDFSYQILYWKNSSDNEEEVKMKETKQTIATVSDLAPSTLYCVKVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.6%; Score 222.5; DB 11; 26.2%; Pred. No. 3.9e-10; tive 47; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clones
                     Created)
Last sequence update)
Last annotation update)
(INTERFERON GAMMA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding
                                                                                                                                                   332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                        BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            路
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SORRER REPORTED TO THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
REBOUL J., GARDINER N., PUNITED TO TECHNOLOGY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding the second chain of Scand. J. Immunol. 44:599-606 EMBL; U69599; AAC52938.1; JOI EMBL; U69594; AAC52938.1; JOI EMBL; U69596; AAC52938.1; JOI EMBL; U69597; AAC52938.1; JOI EMBL; U69597; AAC52938.1; JOI EMBL; U69597; AAC52938.1; JOI
                                                                                                                                                                                                                                                                                                                                                                                              O9YGC8 PRELIMINARY;
O9YGC8;
O1-MAY 1999 (TYEMBLYE1. 1
O1-MAY 1999 (TYEMBLYE1. 1
O1-MAY 1999 (TYEMBLYE1. 1
INTERLEUKIN-10 RECEPTOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U69595; AAC
EMBL; U69596; AAC
EMBL; U69597; AAC
EMBL; U69598; AAC
EMBL; S69336; AAB
MGD; MGI:107654;
                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Entheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                           SEQUENCE FROM N.A.
REBOUL J., GARDINER K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 94170381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EBENSPERGER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97128072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;
"A novel member of the interferon receptor family complements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       functionality of the murine interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LSAAAGG----KNLKSPQKVEVDIIDDNFILRWNRSDES-----VGNVTFSFDYQKTGM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-NWIKL--SGCQNITSTKCNFSS---LKLNVYE-EIKLRIRAEKEN-TSSWYEVDSFTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGAAASSPDSFSQLAAPLNPRLHLYNDEQILTWEPSPSSNDPRPVVYQVEYSF-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76:803-810(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YENVTVGPPKNISVTPGKGSLVIHFSPPFD----VFHGATFQYLVHYWEKSETQQEQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRKAQIGPPE-VHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGSWHRLLEPNCTDITETKCDLTGGGRLKLFPHPFTVFLRVRAKRGNLTSKWVGLEPFQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S., DEMBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC52938.1;
AAB30165.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHEE S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ion and promoter analysis d chain of the mouse inter 44:599-606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.8%;
                                                                                                                                                 MONNERON lalysis of
                                                                                                                                                                                                                                                                                                                                                                                                     10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTHUKUMARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 203;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBF24E9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                 the
                                                                                                                                                 UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۶
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DONNELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ifngr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
```

375

325 512

470

```
RESULT
Q9W6U9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS
                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQ PRESENTATION OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                           Ş
                                                                                밁
                                                                                                                         δ
                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                          문
                                                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 9907608.

MEDLINE: 9907608.

MEDLINE: 9907608.

"The Specification of sympathetic neurotransmitter on gpl30 cytokine receptor signaling.";

Development 125:4791-4801(1998).

EMBL; AJ011688; CAB42084.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
GLYCOPROTEIN 130 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609M60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                359
                                                                                                                                                                                         320
                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGNAL
                                                                                                                                    172
                                                                                                                                                                                                                                                                                                                                                                                                   202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 CLLLCVSGIVPKPRNARISSVNFRSVLLWDPPGVRKGNLSYTVQAKSIFPKQNFNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              υı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIKTTVENELPPPENIEVSVQNQNYVLKWD----YTYANMTFQVQWLHAFLKRNPGNHLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDVTVPNLKPLTVYCVKARAHTMDEKLNKSSVFSDAVCEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKQIPDCENVKTTQC-VFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFNIRSLSDSFHIYIGAP---KQSGNTPVIQDY-PLIYEIIFWENTSNAERKIIE---KK 388
VYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANWTFQVQWLHAFLKRNPGNH 273
                                                                                                                                                                                                                                                                                               NIRYRISSDTNWMEVPP-EDTASPRTSFSIQGLRPYTEYVFSIRCMKEDGVGFWSDWSE-
                                                                                                                                                                                                                                                                                                                                           SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKEN----TSSWYEV 117
                                                                                                                                                                                                                                                                                                                                                                                                   WVEAANALGKAESDHLVFDPIEIVKPPPPRNLSVNSGILPTVLKLSWENQISTVVMELKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVLSAAAGGKN------LKSPQ----KVEVDIIDDNFILRW-NRSDESVGNVTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSEILSQLEPWTIYCIQVQG--VIPEWNKTGERSQELCEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVNVKSESGTLHVDFTGPAADREHDKWSLKQYYGSWIYRILYWKKGSN--KKVIHIDTKH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VTTNLNVTECDVSSLSYY--GAYVLRVRTEWEDEHSDWA-VVRFKPMADTVIGPP
                                                                                                                                                                                                                                           DSFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLS----FTYSLLIWK-- 172
                                                                                EPFEANGVILQYEVTIRAKPPLSHPPSRYNVTTTSLTLKLPNGTY----EVTVVAHNRVG
                                                                                                                                                                                      -----EQIG-----VTTEDKP------SKGPTIWRTIDVSPSPAFWIVRLMWKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 8.2%; 1 Similarity 27.1%; 60; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
102495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%;
                                                                                                                               EERIENIYSRHKIYKLS-----PETTYCLKVKAALLTSWKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 189.5;
; Pred. No. 1.66
41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 138.5; DB
Pred. No. 0.0069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
1; 9DC128C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7433D364 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..6e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E8);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROHRER H.;
er phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      depends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                                                                      358
                                                                                  414
                                                                                                                                    213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q ARESULP Q ARES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÔ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                         Š
                                                                                                                                                                                                               Šõ
                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
     õ
                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sin
Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09YHV9;
01-MAY-1999
01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative genomic analysis receptor gene cluster."; Genome Res. 0.0-0-(1999).
EMBL; AF082665; AAD13670.1; -. HSSP; P13726; ITFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TIEMBLIEL 10, Last sequence up 01-NOV-1999 (TIEMBLIEL 12, Last annotation INTERPERON ALPHA/BETA RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9YHV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REBOUL J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFNAR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415
           352
                                                                                                                                                                                                                    255
                                                                                                                                                                                                                                                                                                                           203
                                                                                                                                                                                                                                                                                                                                                                             162
                                                                                                                                                                                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
                                                                                                                                                                   255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MVVLLGAT----TLVLVAVGPWVLSAAAGGKNLKSPQKV--EVDIIDDNF--ILRWN-RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEIQAFLLP-----PVFNIRSLSDSFHI----YIGAPKQSGNTPVIQDYPLIYEIIFWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYKWKQIPDCENVKTTOCVFPQNVFQKG-----IYLLRVQA--SDGNNTSFWSEEIKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A-SPPSVLLIPSSNSKAPVKNIRTLPKDGKLWVGWTAPNNVLKYVIEWC---LMSNSSDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTSNAERKIIEKKTDVTVPNLKPLTVYCVKARAHT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSVKAYLQQGRPSKGPTVQTKKVGKAEAVLTWNHLTVDEQNG---FIRSYTILYKTVDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITEWQTEPG--NI-----QGTYLKGDIKPFKCYLITVYPLFADGQGSG------
           APKQSGNTPVI-
                                                                                                                                                                                                                                                                                                                  --- KAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEVFNSSLLH----FSPLSETFLGPPEFNLSSCVHCINITIKLPPTHLRKNGKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEKENTSSWYEVDSFTPFRKAQIGPPEVHLEAEDKAIVIHIS-PGT---KDSVMWALDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESVG---NVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEE----IKLRIR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METLMGGPLRFYQLVFVSI----LCAACYSSLSEKIPREPPDNLQMTSNNFQHILSWRAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETAVS---VDPSKTEYTLSSLTSDTLYTVRMMAYT
                                                                                                                                                                                                                                                                         LNKHSIPSAWK------CITTD------SVAEKDY---YGITIAGAICFSI
                                                                                                                                                                                                                                                                                                                                                                             ---LSLFDIYNKVNYEITLRTVGEEHKRSPEKVTEEPFSIVIEELYPNRNYCVSVMVTAS
                                                                                                                                                                                                                                                                                                                                                                                                                              SFTYSLLIWKNSSGVEERIENIYSRHK------IYKLSPETTYCLKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPTVPTYYRVLYS-----SHSNWKIAKQCSRIVQPFCNLTDDFQVVSDEYSAFVQSFVG
                                                                                                           FOKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYI-----G
                                                                                                                                                                ILVVILKCLHL-----GGYILHKKSLPDTLVFTKMFSYLPFTFECEEITSVEIIY-KEV
                                                                                                                                                                                                                  -MTFQVQWLHAFLKRNPGNHLYKWKQIPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GARDINER K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                               --- AEGSVGAVSSEDDSDDSESDAM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%;
21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nalysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.012;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2DC4E498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
        ----QDYPLIYEIIFWENTSNAERKIIEKKTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UZE G., LUTFALLA G.; interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                  -----CENVKTTQCVFPQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
```

Gaps

29

57 52

SNHDYTRRDIVRR

345

351 307

391

297

254 255 218

203

```
RESULT
Q94537
ID Q9
AC Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PP P979 PP P97
                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                   밁
                                                                                                                                                                           Ş
                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.49
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *KEELING S.L., GAD J.M., COOPER H.M.;

*Mouse Neogenin, a DCC-like molecule, has four sp
expressed widely in the adult mouse and during em
Oncogene 15:691-700(1997).

EMBL: Y09535; CAA70727.1; -.

EMBL: Y09535; CAA70727.1; -.

HSSP; P02751; ITTG.

MGD: MGI:1097159; Neo1.

PFAM: PF00041; fn3; 6.

PFAM: PF00047; ig; 4.

PFAM: PF00047; ig; 4.

PFAM: PF00047; ig; 4.

PFAM: PF00041; FNTYPEIII.

PFAM: PF00041; FNTYPEIII.
Q94537
Q94537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P97798 PRELIMINARY; PRT; 1493 AA. P97798; O1-MAY-1997 (TrEMBLrel. 03, Created) O1-MAY-1997 (TrEMBLrel. 03, Last sequence update) O1-NOV-1999 (TrEMBLrel. 12, Last annotation update) NEOGENIN (NEOGENIN PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutharia; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                               684
                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346
                                                                                                                                   793
                                                                                                                                                                           355
                                                                                                                                                                                                                       734
                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 EL--LSPLSKVNCTYSLRSRSN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LSAAAGGKNIKSPQKVEVDIIDDNFI-LRWN--RSDESVGNVTFSFDYQKTGMDNWIKLS
                                                                   œ
                                                                                                                                                                        QSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA 408
                                                                                                                                                                                                                                                                                                                                                 KW---DYTYAN---MTFQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVFQK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVENTSQPGEMQVTIQNEMPATYYIF----KVMAQNKHGSG----ESSAPLRVET--QP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APQSSDTSPVFVQHSTSSTCDGSSSWVSQNPDDGPEVFE---ENEMDAEE---EKDTDS
                                                                                                                                 ENQNI-VVRGYAIGYGI---
                                                                                                                                                                                                                       TEYNFRVAALTVNGTGPATDWLSAETFESDLDETRVPEVPSSLHVRPLVTSI-VVSWTPP
                                                                                                                                                                                                                                                              GIYLLRVQASDGNNT - - - SFWSEEIKFDTEIQAFLLPPV - - - FNIRSLSDSFHIYIGAPK
                                                                                                                                                                                                                                                                                                        HWQPPSSTTQNGQITGYKIRYRKASRKSDVTETLVTGTQL-----SQLI--EGLDRG
                                                                                                                                                                                                                                                                                                                                                                                                  TINGLKKYTEYSFRVVA--YNKHGPGVSTQDVAVRTLSDVPSAAPQNLSLEVRNSKSIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                           KIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVHLEAEDKAIVIHISPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCQNITS-----TKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAPATTGPLPSAPRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTKEGVDR----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVPNLKPLT----VYCVKARAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLPGPAPNIRAYATSPTSITVTWETPLSGNGEIQNYKLYYMEKGTDKEQDIDVSSHSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97407661.
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.6%; Score 130; DB 11; 21.4%; Pred. No. 0.063;
                                                                                                                               -GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98F26676 CRC32;
                       1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splice variants
embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                               842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                  683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          625
                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398
                                                                                                                                                                                                                       792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                         Š
                                                                                                          밁
                                                                                                                                               Š
                                                                                                                                                                                             В
                                                                                                                                                                                                                                     ρ
                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                        뮍
                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S D D D R R R R R R R C C C C S E H H H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfamily and is required for Cell 87:197-204(1996).
EMBL; U71001; AAC47314.1; --
FLYBASE; FBGn0011592; fra.
FFAM; FF00041; fn3; 6.
PFAM; PF00047; 19; 3.
PFAM; PF00041; FNTYPEIII.
                    1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOLODZIEJ P.A., TIM
JAN L.Y., JAN Y.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAZZLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAZZLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "frazzled encodes a Drosophila member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
                                                                                                                                                                                                                                                                                                                                   251
                                                                                                                                                                                                                                                                                                                                                                             793
                                                                                                                                                                                                                                                                                                                                                                                                                       248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                           TDVTVPNLKPLTVYCVKARAHT
                  TMLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                             --HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSMSVLNSTYQNVPVTPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-----NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVYSPVHCIKTTVENELP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGKNLKS------PQKVEVDIIDDNFI-LRW-------NRSDESV
                                                                                                                                                 LSDSFHIYIGAPKQSGNTPVIQDYP------LIYEIIFWENTSNAER-----KIIEKK 388
                                                                                                                                                                                                                                       DCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS
                                                                                                                                                                                                                                                                                     APTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY----
                                                                                                                                                                                                                                                                                                                            WGRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEWNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL-----TSWKI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSFTPFRKAQIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97015076
                                                                                                          REVTVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIMPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNTYPEIII.
A; 151692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L., MITCHELL K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02, Created)
02, Last sequence update)
12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PPEVHLE-AEDKAIVIHISPGTKDSVMWAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for CNS and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                              410
                  1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 129; DB 5; Length 1375; Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43806DBC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the DCC motor axon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------PPENIEVSVQNQNYVLK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOODMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     guidance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
```

341

909

960

852

792

743

686 158 117

566 104 506

22;

```
RESULT

OPERATOR

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                              ş
                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                               Ş
                                                                                                            밁
                                                                                                                                                              Ş
                                                                                                                                                                                                                         밁
  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KOLODZIEJ P.A., TIMPE L., MITCHELL K.J., GOODMAN C.:
JAN L.Y., JAN Y.N.;
"frazzled encodes a Drosophila member of the DCC im
subfamily and is required for CNS and motor axon gu-
Cell 87:197-204(1996)
EMBL; U71002; AAC47315.1; -.
FIYBASE; FBGN001592; fra.
FFYBASE; FBGN001592; fra.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 19; 3.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94538
Q94538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAZZLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658
                                                                                                                                                                                                                                                                                                                                         944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGKNLKS-----PQKVEVDIIDDNFI-LRW-------NRSDESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYARSHKEIYVKWEEPTVTNGEILKYRVYYSENDSGADLYHDSTALEAVLTELRPHTDYV 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KMVTKSHDDQQVNIQSLLPGRTYQFRVEANTNFGSGASSAPLEVSTQPEVNIAGPPRNFE 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFSS-----LKLNVYEEIKLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGKPLDSGLQARLPSQPRDLVAQIVKSRFVTLSWVEPLQNAGDVVYYTVYYKMNNSEREQ 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-----NTLENDLDETQVPGKPIWISIHPGANNIALHWGPPQHPEIKI--RNYVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGYKIRYRK--FKDAPQVKSTPANI-RYFELSNLDRNAEYQVKIAAMTVNGSGPFTEWNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALL-----TSWKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISVVPFNRNGMGDSSAEIRVKTFSSTPSEPPNNVTLEVTSSSSITVHWEPPAEEDRNGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSDSFHIYIGAPKQSGNTPVIQDYP------LIYEIIFWENTSNAER-----KIIEKK
                                                                                                            --HNTTDLNCMI-NDLRPNTQYEFAVKVVKGRRESSWSWSVLNSTYQNVPVTPP-----
                                                                                                                                                                 DCENVKTTQCVFPQNVFQKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRS
                                                                                                                                                                                                                               APTPLEVPVGLRAITMSSSSIVVYWIDTMLNKNQHVTDNRHYTVSYGITGSNRYRY----
                                                                                                                                                                                                                                                                                                                                         WGRGIPDENTIELKETERYHILKNLESNMDYVVSLRARNVKGDGPPIYDNIKTRDEEPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVYSPVHCIKTTVENELP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97015076.
REVTVRLDEMNPPTVIVQWIPPKHTLGQITGYNIYYTTDTTKRDRDWSVEAFAGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                 -TYANMTFQVQWLHAFLKRN-------PGNHLYKWKQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%;
16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02, Created)
02, Last sequence up
12, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 129; DB 5; Length 1526; Pred. No. 0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F17B1EC9 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------PPENIEVSVQNQNYVLK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        guidance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----V 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
                                                             388
                                                                                                                                                                                                                                  1060
                                                                                                                                                                                                                                                                                          281
                                                                                                                                                                                                                                                                                                                                               1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                            943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212
                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
```

```
RESULT
Q90610
ID QS
AC QS
DT 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                             밁
                                                                                                                                    Š
                                                                                                                                                                   밁
                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                     გ
                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q90610 PRELIMINARY; PKI; 1777....
Q90610;
Q90610;
Q1-NOV-1996 (TIEMBLrel. 01, Created)
Q1-NOV-1996 (TIEMBLrel. 02, Last sequence update)
Q1-NOV-1999 (TIEMBLrel. 12, Last annotation update)
NEOGRIV (FRAGMENT).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Eukaryota; Metazoa; Chordata; Craniata; Phasianinae; Gallus.
Q98949;
Q98949;
01-FEB-1997
01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Neogenin, an avian cell surface protein expressed during neuronal differentiation, is closely related to the human suppressor molecule deleted in colorectal cancer."; J. Cell Biol. 127.2009-2020(1994).

EMBL; U07644; AAC59662.1; -.

HSSP; P80362; INTL.

PFAM; PF00041; fn3; 6.

PFAM; PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
MEDLINE; 95105243.
VIELMETTER J., ROMAN J.M., DREYER W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389
                                                                                                                                                                    889
                                                                                                                                                                                                                          645
                                                                                                                                                                                                                                                                                 587
                                                                                                                                                                                                                                                                                                                                       527
                                                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                                                                                                               472
                                                                                                                                                                                                                                                                                                                                                                                                                                                     416
                                                                                                              747
                                                                                                                                       355
                                                                                                                                                                                              303
                                                                                                                                                                                                                                                      253
                                                                                                                                                                                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TMLMLPNLKPYTTYYFKVQART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDVTVPNLKPLTVYCVKARAHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSAAAGGKNLKSPQKVEVDIIDDNFI-LRWNR--SDESVGNVTFSFDYQKTGMDNWIKLS 77
                                                                                                                                                                                                                                                                                                                                                                                                                       GCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRKAQIGPPEVHLEA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAPATTGPLPTAPRDVVATLVSTRFIRLTWRTPVSDPQGDNLTYSIFYTKEG----INRE 471
                                                                                                              ENQNI-VVRGYAIGYGI----GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLKA
                                                                                                                                       OSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA
                                                                                                                                                                   TEYNFRIAAMTVNGTGPATDWVSAETFESDLDESRVPEVPSSLHVRPLVTSI-VVSWTPP
                                                                                                                                                                                             --YLLRVQASDGNNT---SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHIYIGAPK
                                                                                                                                                                                                                                                                                                         PETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN-QNYVLKWDYTY
                                                                                                                                                                                                                                                                                                                                   PAPNIRAYAGSPTSVTVTWETPLSGNGEIQNYKLYYMEKGODSEODVDVAGLSYTITGLK
                                                                                                                                                                                                                                                                                                                                                                  EDKAIVIHISPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                                                                                                            RVEN-TSRPGETQVMIQNLMPETVYVFRVVAQNKHGHGE--SSAPLKVAT--QPEVQLPG
                                                                                                                                                                                                                                                    ANMIFQVQWLHAFLKRNPGNHL----YKWKQIPDCENVKTTQCVFPQNVFQ--KGI---
                                                                                                                                                                                                                                                                                 KYTEYSFRVVA--YNKHGPGVSTQDVVVRTLSDVPSAAPQNLTLEARNSKSIMLHWQPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
 (TrEMBLrel.
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158050 MW;
                                                                                                                                                                                                                          GTHSGQITGYKIRYRKVSRKSDVTESVGGTQLFQLIEGLERG
 02,
02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 127.5; I
%; Pred. No. 0.095
61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410
 Last sequence update)
                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270B77DC CRC32;
                                           873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                           408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                   354
                                                                                                                                                                                                                          687
                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                    644
                                                                                                                                                                                                                                                                                                               252
                                                                                                                                                                                                                                                                                                                                          586
                                                                                                                                                                                                                                                                                                                                                                      193
                                                                                                                                                                       746
```

19;

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SO DE RESERVATION DE LA COMPTANTA DE LA COMPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim.
Matches 102;
                                                                                                                092859 PRELIMINARY;
092859;
01-FEB-1997 (TIEMBLIEL 0
01-FEB-1997 (TIEMBLIEL C
01-NOV-1999 (TIEMBLIEL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE: 97067156.

BISCARDI J.S., DENHEZ F., BUEHLER G.F., CHESNUTT D.A., BARAGONA O'BRYAN J.P., DER C.J., FIORDALISI J.J., FULTS D.W., MANESS P.F. "Rek, a gene expressed in retina and brain, encodes a receptor tyrosine kinase of the Axl/Tyro3 family.";

J. Biol. Chem. 271:29049-29059(1996).
Eukaryota; Metazoa;
Eutheria; Primates;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSOÓ107; PROTEIN_KINASE_TYR; PROSITE; PSO0109; PROTEIN_KINASE_TYR; PFAM; PF00041; fn3; 2.
PFAM; PF00047; ig; 1.
PFAM; PF00069; PK1nase; 1.
SEQUENCE 873 AA; 96402 MW; 2918D55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                      Homo sapiens (Human)
                                                                                                   NEOGENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U70045; AAC60041.1; HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999
AXL-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                     351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ü
                                                                                                                                                                                                                                                                                                                                                  QDNVTQGEMIVQDTKANLTTWNPLKDLIIRVCV
                                                                                                                                                                                                                                                                                                                                                                                                 -ENTSNAERKIIEKKTDVTVPN-LKPLTV-YCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIKEDTEIQAFLLPPVFNIRSLSDSFHIYIGAP----KQSGNTP-VIQDYPLIYEIIFW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-GNHLYKWKQIPDCENVKTTQCVFPQNVFQKGI-----YLLRVQASDGNNTSFWSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKYWCQVENGGKKEESQQVWLIVEGVPYFTVEPED----VSVSPNAPFHMACAAVGPPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVAVGPWVL-----SAAAGGKNLKSPQKVEV------DIIDDNFILRWNRSDES
                                                                                                                                                                                                                                                                                                                                                                                                                                              RVYF----QTLELAP----SSTPQNIHVIQRDPGLVLEWEGVAPDVLKENVLGYR-LEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLHSCTLQVAESPDGQEVSTE--VAPVPPFAYGVQGLKHSTNYSVRVQCSNEMGSSPFTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYANMTFQVQWLHAFLKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTIVWWMGDSRVGLPDISPSILNVSGINQSTMFSCEAHNVKGLSSSRTATVQIKAMPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSLLIWK-------NSSGVEERIENIYSRHKIYKLSPETTYCLKVKAALLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---WYEVDSFTPFRKAQ-----IGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGNVTFSFD--YQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLLGLWAAALRDGAVAAGMKFTGSPIKLKVSQGQPVKLNCSLEGMEDPEML-WIKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GAVVQSVDQVYIPVDEDHWI--------GFLSLK------SVERTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TremBLrel. 12, Last annotation update) RECEPTOR TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%;
                    Catarrhini;
                                               Chordata;
                                                                                                                      12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLNVTVS------QVTSSNAS--VVWVPGFDGRA
                                                                                                                   Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 123; DB 13; Pred. No. 0.11;
                                         Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2918D550 CRC32;
                    Hominidae;
                                                                                                                                                                                                                    1461 AA
                                                                                                                                                                                                                                                                                                                                                  383
                                                                                                                                                                                                                                                                                                                                                                                               404
                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aves
                                                                                                                                                                                                                                                                                                                                                                                                                                                350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                  끊
                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOR DR RAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 87
Genomics 41:414-421(1997).

EMBL; U72391; AAC51287.1; -

HSSP; P02751; lTTG.

PFAM; PF00041; £n3; 6.

PFAM; PF00047; 1g; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEYERHARDT J.A., LOOK A.T., B
ONCOGENE 0:0-0(0).

EMBL; U61262; AAB17263.1; -.

HSSP; P02751; 1TTG.
PFAM; PF00047; 1g; 4.

PRINTS; PR00014; FNTYPEIII.

PRINTS; PR00014; FNTYPEIII.

PROUDENCE 1461 AA; 159958 M
                                                                                                                                                                                                                            O00340; PRELIMINARY;

O00340; PTEMBLrel. 04,

O1-JUL-1997 (TrEMBLrel. 04,

O1-NOV-1999 (TrEMBLrel. 12,
              EMBL;
HSSP;
PFAM;
                                                                and
q23.
                                                                                    TISSUE-BRAIN;
MEDLINE; 97312699.
WILLNE; 97312699.
VIELMETTER J., CHENG X.N., MISKEVICH
KORENBERG J.R., DREYER W.J.;
"Molecular characterization of human."
                                                                                                                                                                  Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Entheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NEOGENIN
                                                                                                                                                                                                                                                                                                                                                                          408
                                                                                                                                                                                                                                                                                                                                                                                                                                                      697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589
                                                                                                                                                                                                                                                                                                                                                 811 A 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425
                                                                                                                                                                                                                                                                                                                                                                                                  756 VSWTPPENQNI-VVRGYAIGYGI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LYLVAVGPWYLSAAAGGKNLKSPQKYEVDIIDDNFI-LRWN--RSDESYGNVTFSFDYQK
                                                                           the mapping of its gene
                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNVFQKGIYLLRVQASDGNNT---SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QNYVLKWD-----YTYANWT-FQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQIGPPEVHLEAEDKAIVIHISPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGM--DNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIILEHAP-----ATTGPLPSAPRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTK
                                                                                                                                                                                                                                                                                                                                                                                                                         YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGLDRGTEYNFRVAALTINGTGPATDWLSAETFESDLDETRVPEVPSSLHVRPLVTSI-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKSIMIHWQPPAPATQNGQITGYKIRYRKASRKSDVTETLVSGTQL-----SQLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSSHSYTINGLKKYTEYSFRVVA--YNKHGPGVSTPDVAVRTLSDVPSAAPQNLSLEVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGIARERVENTSHPGEMQVTIQNLMPATVYIF-----RVMAQNKHGSG-----ESSAPLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         et---Qpevqlpgpapnlrayaasptsitvtwetpvsgngeiqnyklyymekgtdkeqdvd
                                                                                                                                                                                                                                                                                                                                                                          408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,08
                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                         Created)
                                                                           (NEO1) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 122.5; |
Pred. No. 0.24
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIGNER S.H.,
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 -GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0AB7247E CRC32
                                                                         neogenin, a DCC-related protein, o chromosomal position 15q22.3-
                                                                                                               ,
M
                                                                                                               LANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEARON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197;
                                                                                                                                                                                                                                update)
                                                                                                               R.P., YAMAKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 810
                                                                                                                                                                                                                                                                                                                                                                                                                           407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
```

```
RESULT 14
Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           몽
                                                                                                               Matches
Query Match
Best Local Similarity
Matches 93; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; F
                                                                                                        "Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the nervous system of developing Xenopus embryos.";
Dev. Blol. 166:654-665(1994).
EMBL; U10986; AAA70168.1; -.
HSSP; P56276; lTLK.
PFAM; PF00041; fn3; 6.
PFAM; PF00047; 1g; 4.
PRINTS; PRO0014; ENTYPEIII.
SEQUENCE 1427 AA; 156533 MW; E50B7475 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 95113183.
PIERCEALL W.E., REALE M.A., CANDIA A.F., WRIGHT C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR SUPPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425
                                                                                                                                                                                                                                                                                                                  FEARON E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                             xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       811 A 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFI-LRWN--RSDESVGNVTFSFDYQK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGM--DNWIKLSGCQNITSTKCNFSSLKLNVYEEIKLRIRAEKENTSSWYEVDSFTPFRK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIILEHAP-----ATTGPLPSAPRDVVASLVSTRFIKLTWRTPASDPHGDNLTYSVFYTK 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQIGPPEVHLEAEDKAIVIHISPGTKDSVMWAL----DGLSFTYSLLIWKNSSGVEERIE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGIARERVENTSHPGEMQVTIQNLMPATVYIF-----RVMAQNKHGSG----ESSAPLRV 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSWTPPENQNI-VVRGYAIGYGI----GSPHAQTIKVDYKQRYYTIENLDPSSHYVITLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGLDRGTEYNFRVAALTINGTGPATDWLSAETFESDLDETRVPEVPSSLHVRPLVTSI-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSSHSYTINGLKKYTEYSFRVVA--YNKHGPGVSTPDVAVRTLSDVPSAAPQNLSLEVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ET - - QPEVQLPGPAPNLRAYAASPTSITVTWETPVSGNGEIQNYKLYYMEKGTDKEQDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNVFQKGIYLLRVQASDGNNT---SFWSEEIKFDTEIQAFLLPPV---FNIRSLSDSFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKSIMIHWQPPAPATQNGQITGYKIRYRKASRKSDVTETLVSGTQL-----SQLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QNYVLKWD-----YTYANMT-FQVQWLHAFLKRNPGNHLYKWKQIPDCENVKTTQCVFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00014; FNTYPEIII.
E 1461 AA; 160015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
  5.18;
(larity 22.28;
Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80;
    70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 122.5; DB 4; Length Pred. No. 0.24; Indels 197; Indels
  Score 117.5; D
Pred. No. 0.59;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9D5AE1C4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                              DB 13;
      163;
      Indels
                                              Length 1427;
      93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOUR REPORT OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                               Ş
                                                                                                                                                             В
                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                           Ş
                         Ş
                                                                          g
```

```
Query Match 5.1%; Score 117.5; D Best Local Similarity 19.7%; Pred. No. 0.68; Matches 86; Conservative 74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q17859; Q20137;
Q17859; Q20137;
Q1.00V-1996 (TEMBLrel. 01,
Q1.MAY-1999 (TEMBLrel. 10,
Q1-NOV-1999 (TEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z46811; CAA86842.1; -...
EMBL; Z49938; CAA86842.1; JOINED.
EMBL; Z49938; CAA90189.1; -..
EMBL; Z46811; CAA90189.1; JOINED.
HSSP; P28827; 1RPM.
PFAM; PF00041; fn3; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C09D8.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 GAPKQSGNTPVIQDYPLIYEIIFWENTSNAER-KIIEKKTDVTVPNLKPLTVYCVKARA 408
  179
                                                    380
                                                                                                                                                                                                                                                      263
                                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                        \omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTPPLNPNI-VVRGYIIGYGV----GSPYAETVRVDSKQRYYSIENLEPSSHYVISLKA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEKGSQYSFQVAAMTVNGTGPSSDWYTAETPENDLDESQVPDQPSSLHVRPLTTSI-IMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMTFQVQWLHAFLKRNPGNHL-----YKWKQIPDCENVKTT-----QCVFPQNVF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFTEYSIRVLA--YNRYGPGVSSEEHTVVTLSDVPSAMPQNVSLEVAN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAIVIHISPGTKDSVMWALDGLSFT-----YSLLIWKNSSGVEERIENIYSRHKIYKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SLQITYGNLTPEETYNFRYVAYNE----WGPGESSQEVKVVTQPELQVPGPVENLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APRDVVPVLVSSRFVRLSWRPPVESKGNIQTYTVYFSKQGVQRERAVNTSQPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPOKVEVDIIDDNFI-LRWNRSDESVGNV-TFSFDYQKTGMDNWIKLSGCQNITSTKCNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKWDYTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VVSTAP---TSVLISWDPPAYANGPVQGYRLFCAETFSGREQNIEVDGIVYRLEGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLKLNV - - - - YEEIKLRIRAEKENTSSWYEVDSFTPFR - - - - KAQIGPPEVHLEAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QKGI-YLLRVQASDGNNTSFWSEEIKFDT-----EIQAFLLPPVFNIRSLSDSFHIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRSIKVSW----LPPPPGTQNGFITGYK-----IRHRKTTRRGELETLEPNNLWYLFTG
                                                                                                                                                                                                                                                    PIDVQYEVMKGKIVVSWRPPSEEKRNGNIT-SYKAILSAMD--ATADRYEQPVPAPSTSS
                                                                                                                                                                                                    SLKLNVYEEIKLRIRA-------
RIENIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEV-
                                                                                                 SFTPFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLLIWKNSSGVEE
                                                                                                                                                     TFEVNVRRAYLFKVAAATMKGIGPYSPVLTINPDPADLILDNNIEEEEGNQDPGEATMGE
                                                                                                                                                                                                                                                                                                   PQKVEVDIIDDNFILRWNRSDESV--GNVTFSFDYQKTGMDNWIKLSGCQNITSTKCNFS
                                                    NRNPPKKSKISTADVY-----SAILHHAPGP------LTHPISAALAKAKPTIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; fn3; 3.
1585 AA; 178386 MW; E403A8DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                            DВ
                                                                                                                                                                                                                                                                                                                                                             171;
                                                                                                                                                                                                                                                                                                                                                                                                            ű
                                                                                                                                                                                                                                                                                                                                                             Indels 105;
                                                                                                                                                                                                          ·EKENTSSWYEV---D 118
                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536
                                                                                                           178
          238
                                                                                                                                                                                                                                                           319
                                                                                                                                                                                                                                                                                                                90
                                                                                                                                                                                                                                                                                                                                                                  24;
```

```
A_Geneseq_36:W97861
A_Geneseq_36:R97469
A_Geneseq_36:R79749
A_Geneseq_36:R7013
A_Geneseq_36:R1641
A_Geneseq_36:R14641
A_Geneseq_36:R71139
A_Geneseq_36:W41803
A_Geneseq_36:W41803
A_Geneseq_36:R57139
A_Geneseq_36:R57139
A_Geneseq_36:R13144
A_Geneseq_36:R13144
A_Geneseq_36:R1013
A_Geneseq_36:R1013
A_Geneseq_36:R1013
A_Geneseq_36:W42086
A_Geneseq_36:W42086
A_Geneseq_36:R142087
A_Geneseq_36:W42086
A_Geneseq_36:R144038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_36:W21806
A_Geneseq_36:W52296
A_Geneseq_36:R75782
A_Geneseq_36:W9159
A_Geneseq_36:R71035
A_Geneseq_36:R75783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
Query: US-09-240-675-1
Query length: 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database: A_Geneseq_36:*
Database sequences: 188963
Database length: 23686106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_36:R28496
A_Geneseq_36:R42635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score_list:
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_36:W21805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_36:R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_36:R14487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search time (sec): 79.530000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -Q-/gn2_1/USPTO_spool/US09240675/runat_30052000_165117_2964/app_query.fasta.
-DB-A_Geneseq_36 -OPMT-fastan -SUFFIX-modif.rag -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QAPEXT-500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOOF-6.000 -DELEXT-7.000 -START-1 -MATRIX-bLosum52
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-PCt
-ALICN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-100000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -MODEL-frame+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _Geneseq_36:W21804
_Geneseq_36:R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geneseq_36:R28495
                          _Geneseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geneseq_36:R14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of: US-09-240-675-1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _n2p.model -DEV-xlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strd Orig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2313.
2313.
2313.
2313.
2313.
2313.
2313.
2309.
2308.
2304.
2260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198
153
153
151
131
124
122
                                                                                                                                                                                                                          118
118
117
117
117
115
115
115
1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                   5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4101.48
4099.69
4095.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2Score
4111.17
4111.17
4095.09
4005.09
3922.16
388.62
3282.254.19
2254.19
2254.19
2254.19
2197.60
1194.85
1194.85
1194.85
1194.85
1194.85
1194.85
1195.80
1197.80
1197.80
1187.80
1187.80
1188.30
1187.80
1187.80
1187.80
1188.30
1188.30
1189.30
1189.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
1180.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4108.62
4108.62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4108.62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4108.62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCORE Len
3.7e-222 43
3.7e-222 43
4.0e-222 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1e-14
.8e-12
.4e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .9e-221
.0e-217
  .0036
.0022
.0065
.0065
.0069
.0089
.0131
.0134
.0134
.0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3e-07
.9e-07
.3e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0e-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0e-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1e-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         out_format :
  5557

5557

5557

5557

5557

5557

5557

5557

5557

5557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

557

5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble interferon-alpha/beta z Sequence of a soulble form of thuman alpha-interferon receptor Complete interferon-alpha/beta Sequence of a soulble form of thuman interferon receptor. Monch Human interferon receptor. Monch Human interferon receptor. Monch Human interferon alpha in receptor extracellular doma spliced-deleted interferon alpha if receptor extracellular doma spliced-deleted interferon alpha if receptor beta-subunit in receptor beta-subunit in receptor beta-subunit in receptor beta-subunit receptor beta-subunit receptor beta-subunit receptor beta-subunit in receptor beta-subunit receptor beta-subunit receptor beta-subunit receptor beta-subunit receptor beta-subunit receptor beta-subunit receptor til receptor in recep
                                                                                                                                                                                                                                                                                                                        Gamma interferon receptor. New Gamma interferon receptor. New Rat receptor tyrosine kinase F Interleukin-10 receptor subunit Mouse IL-10 receptor interleuk Human LDL receptor analogue. If Gamma interferon receptor. New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Documentation
                       Human Down syndrome-cell adhes Human Down syndrome-cell adhes Rabbit LDL receptor analogue. Extracellular domain of hybrid Rat REK7 eph-related tyrosine k EPH-like receptor protein tyros Human interleukin-12 receptor a
                                                                                                                                                                                           Soluble human interferon gamma Human neuronal calcium channe Human calcium channel alpha-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cytokine receptor 11 (2c) Human cytokine receptor 11 (2c) Plasmid pBABLUE human interferc Extracellular domain of human I Gamma-IFN-R-GBP 130 fusion prot
                                                                                                                                                                                                                                                                            Sequence encoded by human insu
Deleted in Colorectal Carcinon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_36:R57138
A_Geneseq_36:W41804
A_Geneseq_36:W83927
A_Geneseq_36:R15049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID R14487 standard; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1
                               327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6-JAN-1992
                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
```

```
A_Geneseq_36:R57138 + 107.00 165.48 0.0167 578 ! Interleukin-10 receptor s
A_Geneseq_36:W41804 + 107.00 165.48 0.0167 578 ! Human II-10 receptor. Int
A_Geneseq_36:W41807 + 107.00 162.73 0.0182 753 ! Human II-10 receptor. Int
A_Geneseq_36:R15049 + 107.00 160.33 0.0197 948 ! Hybrid human insulin-IGF-
seq_name: A_Geneseq_36:R14487

seq_documentation_block:
ID R14487 standard; Protein; 436 AA.
AC R14487.
DT 16-JAN-1992 [first entry)
DE Soluble interferon-alpha/beta receptor.
KW IIP; autoimmune disease; graft rejection; histocompatibility.
DF R2657881-A.
DN R2657881-A.
DN 9-AUG-1991;
DF 05-FEB-1990; D01298.
DR 05-FEB-1990; FR-001298.
DR (FUST) LAB EURO BIOTECHNO.
DI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;
DI TOVEY MG, Uze G;
DR WPJ; 91-319778/44.
DR N-PSDB; Q14239.
DR N-PSDB
```

Quality: 2313.00 Length: 436
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
plignment\_block:
US-09-240-675-1 x R14487 from: 1 to: 436

ign seg 1/1 to: R14487 from: 1 to: 436

127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 17-

AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376

```
977
                                                                                                                                                                                                                                                                                                                                                           827
                                                                                                                                                                                                                                                                                                                                                                                                    777
                                                                                                                                                                                                                                                                                                                                                                                                                                              727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                               284
                                                                                                                                                                                                                                                                                                                                                                                251
                                                                                                                                                                                                                                                                                                                                                                                                                       234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT
                                                                                                                         GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                        AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTTCCAAAAA
                                                                                                                                                                                                                                                                                                                                              AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                             ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                 TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC
                                                                                                                                                                                                                                                   GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                                                                                                                                                                                                                                      sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                          leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr
                                                                                                                                                                                                                                                                                              luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                           400
                                                                                                                                                                                         1076
                                                                                                                                                                                                                                1026
                                                                                                                                                                                                                                                                         976
                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                   926
                                                                                                                                                                                                                                                                                                                                                                                                                                           776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426
                                                                                   384
                                                                                                                                                                    350
                                                                                                                                                                                                             334
                                                                                                                                                                                                                                                                                                                                                           876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                       250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150
                                                                                                                                                                                                                                                                                                                                     284
```

```
seq_documentation_block:
ID R28495
AC R28495
DT 31-MAR-1993 (first e
DE Sequence of a soulble
DE with a high affinity
Interferon receptor;
OS Synthetic.
PN W99218626-A.
PD 29-OCT-1992.
PF 17-APR-1991; WO-F00318.
PF 17-APR-1991; WO-F0031
PA 1814 P, Gresser I, Lut
PI Tovey M, UZe G;
DR WPI; 92-382110/46.
DR N-PSDB; Q30532.
PT Water soluble polyper
and beta - useful as
PS Claim 2; Fig 1; 58pp;
CC DNA encoding the wate
CC IFN-alpha and -beta al
CC oligonucleotides as placeteriophage lambda
CC the IFN-alpha and -beta for the IFN-alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality: 2313.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-240-675-1 x R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: A_Geneseq_36:R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta useful as immunosuppressants, for treating auto:immune diseases and transplant rejection Claim 2; Fig 1; 58pp; English.

DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and beta receptor (30533), was incubated with oligos (30534 and 030535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the
                                                                                                                                                              177
                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1993 (first entry)
Sequence of a soulble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta.
Interferon receptor; alpha-interferon; beta-interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EUBI-) LAB EURO BIOTECHNOLOGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxic side-effects of known immunosuppressants such as steroids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-1991; F00318.
17-APR-1991; WO-F00318
                                                                                                51
                                                                                                                                                                                                                            34
                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                        CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                           yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                  AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrSerLys 436
to: R28495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436
                                                                                                                                                              226
                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                             176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                  276
                                                                                                67
                                                                                                                                                                                                                                                                                                                                                           34
```

```
1077
                                                                                  1027
1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                          627
                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277
                    351
                                                             334
                                                                                                      317
                                                                                                                           977
                                                                                                                                                301
                                                                                                                                                                     927
                                                                                                                                                                                        284
                                                                                                                                                                                                             877
                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                     827
                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                                                                                                                               777
                                                                                                                                                                                                                                                                                                                   234
                                                                                                                                                                                                                                                                                                                                       727
                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                 677
                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                           AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTAGAAGCTGAAGATAAGGGAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                                                                                                                                                                                                    GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                            TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC
                                                                                                                                              GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                                                          GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                        ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA
                             GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
                                                                                                                                                                                                                                                     AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                    GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
                                                                                                      eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                           AMANTGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
                                        1126
                                                                                  1076
                                                                                                                           1026
                                                                                                                                                                     976
                                                                                                                                                                                         300
                                                                                                                                                                                                              926
                                                                                                                                                                                                                                                                                               826
                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                              350
                                                                                                                                                317
                                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                      876
                                                                                                                                                                                                                                                                          267
                      367
                                                                                                       334
```

```
alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: A_Geneseq_36:R11958
                                                                                                                                                                              alignment_block:
US-09-240-675-1 x R11958
                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-1991.
19-OCT-1990; F00758.
20-OCT-1989; FR-013770.
(CNRS ) CNRS CENT NAT RECH S
(CORS ) LUTEALIA
MOGENSEN KE, UZE G, LUTEALIA
WPI; 91-148740/20.
N-PSDB; 011701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                      New human alpha-interferon receptor protein - useful for testing interferon agonists and in treatment or diagnosis
Disclosure; fig 4; 30pp; French,
This recombinant human alpha interferon (IFN) receptor protein is useful for the testing of IFN agonists and for treatment and diagnosis of viral diseases and tumours. Antibodies raised against this protein can be used for blocking the receptor when required, eg where overexpression of alpha-IFN is harmful. The Abs are also useful for eg drug targetting. Variants of the protein, having residue 14 (Thr) replaced by Arg and an Asp inserted between residues 479 and 480, are also useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human alpha-interferon receptor protein. Human alpha IFN; IFN agonists; antiviral; anti tumour drug targetting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R11958 standard; Protein; R11958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9105862-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-1991 (first entry)
                        127
 34
                                                   17
                                                                                                                              27
                                                                           77
                                                                                                   <u>بــ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr
AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                hrSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIATCGAGAAAAAAACTGATGTIACAGTITCCTAATITGAAACCACTGACT
                                                                                                                                                      ;;
                                                                                                                                                                                                                    2313.00
5.305
100.000
                                                                                                                                                       R11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .2/
/label- signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AT RECH SCI.
Lutfalla G,
                                                                                                                                                       from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           557
                                                                                                                                                                                                                    Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gresser
                                                                                                                                                       .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H
                                                                                                                                                                                                                     436
0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1226
                          176
                                                                            126
                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400
                                                    34
    50
```

```
827
                                                                                                                                                                                                                                                                                                                                                                                                                        477
                                    317
                                                                                                                                                                                  251
                                                                                                                                                                                                    777
                                                                                                                                                                                                                     234
                                                                                                                                                                                                                                       727
                                                                                                                                                                                                                                                        217
                                                                                                                                                                                                                                                                           677
                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                             627
                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                 577
                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                    527
                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                                                                                                                            427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                    CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076
                                                                                                                                                      AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                              AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                         TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                             AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                                                                                                     ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                          ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
                                                                                                                                            sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                  uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT
                                                                                                                                                                                                                                                                                                                                                                                                    LysaspSerValMetTrpalaLeuaspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                      976
                                                                                                                           926
                                                                                                         300
                                                                                                                                                                                                                   250
                                                                                                                                            284
                                                                                                                                                              876
                                                                                                                                                                                267
                                                                                                                                                                                                                                    776
                                                                                                                                                                                                                                                                                                            676
                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                        150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376
                                                                                                                                                                                                                                                                                         217
                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                                  576
                                                                                                                                                                                                                                                                                                                                                                                                                     526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: A_Geneseq_36:R14488
Quality: 2313.00
Ratio: 5.305
Percent Similarity: 100.000
                                                                                                                                                                                                               09-AUG-1991.

05-FEB-1990; 001298.

05-FEB-1990; FR-001298.

(EUBI-) LAB EURO BIOTECHNO.

Eld P, Greeser I, Lutfalla G

Tovey MG, Uze G;

WPI; 91-319778/44.

N-PSDB; 014240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                  documentation_block:
R14488 standard; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1177
                                                                    New water soluble polypeptide(s) with affinity for IFN-alpha and beta - used to treat e.g. lupus erythematosus, Behcet's disease, aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc. Disclosure; Page 47; 52pp; French.

The invention covers derivatives of the interferon-alpha and/or beta receptor obtained by deleting the transmembrane and cytoplasmic domains of the native receptor or by substitution. Potentially immunogenic epitopes are eliminated and the deriv. can be secreted from transformed cells. Soluble deriv.s block the activity of IFN alpha/beta and can be used to treat autoimmune diseases or to inhibit graft rejection. See also Q14239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1077
                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1992 (first entry)
Complete interferon-alpha/Deta receptor.
IFN; autoimmune disease; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hrSerLys 436
                                                                                                                                                                                                                                                                                                                            /label= transmembrane
458. .557
/label= cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 437. .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
  Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                    557
                                                                                                                                                                                                                                                       ç,
                                                                                                                                                                                                                                                       Meyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
 Identity:
                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                    Mogensen
                                                                                                                                                                                                                                                                                                                                                                                                   histocompatibility
436
0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1226
```

alignment\_block: US-09-240-675-1

x R14488 R14488

Align seg 1/1

. :

from:

Н

; 6

557

27

ATGATGGTCGTCCTGGGGCGCGACGACCTAGTGCTCGTCGTCGCCTGGG

```
377
                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                              477
                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                                                             427
                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                   627
                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                   577
                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                527
                                                                                                                                                                                                                                                                               151
                                                                            827
                                                                                                         777
                                                                                                                                                       217
                                                                                                                                                                      677
                                                                                                                                                                                     201
301
                927
                              284
                                             877
                                                             267
                                                                                           251
                                                                                                                        234
                                                                                                                                       727
                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77
                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                              ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                        AACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                   ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                                              isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr
                                                                                                                                                                                                                                                                                                                                           lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                          OValHisCysIleLysThrThrValGluAsnGluLeuProProProGluA
                                                                                                                                                                                                                                                 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT
AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                            AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                              luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                         376
                                                                                                                                                                                                     676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                   626
                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                 576
                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                              150
                                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                                                                                                                                                                            426
                                                                                                                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                                                                      217
                                                                                                                                                                                                                    200
                976
                                                                            876
                                                                                           267
                                                                                                                         250
                                                                                                                                                       234
                               300
                                                              284
 317
```

```
seq_documentation_block:
ID R28496; standard; Prot
AC R28496;
DT 31-MAR-1993 (first e
DE Sequence of a soulbie
DE MITT a high affinity
KW Interferon receptor;
OS Synthetic.
PN W09218626-A.
PD 29-OCT 1992.
PF 17-APR-1991; F00318.
PF 17-APR-1991; MO-F0031
PA 17-APR-1991; MO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-APR-1991; WO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-APR-1991; WO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-APR-1991; WO-F0031
PA (EUBI-) LAB EURO BIOD
PR 17-YW M, UZE G;
DR WATER SOUNDLE POLYPER
PT and beta useful as
PT diseases and transple
PT and beta useful as
PT diseases and transple
PT and beta useful as
PT claim 3; F19 2; 58pp)
CC IFN-alpha and -beta i
CC oligonucleotides as;
CC oligonucleotides as;
CC oligonucleotides as of the IFN-alpha and -be
CC oligonucleotides as of the IFN-alph
DE Sequence of a soubble form of the interferon (IFN) receptor

DE with a high affinity for IFN-alpha and -beta.

KW Interferon receptor; alpha-interferon; beta-interferon.

Synthetic.

PN W09218626-A.

PF 17-APR-1991; F00318.

PF 17-APR-1991; W0-F00318.

PR (EUBI-) LAB EURO BIOTECHNOLOGIE.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE.

PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,

PI TOVEY M, Uze G;

DR WPI; 92-382110/46.

DR N-PSDB; 030533.

PT Water soluble polypeptide(s) strongly bind interferon(s) alpha

PT TOVEY M, Uze G;

DR WPI; 92-382110/46.

DR N-PSDB; 030533.

PT Water soluble polypeptide(s) strongly bind interferon(s) alpha

PT diseases and transplant rejection

PS Claim 3; F12 2; Sep; English.

CC DNA encoding the water-soluble polypeptide with a high affinity for

CC INN-alpha and -beta is isolated by PCR, using appropriate

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC DNA encoding the water soluble polypeptide with a high affinity for

CC DNA encoding the water soluble polypeptide with a stemplate. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC DNA encoding the water soluble polypeptide with a high affinity for

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as template. For example,

CC Oligonuclectides as primers and cloned cDNA as templates. For example,

CC Oligonuclectides as primers and cloned cDNA as templates. For example,

CC Oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hrSerLys 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_36:R28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
```

alignment\_scores: Quality:

Ratio: Similarity:

2313.00 5.305 100.000

Gaps: Percent Identity:

Length:

: 436 : 0 : 100.000

```
alignment_block:
US-09-240-675-1 x
                                                                                                                                                                                                                                                                                                    Align
                          777
                                                    217
                                                                     201
                                                                                       184
                                                                                               577
                                                                                                       167
                                                                                                                527
                                                                                                                        151
                                                                                                                                477
                                                                                                                                                 427
                                                                                                                                                          117
                                                                                                                                                                   377
                                                                                                                                                                            101
                                                                                                                                                                                    327
                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                      177
                                   234
                                           727
                                                                                                                                          134
                                                                                                                                                                                                      277
                                                                                                                                                                                                              67
                                                                                                                                                                                             84
                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                       77
                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                   seg 1/1 to:
ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT
                                                                                    AACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                             AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA
                                                                   ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA
                                                                                                                                                         AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                   oValHisCysIleLysThrThrValGluAsnGluLeuProProProGluA
                                                                                                                                                                                                                                                                                                   from:
                                                                                                                                                                                                                                                                                                   _
                                                                                                                                                                                                                                                                                                   8
        876
                                                                                                                                                          134
                                                                                                                                                 476
                 267
                                   250
                                                   234
                                                            726
                                                                    217
                                                                            676
                                                                                     200
                                                                                              626
                                                                                                       184
                                                                                                               576
                                                                                                                        167
                                                                                                                                526
                                                                                                                                         150
                                                                                                                                                                   426
                                                                                                                                                                           117
                                                                                                                                                                                   376
                                                                                                                                                                                            100
                                                                                                                                                                                                    326
                                                                                                                                                                                                             84
                                                                                                                                                                                                                      276
                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                 17
```

```
seq_name:
                                                                                     EP-563487-A.
06-CCT-1993; 400902.
31-MAR-1992; EP-400902.
31-MAR-1992; EP-400902.
(EUBI-) LAB EURO BIOTECHNOLOGIE SI
Benoit P, Maguire D, Meyer F, I
WPI; 93-312951/40.
P-PSDB; R42635
                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                     1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1177
                                                                                                                                                                                                                                                                                                                                                                                                                              1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1127
Monoclonal antibody to human interferon type-I receptor - having neutralising activity against human type I interferon, used for therapy and diagnosis
Disclosure; Fig 3; 21pp; English.
Monoclonal antibodies produced against soluble forms of the human interferon alpha-beta receptor based on the full-length human IFN-R sequence are claimed. The antibodies are useful for treatment and prophylaxis of disorders involving cell proliferation and/or viral
                                                                                                                                                                                                 Key
domain
                                                                                                                                                                                                                              IFN-R, extracellular domain; monoclonal antibody; viral infection; cell proliferation; allograft rejection; systemic lupus erythematosus; psoriasis; multiple sclerosis; behoet's Disease; aplastic anaemia; immunodeficiency; measles virus; interferon-alpha-beta.
                                                                                                                                                                                                                                                                                               R42635 standard;
R42635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1027
                                                                                                                                                                                                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                         Human interferon receptor
                                                                                                                                                                                                                                                                                    20-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                              434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  877
                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrSerLys
                                                                                                                                                                                                                                                                                                                                                                                   CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                      sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
                                                                                                                                                                                                                                                                                                                                         A_Geneseq_36:R42635
                                                                                                                                                                                                                                                                                                                                                              436
                                                                                                                                                                        Location/Qualifiers
1. .436
/label= extracellular_domain
/note= "soluble, immunogenic
                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                           557
                                                                                                                                                                                                                                                                                                          ₿
                                                                                                           SA.
Plavec
                                                                                                           Ļ
                                                                                                           Tovey
                                                                                                                                                                          form
                                                                                                           ă
                                                                                                                                                                          of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                   417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
```

ì

ဗ္ဗ ဂ

infection Sequence

```
alignment_scores:
Quality: 2313.00
Ratio: 5.305
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-240-675-1 x R42635
                                                                                                                                                                                                                                                                                                                                                                                   Align
                                                                                                                                        477
                                                                                                                                                    134
                                                                                                                                                                                         377
                                                                                                                                                                                                      101
                                                                                                                                                                                                                 327
                                                                                                                                                                                                                                                                    227
                                     677
                                                              627
                                                                          184
                                                                                       577
                                                                                                   167
                                                                                                               527
                                                                                                                           151
                                                                                                                                                                427
                                                                                                                                                                             117
                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                            177
                                                                                                                                                                                                                                                                                                                     127
             727
                         217
                                                  201
                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                          \vdash
                                                                                                                                                                                                                                                                                                                                                                                  seg 1/1 to:
                                                                                                                                                                                                                                                                                                       AAAAAGTAGAGGTCGACATCATAGATGACAAĊTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                         ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                               GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                            AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA
                                                                                                                                                                             TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                              erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                      sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                   R42635
                                                                                                                                                                                                                                                                                                                                                                                   from:
                                                                                                                                                                                                                                                                                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                                                                                   ب
                                                                                                                                                                                                                                                                                                                                                                                   ç
O
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
: Identity:
                                                                                                                                                                                                                                                                                                                                                                                   557
                                                                                                                                                                                                                                                                                                                                                                                                                  100.
                                      726
                                                              676
                                                                                       626
                                                                                                   184
                                                                                                                576
                                                                                                                            167
                                                                                                                                        526
                                                                                                                                                    150
                                                                                                                                                                 476
                                                                                                                                                                             134
                                                                                                                                                                                          426
                                                                                                                                                                                                                 376
                                                                                                                                                                                                                              100
                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                                                                          17
                                                  217
                                                                           200
                          234
```

```
seq_documentation_block:
ID R75356 standard; Pr
                                                                                                                                                                                                                 seq_name:
23.MAR-1995.
16.SEP-1994; E03114.
17.SEP-1993; EP-402279.
(EUBI-) LAB EURO BIOTECHNOLOGIE SA.
Benizri EJ, Tovey MG;
WPI; 95-131187/17.
N.PSDB; OB6458.
N.PSDB; OB6458.
Compsn. of monoclonal antibodies against interferon recuseful as immuno:modulator, eg. for treating AIDS Disclosure; Fig.3A-2B; 105pp; English.
                                                                                                                                                                                                                                                     1327
                                                                                                                                                                                                                                                                                           1277
                                                                                                                                                                                                                                                                                                                              1227
                                                                                                                                                                                                                                                                                                                                                                                                                                          1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1027
                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                            334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        927
                                                                                                                                                                                                                                     434
                                                                                                                                                                                                                                                                                                            401
                                                                                                                                                                                                                                                                                                                                                 384
                                                                                                                                                                                                                                                                                                                                                                                     367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   777
                                                                                             WO9507716-A.
                                                                                                                domain
                                                                                                                        Homo sapiens.
Key
                                                                                                                                           IFN receptor; int
interferon-beta;
                                                                                                                                                            Human IFN receptor
                                                                                                                                                                     16-OCT-1995 (first entry)
                                                                                                                                                                                                                                  |||||||||
hrSerLys
                                                                                                                                                                                                                                                                     GTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA
                                                                                                                                                                                                                                                     CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                               ulleTyrGlullellePheTrpGluAsnThrSerAsnAlaGluArgLysI
                                                                                                                                                                                                                                                                                                                                                                                            GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLy
                                                                                                                                                                                                                                                                                                            ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                 A_Geneseq_36:R75356
                                                                                                                                                  interferon
                                                                                                      1. .436
/label=
                                                                                                                       Location/Qualifiers
                                                                                                                                           terferon receptor; interferon-alpha;
monoclonal antibody; immunomodulate
                                                                                                                                                                                       Protein;
                                                                                                       Extracellular_domain
                                                                                                                                                                                        557
                                                                                                                                                                                        Z
                                                                                                                                            immunomodulator; AIDS
                                                                                                                                                                                                                                                                                                                                                                   1226
                                                                                                                                                                                                                                                                                                                                                                                                       1176
                                                                                                                                                                                                                                                                                           1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826
                                                                                                                                                                                                                                                                                                                                                  400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                876
                                                                                                                                                                                                                                                                          434
                                                                                                                                                                                                                                                                                                             417
                                                                                                                                                                                                                                                                                                                                                                                     384
                                                                                                                                                                                                                                                                                                                                                                                                                         367
                                                                                                                                                                                                                                                                                                                                                                                                                                                              350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
```

```
alignment_block:
US-09-240-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ន្តន្តន្តន្ត
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouality: 2309.00
Ratio: 5.296
Percent Similarity: 100.000
                                                                                    184
                                                                                                                              167
                                                                                                                                                 527
                                                                                                                                                                                          477
                                                                                                                                                                                                               134
                                                                                                                                                                                                                                    427
                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                           377
                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence of human interferon class I receptor is given in R75356. A recombinant soluble form of the extracellular domain of this receptor (R71723) has been used to raise immunomodulatory monocional antibodies.

Sequence 557 AA;
                                                                                                                                                                                                                                                                                                                                                             277
                                                                                                                                                                                                                                                                                                                                                                                                       227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ب
AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                        AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
                                                                                                                         ATTCCAGACATAAAATTTATAAACTCTCACCAGAGAGACTACTTATTGTCTA
                                                                                                                                                                                                         ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA
                                                                                                                                                                                                                                                               TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                                                                           LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                          AAATTGCGTATAAGAGCAGAAAAAGAAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                    AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                    lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH
                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x R75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R75356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 436
Gaps: 0
Percent Identity: 99.771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             557
                                                                                                                                                                                                                                 476
                                                                                                                                                                                                                                                                          426
                                         217
                                                             676
                                                                                  200
                                                                                                     626
                                                                                                                           184
                                                                                                                                               576
                                                                                                                                                                   167
                                                                                                                                                                                        526
                                                                                                                                                                                                           150
                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                  376
                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                            226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
```

```
Sed Control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: A_Geneseq_36:W21804
                                                                                                                                                                                                                                                                                                                                                                                         _documentation_block:
W21804 standard; Pro
  AU9475977-A.
11-MAY-1995.
20-OCT-1994;
24-OCT-1993;
(YEDA ) YEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1077
                                                                                                                                            domain
                                                                                                                                                                                       domain
                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                            Transmembranal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                 23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   777
                                                                                                                                                                                                                                                                                               Interferon alpha-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hrSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATATTGTGTGAAAGCCAGAGCACACACATGGATGAAAAGCTGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA
IL-107378.
RES & DEV (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436
                                               075977
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                     interferon alpha-receptor
                                                                                                                                         /label=
458. .55
                                                                                                                                                                                  /label= Extracellular_domain 437. .457
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                       L= Transmembrane_domain
.557
    CO LTD
                                                                                                                                                                                                                                                                                                                                                                                         557
                                                                                                                                                                                                                                                                                                  IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      776
```

```
ALERE SOUDOUDOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-240-675-1 x W21804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg
                                                                                                                                                                                                                                               377 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTÄC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   includes a 21-amino acid transmembrane region. Novel, splice-deleted IFWAR forms 1 (W21805) and 2 (W21806) have been detected that lack this transmembrane domain. These, soluble non-membrane bound polypeptides can be expressed in host-cells and used to inhibit, modulate or modify the activities of interferons alpha and beta in cells, tissues and organisms, or for diagnostic
                                                                                                                                     477 AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT
                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                                                                 327
                                                     167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purposes.
Sequence : 557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian soluble interferon alpha-receptor forms - used for inhibiting, modulating or modifying the activities of interferon(s) Disclosure; Fig 7; 46pp; English.

Human transmembranal interferon alpha receptor (IFNAR) (W21804)
                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 95-200634/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dramovich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABRA/) ABRAMOVICH C
                                                                                                                                                                                        isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr
                                                                                                                                                                                                                                                                                                                   LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA
                                                                                                                                                                                                                  ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                              GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                  ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                                                    LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                              AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                              erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1/1 to: W21804 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 2308.00
Ratio: 5.306
milarity: 99.771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratovitski E, Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 436
Gaps: 0
Percent Identity: 99.771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626
                                                                                  576
                                                                                                                                                      526
                                                                                                                                                                                        150
                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                          426
                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                              376
                                                   184
                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
```

Ä,

IFN receptor extracellular domain.

IFN receptor; interferon receptor; interferon-alpha; interferon-beta; monoclonal antibody; immunomodulator; Homo; sapiens.

W09507716-A.

AIDS

```
seq_documentation_block:

ID R71723 standard; Protein; 436 AA.

AC R71723;

DT 16-OCT-1995 (first entry)

DE IFN receptor extracellular domain

KW IFN receptor; interferon receptor
                                                                                                                       seq_name: A_Geneseq_36:R71723
                                                                                                                                                                                                                                         384 lelleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1077
                                                                                                                                                                                                                                                                                                                                       1227. GTATATTGTGAAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAA. 1276
                                                                                                                                                                                                                                                                                                                                                                                                                  1177 TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1127 GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA
                                                                                                                                                                                                      1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                              401 ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                                       417
                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 ulleTyrGlulleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1027
                                                                                                                                                                   434, hrserLys 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 roProValPheAsnIleArgSerLeuSerAspSerPheH1sIleTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 eTrpSerGluGluIleLyspheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 snileGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              877 AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    727 ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTÄT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217. ovalHisCysTleLysThrThrValGluAsnGluLeuProProProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       677. AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  777 ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                               .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367
                                                                                                                                                                                                                                                                                                                                                                                                                                1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926
                                                                                                                                                                                                                                                                                                                    417
                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676
```

```
alignment_scores:
Quality: 2304.00
Ratio: 5.284
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-240-675-1 x R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: R71723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EUBI-) LAB EURO BIOTECHNOLOGIE SA.
Ben1zri EJ, Tovey MG;
WPI; 95-131187/17.
N-PSDB; 086457.
Compsn. of monoclonal antibodies against interferon receptor useful as immuno:modulator, eg. for treating AIDS
Disclosure; Fig.2A-2B; 105pp; English.
Disclosure; Fig.2A-2B; 105pp; English.
A recombinant soluble form of the human interferon class I receptor protein extracellular domain, given in R71723, was expressed in either E. coli or COS cell hosts; The protein was used to raise
                                                                                                                                      477
                                               167
                                                                                                          151
                                                                                                                                                                    134
                                                                                                                                                                                                                                                            377
                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                         227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulatory monoclonal antibodies. Sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \mathbf{\mu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTÄCATATAGCTT 526°
                                                                                                                                                                                                                                                                                  ATTTAGAAGCTGAAGATAAĞGCAATAGTGATACACATCTCTCCTGGAACA 476
ATTCCAGACATAAAATTTATAAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                           AspSerPheThrPropheArgLysAlaGlnileGlyprophrogluValH
                                                                                                                                                                                                                                                       TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                                                                                                                               erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                           GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                      AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGAGCGATGAGTCTGTCGAGATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                          ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                              LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                        sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 99:312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436
                                                                        576
                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                                                                                                                                      276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                     167
                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
```

FINAL DE LOS

w21805;
23-SEP-1997 (first entry)
Spliced-deleted interferon alpha-receptor form
Interferon alpha-receptor; IFNAR.

Key

Location/Qualifiers
1. .427

Homo sapiens.

seq\_name: A\_Geneseq\_36:W21805

\_documentation\_block:

W21805 standard; Protein; 434 AA.

```
1227
                                                                                                                                                   1177
                                                                                                                                                                                                      1127
                        1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                  1077
                                                                                                                                                                                                                                                                                               1027
                                                                                                                                                                             367
                                                                                           401
                                                                                                                               384 leileGluLysLysThrAspValThrValProAsnLeuLysProLeuThr
                                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                                        334
                                                                                                                                                                                                                                                                                                                   317
                                                                                                                                                                                                                                                                                                                                        977
                                                                                                                                                                                                                                                                                                                                                                                     927
                                                                                                                                                                                                                                                                                                                                                                                                         284
                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217
hrSerLys
                                         ValTyrCysLeuLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy, 417.
                                                                                                   GTATATTGTGTGAAAGCCAGAGCACCACCATGGATGAAAAGCTGAATAA, 1276
                                                                                                                                                TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                               TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC
                                                                                                                                                                                                                                                                                                                                                           AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA
                                                                                                                                                                                                     GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                         ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yrSerArgH1sLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                 GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oValHisCysIleLysThrThrValGluAsnGluLeuProProFluA
                                                                                                                                                                                                                                                                                                                  eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snIleGluValSerValGlnAsnGlnAsnTyrLeuLeuLysTrpAspTyr
   436
                                                                                                                                   400
                                                                                                                                                                                384
                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                             1076
                                                                                                                                                                                                                                                                                                                                       1026
                                                                                                                                                                                                                                                                                                                                                              317
                                                                                                                                                                                                                                                                                                                                                                                  976
                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                              926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             726
                                                                                                                                                                                                                            367
                                                                                                                                                                                                                                                                                                                 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                    284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676
```

```
alignment_scores:
Quality: 2260.00
Ratio: 5.305
Percent Similarity: 99.766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1 x W21805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: W21805 from: 1 to: 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (W21805) is characterised by a new domain (S) which follows an end-deleted extracellular domain when compared to transmembranal IFNAR (W21804). There is no transmembrane domain. The amino acid sequence is predicted from a cDNA clone (see also T73520) obtd. from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 and 2 (see also W21806) probably regulate the response of human cells to IFNs, either by acting as IFN antagonists or by regulating the activity of the multiple IFN subtypes. They can be expressed in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms, or for diagnostic purposes.
101
                                                                                                                                                                                                                                                                                                  227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                            277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibiting, modulating or modifying the activities Example 2; Fig 7; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEDA ) YEDA RES & DEV CO LTD.
ABRA/) ABRAMOVICH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl 17
                                                                                          ANATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                  ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                        AGGAGCGATGAGTCTGTCGGGAATGTGÄCTTTTCÄTTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                InLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , 95-2005-9/2/.
mammalian soluble interferon alpha-receptor forms
madifying the activities of
                                                   TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                                                                        sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splice-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratovitski E, Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon alpha-receptor (IFNAR) form 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 99.766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ino acids 1-427 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - used for
interferon(s)
                                                                                                                                                                                                                                                                                                                                                                                                             226
                                                                                               117
                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
```

$\mathcal{Z}_{t}$ .																	
1277 417	1227	1177 384	1127 367	1077 351	1027 334	977 317	927 301	877 284	827 267	777 251	727 234	677 217	627 201	577 184	527 167	477 151	427 134
AAGCAGTGTTTTTAGTGAGGCTGTATGTGAG 1307	ACACACC	AAAAACTGATGTTACAGTTCCTAATT 	GATTTANGAAATTATTTTTTTGGGAAAACACTTCAAANGCTGAGAGAA 	GTTCTCCAAAACAGTCTGGAAACAGGCTGTGATCCAGGATTATCCACT	CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC	TIGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC	GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA 	AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 	AAGGAATCCTGGAAACCATTTGTATAAATGGAAAC	ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTÄAA	/ ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 	AGTACATTGTATAAAGACCACAGTTGAAAATGAA 	7 AAAGTTAAAGCAGCACTACTTACGTCATGĞAAAATTGGTGTCTATAGTC 	ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACCTACTTATTGTCTA	ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT	7 AAAGATAGTGTTATGTGGGCTTTGGÅTGGTTTAAGCTTTÄCATATAGGTT 	7 ATTTÄGAAGCTGAAGATAAGCCAATAGTGATACACATCTCTCCTGGAACA 
	1276	1226	A 1176   I 384	1126 367	1076	1026	r 976   n 317	1 926 300	3 876	826   826   267	r 776	726 1 1 234	C 676	A 626	r 576 l r 184	T 526	A 476

```
alignment_block:
US-09-240-675-1 x-w21806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: W21806 from: Il to: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intracellular domain. There is no transmembrane region. The amino acid sequence is predicted from a cDNA clone (see also T7352) obtd from human myeloma U266 cells. Soluble, non-membrane bound IFNAR splice-deleted forms 1 (see also W21805) and 2 may regulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1997 (first entry)
Spliced-deleted interferon
                                                                                                                                                                             127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in host cells and used to inhibit, modulate or modify the activities of IFNs alpha and beta in cells, tissues and organisms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response of human cells to IFNs, either by acting as antagonists or by regulating IFN activities. They can host cells and used to inhibit, modulate or modify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shortened by 6 amino acid residues and is followed by a truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting, modulating or modifying 
Example 3; Fig 7; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apramovich C, Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    √21806 standard;
        67
                                                                                                                                                    34 lnLysValGluValAsplielleAspAspAspAsnPheileLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iPI; 95-200634/2/.
New mammalian soluble interferon alpha-receptor forms -
interferon the activities of ir
                                                                                                                                                                                                                                                                                                                                                            27 ATGATGGTCGTCCTCGGGCGCGACGACCCTÄGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interferon alpha-receptor;
                                                                                                                                                                                                                                                           77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCTCCTC 126
sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                          AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                       MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl 17
                                                                                ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                     AGGAGCGATGAGTCTGTCGGGAATGTGAČTTTTTČATTCĞATTATCAAA 226
                                                                                                                                                                                                                                       yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l splice-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 2208:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is characterised by a double deletion when compared to branal IFNAR (W21804). The extracellular domain is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratovitski E, Revel M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "comprises amino acids 481-557 of transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.282
97:892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label - Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ote= "comprises amino acid residues 1-413 and 2-427 of transmembranal IFNAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abel- Intratellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon alpha-receptor (IFNAR) form 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctivities. They can be modulate or modify the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interferon(s)
      84
                                                                                  67
                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used for
```

1176 384	1127 GATTTATGAAATTATTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA	
1126 367		
1076 350	ACATTAGATCCCTTÁGTGATTCÁTTCCATATCTATÁTC 	
1026 334	TACAAGCTTTCCTACTTC	
976 317	AAATAACACATĈITT 	
926	CCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 	
876 284	827 AAGGAATCCTGGAAACCATTTGTATAATGGAAACAAATACCTGACTGTG	
826	ATĞCAAACATĞACCTTTCAAĞTTCAGTGGC 	
776 250	727 ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 	
726 234	TTGAAAA         alGluas	
676 217	627 AAAGTTAÄAGCAGCACTACTTACGTČATGGAAAATTGGTGTCTATAGTCC 	
626 200	577 ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA	
576 184	CTTCAGGTGTAGAAGAAAGGATTGAAAATATTT 	
526 167	477 AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT 	
476 <sub>.</sub> 150	ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA	
426 134	GCAAAGCTCAGATTGGTCCTCCAGAAGTAC 	
376 117	NTTGCGTNTAAGAGCAGAAAAAGAAAACACTTCTTCATGGTNTGAGGT 	
326 ·	GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAATTT	

08

259 52 209

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: A_Geneseq_36:W52296
                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 60.268
                                                                                                                                                                                                                                                                                                                          US-09-240-675-1 x W52296
        159 123 11 ...... CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1997; U12455.
17-JUL-1996; US-683743.
(UYNE-) UNIV NEW JERSEY.
KOTENIKO SV, Pestka S;
WPI; 98-110590/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1277 AAGCAGTGTTTTTAGTGACGCTGTATGTGAG 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1227 GTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             measure and localise CRBF4, for diagnosis of derective in the measure and localise CRBF4, for diagnosis of derective in the measure and localise CRBF4, for diagnosis of probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes to assay CRFB4-specific Fragments of (I) are used as primers or probes of (I) are used as primers or probes of (I) are used as primers or probes of (I) are used as primers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection, as vaccine adjuvants, for treatment of photosensitivity, inflammation, autoimmune disease and septic shock, while antagonists are potentially useful for increasing immune responses against tumours, viruses, bacteria and parasites (especially intracellular pathogens) and for preventing organ rejection: A vector containing (I) is used to restore, e.g. by gene therapy, II-10 sensitivity to a cell that expresses a dysfunctional IIIOR and is able to bind II-10 but not to transduce a signal. Antisense CRFB4 sequences (especially ribozymes), can inhibit II-10 activity in cells. Antibodies specific for CRFB4 are used to measure and localise CRBF4, for diagnosis of defective II-10 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2) encoding CREM4, both operably linked to expression control sequences. Cells containing (I) may be used to identify agonists/antagonist of IL-10. Agonists are potentially useful, e.g. for preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRFB4 protein.
CRFB4; interle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 lelleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and CRFB4 linked to operator, useful, e.g. preventing allograft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human CRFB4 sequence, recombinant DNA (I) of the invention (I)
                                                                                                                                                         81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eptic shock; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laim 2; Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant DNA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValTyrCysValLysAlaArgAlaH1sThrMetAspGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                    TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin-10; IL-10; IL-10 receptor; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                photosensitivity; inflammation;
                                                                                                                                                                                                                             to: W52296, from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228.50
                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 29.91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linked to expression control sequences.
sed to identify agonists/antagonist of
useful, e.g. for preventing allograft
                                                                                                                                                                                                                                              to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding it is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413
                        1100000
                                                                                                                                                             꼽끕
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: A_Geneseq_36:R75782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh
W09516036-A.
15-JUN-1995.
07-DEC-1994; U14277.
                                                                                                                                                                                                                                                                                                              domain:
                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 GATTGGTCCTCCAGAAGTACATTTAGAAGCT...GAAGATAAGGCAATAG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310
                                                                                                                                                             domain
                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R75782 standard; Protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 GATGGTTTA.....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 ACTICITCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 TCATTCGATTATCAAAAAACTGGGATGGATAAATTGGATAAAATTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interferon-gamma receptor beta subunit; muIFN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFN-gamma receptor beta-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interferon-gamma-antagonist:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 ThrAlaGlnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 yMetValProProFroGluAsnValArgMetAsnSerValAsnPheLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATRAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rThrHisAspGluThrValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTACGTCATGGAMAATTGGTGTCTATAGTCCAGTACATTGTATMAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATACACATCTCCCTGGAACAAAAGATAGTGTT...ATGTGGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elleGlyProProGlyMetGlnValGluValLeuAlaAspSerLeuHisM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet
                                                                                                                    267. .3:
/label=
                                                                                                                                                                                                                                     243 . . 266 .
                                                                                                                                                                                                                                                                  /label-
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                 label-
                                                                                                                                                                                                                                                                                                                                                  label- Sig_peptide
                                                                                                                                                                                                                                 Extracelular domain
                                                                                                                    Cytoplasmic_domain
                                                                                                                                                                                         Transmembrane_anchoring_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .LeuSerTyrArgIlePheGlnAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   produce the second second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . .
                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36
```

694 195 644 179 594 162 544 145 500 129

```
SCCCCCCPPT PAR PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 203.00
Ratio: 1.471
Percent Similarity: 60.262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: R75782 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-240-675-1 x R75782
                                                                                                                                                                                                                                                                                                                                                                                              336 ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel interferon gamma receptor beta chain polypeptide - for treatment of inflammatory bowel disease and liver damage Claim 3; Fig. 2A; 86pp; English.

The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGUE/) AGUET M.
(BOEH/) BOEHNI R
(HEMM/) HEMMI S.
171 sTyrTrpGluLysSerGluThrGlnGlnGlnGlnValGluGlyProPheL 188
                                                                                          160
                                                                                                                                                                                                                                                                                                       383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT
                                                                                                                                                                                                                                                                                                                                                        110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from mouse B-cells is given in R75782. Recombinant be pref. with the transmembrane anchoring domain deleted inactivated and with the cytoplasmic domain deleted, may be used to treat pathological conditions associate may be used to treat pathological conditions.
                                         480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 ACAGGAGCGATGAGTCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFN-gamma production 
Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q90808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aguet M, `Boehni F
WPI; 95-224321/29.
                                                                                                                                                                                                                                                             126 oPheGlnH1sTyrGluAsnValThrValGlyProProLysAsnIleSerV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                              93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr 32
                                                                                                                         GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTCATTCGATTATCAAAAACTGGGATGGAT...AATTGGATAAAATT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                                                                                                      TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrSerPhe......IleAspGlySerTrpHisArgLe 76
                                                                                                                                                                            alThrProGlyLysGlySerLeuValIleH1sPheSerProProPheAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oLeuAsnProArgLeuH1sLeuTyrAsnAspGluGlnIleLeuThrTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCC 124
                                                                                      .....ValPheHisGlyAlaThrPheGlnTyrLeuValHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boehn1 R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-164596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hemm!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 13
Percent Identity: 30.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions associated with endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGGGAATGTGACT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-subunit,
                                                                                                                                                                                                                                                                                                            429
                                                                                                                                                                                                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
```

alignment\_block:

Ratio: 0.908
Percent Similarity: 50.346

Gaps: 17
Percent Identity: 21.016

Length:

can

Quality: 198.00

US-09-240-675-1 x W79159

·

Align seg 1/1 to: W79159 from: 1

6

18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 57 CIAGIGCICGICGCCGIGGGCCCAIGG.....GIGITGICCGCAGCCGC

34

alignment\_scores:

```
seq_name: A_Geneseq_36:W79159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _documentation_block :
                                                                                                                             binding receptor polypeptide and is a novel member of the type 2 cytokin receptor. family (CRF2). An expression vector containing the Zcytor polynucleotide, operably linked to transcription promoter, a sequence encoding a transmembrane and intracellular domain, or both, and a transcriptional terminator can be used to transform host cells for the recombinant production of the polypeptide. The sequences can be used to study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is
Sequence
                                    preferentially expressed in the kidney, pancreas, prostate or nervous tissue. Agonists of Zcytor? can be used to stimulate prolliferation and differentiation of cell in these organs. The antagonists and agonists or also be used in the treatment of renal, neural, pancreatic and prostate
                                                                                                                                                                                                                                                                                    for treating renal, neural, pancreatic and prostatic diseases Claim 1; Pages 55-59; 72pp; English.
This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-
                                                                                                                                                                                                                                                                                                                                                                                                                Adams RL, Farrah TM, Jelmberg AC, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20'Nov'-1970

ZCYTOT? cytokine receptor polypeptide.

ZCYTOT?; cytokine receptor: ligand-binding polypeptide; kidney; pancreas;

ZCYTOT?; cytokine receptor: CRF2; prostate tissue; nervous tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 ... GGTGTCTATAGTCCAGTACATTGTATAAAGACCACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  624 CTAAAAGTTAAAGCAGCACTA...CTTACGTCATGGAAAATT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 CCAGACATAAAATTTAT.....AAACTCTCACCAGAGACTACTTATTGT
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; V5751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type 2 cytokine receptor family; CRF2; prostate tis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W79159 standard; Protein; 553 AA.
                                                                                                                                                                                                                                                                                                                                                    Novel human Zcytor7
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 98-480798/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1998; U03029.
02-OCT-1997; US-943087.
20-FEB-1997; US-803305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO9837193-A1
                                                                                                                                                                                                                                                                                                                                  or treating renal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural disease; pancreatic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-1998 (first entry)
  553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "extracellular (ligand-binding) domain;
sequence claimed in claim 1"
275. .553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "intracellular domain"
                                                                                                                                                                                                                                                                                                                                DNA encodes a type
neural, pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kho CJ, Lok S,
                                                                                                                                                                                                                                                                                                                                2 cytokine receptor - useful and prostatic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    662
                                                                                                                                                                                                                                                             2 cytokine
```

923 AAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACAT 972	290LeuIleTyrGlyAsnGlupheAs 297	281 ysGluLysHisproAlaAsnLeuIle	264 eLeupheSerValMetGlyTyrSerIleTyrArgTyrIleHisValGlyL 281 823 TAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGAC 872	775 TACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTT 822	erGluPheLysAlaLysIleIlePheTrpTyrValLeuPro	662 TGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA. 710 :::::::::::::::::::::::::::::::::::	612 ACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAAT 661 	568 AAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAG 611       :::       :::       :::       :::       :::       :::         :::         :::         :::         :::           :::	518 ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG 567	480GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC 517	445 AGGCAATAGTGATACACATCTCTCCTGGAACAAAA	395 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA 444	345 GAAAAAGAAAACACTICTTCATGGTATGAGGTTGACTCATTTACACCATT 394 :::    :::        116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh 132	298 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA 344 99 laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaile 115	248 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297 ::::	198 AATGTGACTTTTTCATTCGATTATCAAAAAACTGGGATGGAT	151 ATGACAACTTTATCCTGAGGTGGAACAGGAGGGATGAGTCTGTCGGG 197 ::::::::::::::::::::::::::::::::::::	101 AGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150 :          :::    ::::: 34 rGlyGlyLeuProLysProAlaAsnIleThrPheLeuSerIleA 49
State of the state																		
25 pProLeuSerGlnLeuProAl	108	60 GIGGICGCCGIGGGCCCA :::   :::: :::    9 LeuLeuLeuLeuLeuGlyVal	US-09-240-675-1 x R71035 Align seg 1/1 to: R71035	Quality: Ratio: Percent Similarity: alignment_block:	SQ Sequence 337 alignment_scores:		DR N-ESDS; Q84697.  DR N-ESDS; Q84697.  To Suppressing tumours in map PT for interferon gamma, spe PT antigens, including use of	JR, Don	PN W09505847-A. PN W09505847-A. PD 02-MAR-1995. PE 22-AUG-1994; U09438. PR 20-AUG-1994 PR- 20-AUG-1993	11-00 Human Inter	seq_name: A_cemeseq_so: x/1035 seq_documentation_block: ID R71035 standard; Protein, AC B71035.	5 · · b				327 MetSerLeuLeuGlyLysSe		

Align seg 1/1 to: R71035 from: 1 to: 337

25 pProLeuSerGinLeuProAlaProGinHisProLysIleArgLeuTyrA 42

108 .....AAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150

: •				
280000 20000	POS	Sed Sed		
igens, including use of AF-1 DNA in gene therapy closure; Fig 21A; 114pp; English. sequence is that of human interferon-gamma accessory orporation of AF-1 into immune and tumour cells re-esmal function with elimination of mallgnant cells. mal function AF-1 into immune and tumour cells.	Homo saplens.  Homo saplens.  W09505847-A.  02-MAR-1995.  22-AUG-1994; U09438.  20-AUG-1993; US-110119.  (UYNE-) UNIV NEW JERSEY.  COOK JR, Donnely RJ, Emanuel S, Kotenko S, Mariano TM;  Pestka S, Schwartz B, Soh J;  WPI; 95-106679/14.  N-PSDB; 084697.  Suppressing tumours in mammals with accessory factor 1 (AF-1) for interferon gamma, specifically induction of class I HIA	385 nGluSerLeuSerArgThri q_name: A_Geneseq_36:R71035 q_documentation_block: R71035 standard; Protein R71035 (first entr 11-OCT-1995 (first entr	<b>⊢</b>	297 pLysargPhePheValProAlaGluLysIleValIleA 310 973 CTTTTTGGTCTGAAGATAAAGTTTGATACTGAAATACAA 1013 :::   :::
<b></b>		•		•

σ.	259 uSerValL 757 ATGTTCTT	744	711 CTACCTCC	و	я и — н		529 TTATCTGG:         18 1sTyrTrp	179 AGATAGTG	35GC:	88 CACCATTY:::: 33 lnHisTyr	41 AGCAGAAA         16 galaGluL	00 04 GlyPhePro	87 hrGlnile	74		
eulleLysTyrTrpPheHisThrProProSerlleProLeuGlnileGlu	uServalleuAlaGlyAlaCysPhePheLeuValle		CTACCTCCACCAGAAAATATAGAAGTCAGTGTC. :::    :::        ThrGluLeuGlnGlnValI  eLeuIleSerValG	I   I   I   I   I   I   I   I   I   I	AAAAGTTAAAGCAGCACTACTTAGGTCA.  :::  :::    :::   :::    ::::    ::::    ::::    ::::    :::    :::	TCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTG ::::::!   :::   :::    argSerAsnSerIleSerLeuAspAsnLeuLysProSerArgValTyrCy	TTATCTGGAAAAACTCTTCAGGTG       ::: ::        styrtrpGluLysGlyG	TGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTAC ::::     :::        ::: pThrSerThrAlaphe	GCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAA :::    ::    ::: GlyGluGlySerLeuIleIleArgPheSerSerProPheAspIl	TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAA :   :::::: rargasnyalthryalGlyproproGluasnileGlu	AGAAAAAGAAAACACTTCTT          aGluLeuGlyAlaLeuHisSerA	CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCG !!! yPheProMetaspPheasnValThrLeuar	TACTAGTACCAAATGCAACTTTTCTTCA     :::   :::   :::   eThrAlaThrGluCysA%pPheThrAla	GATGGATAATTGGATAAAATTGTC     ::: 	GATGAGTCTGTCGGGAATGTGAC      ::::   ArgProValValTyrGlnValGl	ATGACAACTTTATCCTGAGGTGG :: ::         snAlaGluGlnValLeuSerTrp
ThrProProSer	ysPhePheLeuV ACATATGCAAAC		AGAAGTCAGTGT   :::        eLeuIleSerVa	SerCysTyrGlu	AGCAGCACTACTTACGTCA	AAACTCTC :::   :: uAspAsnLeuLy	GGTGTAGAAGAA         	TGGATGGTTTAA :: he	AATAGTGATACACATCT    :::   ullelleargPheSerS	ATTGGTCCTCCAGAA :::            ValGlyProProGlu	TCTTCATGGT    :::     sSerAlaTrpV	FGTTTATGAAGA       Val	rGCAACTTTTCT    :::   :::  ysamppheThr	TGTCT ;;; LaAspIleMetS	ACTITITCATI	TGG     TrpGluProValAlaLeuSe
::: V::::   :   IleProLeuGlnI	alLeuLysTyrA ATGACCTTTCAA	САВАНСАСАВАСТ	C     IGlyThrPheSer	ThrMetAlaAsp	ysSerAsnIleF	ACCAGAGACTACTTAT :   ::: :::    sProSerArgValTyr	TCAGGTGTAGAAGAAAGGATTGAAAATATTTAT :::    LysGlyGlyIleGlnGlnValLysGlyProPhe	GCTTTACATATAGCTTAC	CATCTCTCCTGG        eSerSerProPh	GAAGTACATTTAGAA     ::::::      GluAsnIleGluVal	CATGGTATGAGGTTGACTCATTTA ::    laTrpValThrMetProTrpPheG	AATTAAATTGCGT	TCA ::: AlaAlaSerProS	leGlyval	CTTTTCATTCGATTATCAAAAAACTG    ::::::  nPheLysTyrThrAspSerLys	: H
29	ArgGlyL 276 AGTTCAG 806	AGAACT 756	743 rLeuLe 259	P::} - 2	\$ : \$	TTATTG 622 11111 1174 Cy 209	Prophe 192	GCTTAC 528 ::: YrValH 178	GGAACAAA 478 PheAspIl 165	GAA 434      GluVal 148	ACTCATTTA 387	TATAAG 340   :::    gLeuAr 116	299 SerAla 103	GGGTGTC 264 :::    AsnCysT 87	AACTGG .232	ਂ.ਮ ∙ U
٠.			·				•									

```
Database: Issued_Patents_AA:*
Database sequences: 145308
Database length: 14437401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query: US-09-240-675-1
Query length: 1343
Database: Issued_Patents_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        About: Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: Jun 1, 2000 5:44 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM of: US-09-240-675-1 to: Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search time (sec): 45.740000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgn2_6/ptodata/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -Q-/cgn2_1/USPTO_Spoo1/US09240675/runat_30052000_165118_2973/app_query.fasta.-DB-ISSUed_Patents_AA.-QPMT-fastan-SUFFIX-mod1f_ra1
-GAPOP=12.000 -GAPEXT-4.000 -MINAMCCH-0.100 -LOOPCL-0.000
-LOOPEXT-0.000 -QGAPOP-4.500 -QGAPEXT-0.500 -XGAPOP-10.000
-XGAPEXT-0.500 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000
-XGAPEXT-0.500 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
-MATRIX-blosum62 -TARANS-human40.cdi -LIST-45 -DOCALIGN-200
-THK_SCORE-pct -ALICN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext
-MINLEN-0 -MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODEL-frame+_n2p.model -DEV-xlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ptodata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /5B_COMB.pep:US-08-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -11 + 2265.00 4437.87

-12 + 2213.00 4333.79

1277-3 + 490.50 946.5

1277-4 + 466.50 899.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   version 4.5
                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 8e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9e-43
                                                                                                                                                                                                                           Align seg 1/1 to: US-08-307-588-2 from: 1
                                                                                                             27 ATGATGGTCGTCCTGCGCCGACGACCCTAGTGCTCGTCGCCCGTGGG
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                        77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
```

```
alignment_block:
US-09-240-675-1 x US-08-307-588-2
                                                                                                                                                                                                         # MOLECULE TYPE: protein
US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US93-11110-1
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-469-537A-103 +
/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-424-788-2 + 1
/cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-110-683-4 + 1
                                                   Percent Similarity: 100.000
                                                                                                                                                                                                                                                 TELEPHONE: (202)672-5300
TELEFAX: (202)672-399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,588
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
POLICATION DATA:
POLICATION DATA:
POLICATION DATA:
POLICATION DATA:
APPLICATION DATA:
10-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 92400902.0
FILING DATE: 31-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, BETNATO D.
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 17283/117/
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PLAVEC, Ivan
APPLICANT: TOVEY, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MEYER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K St
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TE: D.C.
20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3000 K Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGUIRE, Deborah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BENOIT, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lcation US/08307588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERFERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MONOCLONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/EP93/00770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N. W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   17283/117/GUPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WITH NEUTRALIZING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite
                                                                   Identity: 100.000
                                                                                                    Length: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210.58 3.6e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0002
```

to: 436

ω 4

1000

```
377 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 isLeuGluAlaGluAspLysAlaIleValIlleHisIleSerProGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
                                                                                                                                                                                                                                                                                        251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                       217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                                                                                                                                                          AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                                                                                                                                                           ACATATGCAAACATGÂCCTTTCAAGTTCAGTGGCTCCAČĞCCTTTTTAAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTCCAGACATAAAATTTATAAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysaspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                           uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGATAGTGTTATGTGGGCTTTTGGATGGTTTAAGCTTTACATATAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAÁAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                   TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                     GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                         GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT 976
                                                                                                                                                                             AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                                                                                                                                 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                    876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
 334
                                                                       317
                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                  284
                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                    TELEX: 248633
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1077 GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT
                                                                                                                                                                          APPLICATION NUMBER: IL 107378 FILING DATE: 24-OCT-1993 ATTORNEY/AGENT INFORMATION: NAME: BROWDY, Roger L.
                                                                                                          REGISTRATION NUMBER: REVEL-
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: REVEL, Michel
APPLICANT: ABRAMOVICH, CAROlina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                                                              FILING DATE: 24-OCT-
                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 hrSerLys 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
                                                                           TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTATATTGTGTGAAAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCAGTCTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H: 557 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 Seventh Street,
                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROWDY AND NEIMARK
9 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                             10MBER: US/08/328,256
24-OCT-1994
                                                                                                                                                                                                                                                                                                                    Release #1.0,
                                                                                                                                                          REVEL-13
                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367
```

MOLECULE TYPE:

STRANDEDNESS: single

linear

CARGO CARGO

US-08-328-256-10

```
alignment_block:
US-09-240-675-1 x US-08-328-256-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 2313.00
Ratio: 5.305
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-328-256-10 from: 1 to: 557
                                                                                                                                                                                                                                                                                                           477. AAAGATAGTGTTATGTGGGCTTTTGGATGGTTTAAGCTTTACATATAGCTT
                                                                                                                                                                                                                                                                                                                                                              427 ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                   167 uLeuIleTrpLysAsnSerSerGlyValGluArgIleGluAsnIleT
                                                                                                                                                                                                                                                                     527
                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                               134 isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                         377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                          727
                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                   ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                           LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                           ATTCCAGACATAAAATTTATAAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snIleGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr
                                       ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                       TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACTGGGATGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGATGGTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436
             250
                                                                                             726
                                                                                                                                                     676
                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                576
                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                     526
                                                                                                                                                                                                                                                                                                                                                    150
                                                                                                                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                   234
                                                                                                                         217
                                                                                                                                                                               200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
以外主か的主製品の
```

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-471-454-2
                                                                                                                                                                                                                                          Sequence, 2. Application US/08471454

Patent, No. 5731169

GEMERAL, INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: UZE, Gilles
APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
COMPUTER: IBM PC compi
COMPUTER: IBM PC compi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1277 AAGCAGTGTTTTTAGTGACGCTGTGTGAGAAAACAAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1027
                                                                                                                                  ADDRESSE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY NALINGFON
STATE VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 lelleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 roProValPheAsnileArgSerLeuSerAspSerPheHisileTyrile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              977 TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        927 GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GlyTleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLy
                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrSerLys 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ulleTyrGlulleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luAsnValLysThrThrGinCysValPheProGlnAsnValPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08471454
                                                                                                                                                                                                                            2 Mary State State S
                                                                                                                                                造がたり、というと
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 大学の大学の大学を大学を
                                                                                                                                                                                    384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       826
```

disk

```
alignment_block:
US-09-240-675-1 x US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-471-454-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 5.305
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200797 NIXN UR
NFORMATION FOR SEQ ID NO:
                                                                                   117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH 134
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                           427 ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                 277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 15
134 isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
                                                                                                                                                                                                                                                                                                                                                                                                            227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77. CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BYRNE, THOMAS E. REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                  TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                           AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                                                      erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                 sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 2313.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FR 89/13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/471,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
```

No.

		•		. ,		•			
13 13	12 12 4	. 11 3 11	10 3 10	92. 97. 97. 31.	N & N &	2 7 2 7	<b>N 5 N 5</b>	<b>н</b> и н и	` ہے ہر
27 CC	27 G 101 V 277 A 117 S	27 G 67 u 77 T	27 C	4 4 H 4	127 A 167 S 1777 A 184 L	27 AT 11 234 Sn 777 AC 11 551 Th	627 A 201 L 677 A 217 o	27 AC       67 UL 77 AT       84 Yr	77 AA     51 Ly
: <u>8</u> <u> </u>	GTATATAT	GATTI	CTCCA IIIII FORTO GGIGCI GIYALI	GGAAT       GlyII TIGGT       eTrpS	AGGA FILL Arga AAAT HILL WASN	ATATAGAAĞ           snileGluV            	Value Ys	TTA TCC	
raaa 1      cLys 4	rigic rcysv grgij	ITATGAAATTI 	GTCT	ATTTÀCCTTCI 	ATCC: SnPro SnPro GTCAL []]]	GAAG:	AGTTAAA(	PATCTGGAA	AGATAGTGT
136	TTTAA	ATTA HILL HILL HILL HAAAA HILL SLys	TAAC HEAST NAACA JIII	GAGA	GGAJ G1yJ S1yJ NAACI	CAGT	CAGC	GAAAAAC          PLYSASD   ATAAAAT 	TTAT
	AGCC       SAla       	Thra	ATTA             I   eA                         n Ser	CCGC	ACCA IIII SnHi ACCC	Valc GACC HILL TIME	ACTA      aLeu aGAC      ysTh	ACTCT        snSer  ATTTA 	tirp 
	AGAGO Arga: Arga: CGCTO PAla	TTGGG HHIH ETTP ATGT HHIH SPVA	GATC	GTAC	SLeu BLeu AGTG	AAAA             InAs   TTTC             PheG	CTTA LeuT	TTCA(	GCTT
٠.	CACAC [       aHis  aHis         valcy	rigggaaacı 	CTCLAGTCTTTAACATTAGATCCCTTAGT	AAGCI       nAla  nAla GATAC       AspTI	TATA	rcaga         Glna    AAGTT	CGTC	GGTGT G1yVa ACTCT	GTGGGCTTTGGATGG              TrpAlaLeuAspGl
<i>,</i>	GTATATTGTGTĞAAAĞCCAĞAĞCACAĞĞATGATGATAAĞCTĞAATAAİIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TATGAAATĀTTTTTTGGAAĀĀCACTTCĀĀATĞCTGAGĀĀĀAA 	AGTCTTTAACATTAGAŤCCCTTAGTGATTCCATATCCATATCCATATCCATATCCATTAACATTAACATTAACATTCCATTAACATTCCATTAACATTCCATTAACATTCCATTAACATTCCATCCATATCCATCCATAACAAC	GGAATTTÄČCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT	AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG	ATATAGAAÓTCAGTGICCAAAATCAGAACTATGTTCTTAAATGGGATTAT	GTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAG	TCTGGAAAAACTCTTCAGGTGTAGAAGAAAGAATGAATATATTT	ATGGTT
	TGGA       etas  aaaa 	TAAT OASD	GATTCATTCCATATCTATATC 	ATAC	AAAC       Lysg   CAA 	TOTT	AAAT      ysil GAAC 	GAAA        GluA        AGAG 	TTTAAGCT           yLeuSer
• • •	TGAA       pGlu CAAA      hrLy	ATGC       snall	Phen CCAG IIII	AAAT IIII YASD AAGC IIIII	AAAT lull lall AACG llll Asnv	CCAC LeuL CCAC LILI	TGGT      eGly eGly euPr	GGAT	CTTT
. 6	AAGC:	IGAGAG          aGluar  AACCAC 	ATATO	AACAC      	ACCTO	AATG	X-00	IGAAAAT          CTTATTG 	CTTTACATATI            PheThrTyr:
•	rGAAT	3AGAĞAĞAAA 	TATA	càici IIIII Draci IIIIII	SACTO ASPCY CCAAL	3GAT1	TATAGT	ATAI IIIII ASDIII TTGTC	ATAGC        YrSer
•					•		E-B P-C		10 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1
	1276 417 1326 434	1176 384 1226 400	1076 350° 1126	976 317 1026 334	876 284 926 300	776 250 826 267	676 217 726 234	576 184 626 200	526 167
					•			•	

seq\_name: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:US-08-466-974-2

```
alignment_scores:
                                                                                                                                                                                                                                                   US-09-240-675-1 x US-08-466-974-2
                                                                                                                                                                                                                  Align seg 1/1 to: US-08-466-974-2
                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992
                                                                                                77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                         MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ication US/08466974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR 89/13770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/466,974
                                                                                                                                                                                                                                                                                                                    Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND PROCESS FOR THE
                                                           34
```

126

```
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1077
                                                                                                        NFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTID Release #1.0, V
CURRENT APPLICATION DATA: 3
APPLICATION NUMBER: US/08/471,453
FILLING DATE: 06-UN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-JUN-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 96
ELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C
                                                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION: NAME: BYRNE, THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: (FILING DATE: 15-JUN-1APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION:
         STRANDEDNESS:
                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lelleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uIleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hrSerLys 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRGINIA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1100 NORTH GLEBE ROAD
                                               557 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UZE, Gilles
LUTFALLA, Georges
GRESSER, Ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOGENSEN, Knud E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ication US/08471453
                                                                                                                                                                                                                                                                     THOMAS E.
                                                                                                                                                                                                                                                                                                                     20-OCT-1989
    single.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA FRAGMENT CODING FOR THE GENE FOR THE ALPHA INTERFERON RECEPTOR AND PROCESS PREPARATION OF THE CORRESPONDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                         US 07/900,642
                                                                                                                                                                                                                                                                                                                                         FR 89/13770
                                                                                                                                                                                                                                                                                                                                                                       1992
                                                                                                                                                                                                                                                                                                                                                                                                                      ".
".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           '...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOR THE
         第十四四十四百八四十二十
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-240-675-1 x US-08-471-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-471-453-2 from:
                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                  577
727. ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT
                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                               527 ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  477 AAAGATÄGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 GTACCAAAIGCAACTTTTCTTCACTCAAGCTGAAIGTTTATGAAGAAAIT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1
                                                                                                 AGTACĂTTGTATĂAĀGACCACAGTTGĀAĀATGAACTACCTCCACCAGĀAĀ
                                                                                                                                                                    LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                 ANAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
                                                                                                                                                                                                                                                                   yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                                                                      ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA
                                                                                                                                                                                                                                                                                                                                                               uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uality: 2313.00
Ratio: 5.305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
```

676

217

234

626

200

576

167 526

184

150

134

426

117

67

84

50 176 34

```
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _documentation_block: The land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land to the land
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1277 AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PLAYEC, IVAN
APPLICANT: TOVET MICHAEL G.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON
TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST
TITLE OF INVENTION: INTERFERON
TITLE OF INVENTION: INTERFERON
TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1227 GTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1177 TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 uTleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1127 GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT BENOT Patrick
APPLICANT MEYER, Francois
APPLICANT MACUIRE, Deborah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927 GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     827 AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777 ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     877 AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLy 267
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 snīleGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hrSerLys 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle 350
                                                                                                                                                                            20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ation_block: The hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the hard of the h
                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                              3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGUIRE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foley's Lardner Care Land Control of Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WITH NEUTRALIZING ACTIVITY AGAINST TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-240-675-1 x US-08-307-588-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 100.000
                                                                                            377 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                            7277 GIACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                           点语言 SThrGlyMetAspAspTrpIleLysLeuSerGlyCysGlnAsnIleThrS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 InLysyalGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                327 AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 2313:00
                                                                                                                                                                                                                                                                                                                                              227 AACTGGGATGGATAATTGGATAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27, AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 557 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                             51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27. ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/EP93/00770 FILING DATE: 30-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/307,588 FILING DATE: 05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 92400902.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAXE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (202)672-5399
                                                                                                                                                                                                 sAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 100.000
                                                426
                                                                                                 117
                                                                                                                                                                                                 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
```

427 ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476

/cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:US-08-328-256-11

```
1127 GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1077 GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                                                                                                                                                                                                                                  1177. TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT. 1226-
                                                                                                                                                                                                                                                                                                                                          384 leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                               367. ulleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 SATGASHPTOGLYASHHISLEUTYTLYSTTPLYSGINILEPTOASPCYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    977 TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               927 GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      777 ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTÄAA: 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 snileGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  727 ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe 167
434 hrserLys 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oValHisCysIleLysThrThrValGluAsnGluLeuProProProGluA
                                                                                                                                                       AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                                                               GTATATTGTGTGAAAGCCAGAGCACCACCATGGATGAAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT. 576
                                                                                                                              sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417
                                                                                                                                                                                                                                                                                                                                             400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
```

```
alignment_block:
US-09-240-675-1 x US-08-328-256-11
                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-328-256-11
                                                                                                                                                                                                                                                            Align seg_1/1 to: US-08-328-256-11 from: 1
                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 100.000 Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: REVEL, Michel
APPLICANT: ABRANOVICH, Carolina
APPLICANT: RATOVITSKI, Edward
TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR,
TITLE OF INVENTION: PREPARATION AND USE
177 AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear, orotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/O FILING DATE: 24-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                         127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          27 ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                     34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                               17
                                                                                                                                 77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-628-51
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: REVEL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                         yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG
                                                                                                                                                                                          MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419-Seventh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ication US/08328256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/328, 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25,618
                                                                                                                                                                                                                                                                                                                                                             Length: 427
Gaps: 0
Identity: 100.000
                                                                                                                                                                                                                                                                    to: 434
                                       50
                                                                           176
                                                                                                                 34
                                                                                                                                                      126
                                                                                                                                                                                          17
                                                                                                                                                                                                                              76
```

15 M. W.

```
1077
                                                                                                                                                1027
351 GlyAlaProLysGlnSerGlyAsnThrProVallleGlnAspTyrProLe
                                                                                                             334
                                                                                                                                                                                                                                                            977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                        927
                                                                                                                                                                                                                                                                                                                                                                                                   284 luAsnValLysThrThrGlnCysValPheProGlnAsnValPheGlnLys 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                     877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577 ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527 ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                            CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076
                                                                                                                                                                                                                                                                                          GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sArgAsnProGlyAsnHisLeuTyrLysTrpLysGlnJleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OValHisCysIleLysThrThrValGluAsnGluLeuProProProGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                           GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                           eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP. 334
                                                                                                                                                                                                                              TIGGICIGAAGAGATAAAGITIGATACIGAAATACAAGCITICCTACTIC 1026
                                                                                                                                                                                                                                                                                                                                                 GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysValLysAlaAlaLeuLeuThrSerTrpLysIleGlyValTyrSerPr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                        roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
```

```
CITY: Washington
STATE: D.C.
COUNTRY: USA
2IP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: Patentin Release #1.0, Version #1.
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,256
FILLING DATE: 24-OCT-1994
PRIOR APPLICATION NUMBER: IL 107378
FILING DATE: 24-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGE L.
                 alignment_scores: 0.0 2213.00 Quality: 2213.00
                                                                                                                                            ; MOLECULE TYPE: protein US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-328-256-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
TELEX: 24863
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1227 GTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1277 AAGCAGTGTTTTTAGTGACGCTGTATGTGAG 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1177 TTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1127 GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: REVEL, Michel APPLICANT: ABRAMOVICH, Carolina APPLICANT: RATOVITSKI, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 TelleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 sSerSerValPheSerAspAlaValCysGlu 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 ulleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401: ValTyrCysValLysAlaArgAlaHisThrMetAspGluLysLeuAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITLE OF INVENTION: PREPARATION AND USE
                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: , REVEL-13
REFERENCE/DOCKET NUMBER: 25,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, Application US/08328256 5643749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EE: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
7: 98.126
Percent Identity: 98.126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417
```

Align seg 1/1 to: US-08-328-256-12

from: 1

ë

US-09-240-675-1 x US-08-328-256-12

alignment\_block:

Percent Similarity:

17 77

350

367

413

600

334

317

```
577 ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
  234 snileGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 LysvallysAlaAlaLenLeuThrSerTrpLysIleGlyValTyrSerPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 uLeuIleTrpLysAsnSerSerGlyValGluGluArgIleGluAsnIleT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lnLysValGluValAspIleIleAspAspAsnPheIleLeuArgTrpAsn
                                                                                                                                                                                                                                 ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126
                                                                                                                                                                                                                                                                                                                                                                                                  oValHisCysIleLysThrThrValGluAsnGluLeuProProProGluA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysaspSerValMetTrpalaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCCTCGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erThrLysCysAsnPheSerSerLeuLysLeuAsnValTyrGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValGl
                                                                                                                                                                                      ThrTyrAlaAsnMetThrPheGlnValGlnTrpLeuHisAlaPheLeuLy 267
                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTACATTGTÁTAAAGACCACÁGTTGAAÁATGAACTÁCCTCCACCÁGAAA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yrSerArgHisLysIleTyrLysLeuSerProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sThrGlyMetAspAsnTrpIleLysLeuSerGlyCysGlnAsnIleThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGG
                                                     AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                                              AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG '876
                                                                                                                                                                                                                                                                                                                                    ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTTTTAAATGGGATTAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANAGTTANAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9414277 GENERAL INFORMATION:
                                                   TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: , yevoy
COMPUTER READABLE FORM:
MEDIUM: TYPE: .. 5,25 inch., 360 Kb floppy, disk
COMPUTER: IBM PC compatible
COMPUTER: THE PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1277 AAGCAGTGTTTTTAGTGACGCTGTATGTGAG 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1077 GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT, APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrIle
LENGTH: 202 amino acid
                                                                                                                                                                           FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 866
                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: '08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Aguet, Michel
APPLICANT: Bohn1, Ruth
APPLICANT: Hemm1, Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           977 TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GlyIleTyrLeuLeuArgValGlnAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 460 Point San Bruno Blvd
CITY: South San Brancisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US94/14277 FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValTyrCysValLysAlaArgAlaHisThrMetAspGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leIleGluLysLysThrAspValThrValProAsnLeuLysProLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uIleTyrGluIleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAspAlaValCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                   866PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419
```

184

经经济

101 327

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
  APPLICANT:
                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:PCT-US94-14277-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US94-14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-240-675-1 x PCT-US94-14277-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: PCT-US94-14277-3
                                                     Sequence 4, Application:
                                                                                                                                                                                                                              201 AsnLys 202
                                                                                                                                                                                                                                                                                                                                                                                           655 GGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           605 ACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCAT 654
                                                                                                                                                                                                                                                                                                                                           184 ysLysHisSerAsnTyrSerThr***G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 LysLysThrIleAsnSerThrTyrTyrValGluLysIleProGluLeuLe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               555 GAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 ysProSerPheSerTyrThrIleArgIleTrpGlnLysSerSerSerAsp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 GTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTA. 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 GATACACATCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATG 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 HisMetSerProProGluValArgLeuGluArgGluAspLysAlaIleLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 GAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAAGAAAAC. 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 CTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 CAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 GGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GluCysGlnHisThrThrThrThrLysC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 heSerAlaGluTyrArgThrLysAspGluArgLysTrpLeuLys***Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 erThrSerSerTrpAsnGluValAspProPheIleProPheTyrThrAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GluAsnLeuLysProProGluAsnIleAsp***TyrIleIleAspAspAs 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                   uProGluThrThrTyrCysLeuGlu***LysAlaIleHisProSefLeuL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uValHisIleSerProProGlyGlnAspGlyAsnMetTrpAlaLeuGluL 134
                                                                                                                                                                                                                                                                                AATGAA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rAsn***TyrIleLysThrGlnPheArgValArgAlaGluGluGlyAsnS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nTyrThrLeuLysTrpSerSerHisGlyGluSerMetGlySerValThrP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                  Application PC/TUS9414277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Aguet, Michel
Bohni, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490:50
3.337
72.772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 1
Percent Identity: 48.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysGluPheSerLeuLeuAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
```

```
alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: PCT-US94-14277-4 from: 1 to: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1 x PCT-US94-14277-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                             858 AAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCC 907
                                          908 TCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTG 957
                                                                                                                                                                                                                                                                                                                                                                                       711 CTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGT 760
                                                                                     51 LysProIleProThrCysAlaAsnValGlnThrThrHisCysValPheSe 67
                                                                                                                                                                                                                                                                                                     761 TCTTAAATGGGATTAT...ACATATGCAAACATGACCTTTCAAGTTCAGT 807
67 rGlnAspThr***TyrThrGlyThrPhePheLeuHisValGlnAlaSerG
                                                                                                                                                                     34 rpLeuProGlyTyrSerLysSerSerSerGlySerHisSerAspLysTrp 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 86 FELECOMMUNICATION INFORMATION: TELEPHONE: 415/25-530 TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                               1 MetProValProGlyAsnLeuGlnValAspAlaGlnGlyLysSerTyrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Love, Richard B. REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                             GGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAAACCATTTGTATAAATGG 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TREET: 460 Point San Bruno Blvd
ITY: South San Francisco
                                                                                                                                                                                                                                                          lLeuLysTrpAspTyrIleAlaSerAlaAspValLeuPheArgAlaGlnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genentech;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.049
73.558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N: Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 44.712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
  84
                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                            34
```

1008 ATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGA 1057

84 luGlyAsnHisThrSerPheTrpSerGluGluLysPheIleAspSerGln

100

(); (); (0) 958 ATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAA 100

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-683-743-4
-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No. 5843697 ... 708683743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1308 AAAACAAAACCAGGAAATACCTCT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1258 TGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAG 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1208 TAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCA 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1158 TCANATGCTGAGAGAAAATTATCGAGAAAAAAAACTGATGTTACAGTTCC 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1108 TGATCCAGGATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACT 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 pThrLeuLeuValTyr***AsnCysGlnAspSerThrCysAsp...... 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1058 TTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTG 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 heArgAlaLeuLeuAsnLysThrSerAsnPheSerGluLysLeuCysGlu 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 sAsnLeuGlnProLeuThrValTyrCysValGlnAlaArgVal...LeuP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 LysHisIleLeuProProProProValIleThrValThrAlaMetSerAs 117
                                           HYPOTHETICAL:
FRAGMENT TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFORMER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 LysThrArgProGlySerPheSer 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 SerAsnThrLysIleSerMetGluLysAspGlyProGluPheThrLeuLy 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800 AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NERAL INFORMATION:
APPLICANT: Pestka
                                                                                                                                   OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              EQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: SCPC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLICANT: Kotenko, Serguei
TLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
TLE OF INVENTION: CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hackensack
                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Jersey
                                                                                                                                                                                                                                                                                                         325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pestka, Sidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABLUMENT STRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601-1-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY
```

seq\_name: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:PCT-US94-14277-2

ķ

seq\_documentation\_block:

Sequence 2, Application PC/TUS9414277
GENERAL INFORMATION:
CARPELICANT: Aguet, Michel

```
alignment_block:
US-09-240-675-1 x US-08-683-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 228.50
Ratio: 1.693
Percent Similarity: 60.268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-683-743-4 from: 1 to:
212 rThrHisAspGluThrValpro 219
                                                                                                                                                                              645 CTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGAC 694
                                                                  695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                            196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh 212
                                                                                                                                                                                                                                              179 rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu 195
                                                                                                                                                                                                                                                                                                          595 ATARACTOTORCOAGAGACTACTTATTGTCTARAAGTTARAGCAGCACTA 644
                                                                                                                                                                                                                                                                                                                                                                          162 yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA 179
                                                                                                                                                                                                                                                                                                                                                                                                                             545 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 GATGGTTTA....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 TGATACACATCTCCTGGAACAAAAGATAGTGTT...ATGTGGGCTTTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 ACTICITCAIGGIAIGAGGIIGACICATIIACACCAITICGCAAAGCICA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 GATTGGTCCTCCAGAAGTACATTTAGAAGCT...GAAGATAAGGCAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 TCATTCGATTATCAAAAAACTGGGATGGATAAATTGGATAAAATTGTCTGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer.....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 ThrAlaGinTyr..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eIleGlyProProGlyMetGlnValGluValLeuAlaAspSerLeuHisM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 8
Percent Identity: 29.911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: PCT-US94-14277-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-240-675-1 x PCT-US94-14277-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/952-9881
TELEX: 910/371-7168
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5:25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                         207 TTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 253
                                                                                                                                                                                                                                                                                                                                                                                  125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                           254 G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                                175 ACAGGAGCGATGAGTCT...
                                                                                                                                                                                                                                                                                                                                      32 oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 TIGTCCGCAGCCGCAGGTGGA......AAAAATCTAAAATCTCC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                   76 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG 93
                                                                                                                                                                                                                                                                                                                                                                                                                            16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                       66 TyrSerPhe...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/10 FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                      luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  South San Francisco : California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruth
Silvio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor Subunit Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US94/14277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/164596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 30.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               866PCT
                                                                                                                                                                     .IleAspGlySerTrpHisArgLe 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from:
                                                                                                                                                                                                                                                                                                ....GTCGGGAATGTGACT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 332
                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                            32
```

```
seq_name: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      documentation_block:
                                                                                                                                                                                                                                                                                                                                                        ZIP: YOLV COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/80
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 sTyrTrpGluLysSerGluThrGlnGlnGlnGlnValGluGlyProPheL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 alThrProGlyLysGlySerLeuValIleHisPheSerProProPheAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProHi 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624 CTAAAAGTTAAAGCAGCACTA...CTTACGTCATGGAAAATT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 CCAGACATAAAATTTAT....AAACTCTCACCAGAGACTACTTATTGT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 oPheGlnHisTyrGluAsnValThrValGlyProProLysAsnIleSerV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 ATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC 382
                                                              REGISTRATION NUMBER: 32,743
                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                         CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1201 F
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .GGTGTCTATAGTCCAGTACATTGTATAAAGACCACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION: CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Jelmberg, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Farrah, Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kho, Choon J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whitmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ication US/08943087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZymoGenetics, Inc.
                                                                                               Paul G
                                                                                                                                                 UMBER: 08/803,305
20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...ValPheHisGlyAlaThrPheGlnTyrLeuValHi 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theodore E
                                                                                                                                                                                                                                                                        US/08/943,087
                                                 96-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  662
```

```
; TOPOLOGY: lin
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1 x US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-943-087-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 50.346 Percent Identity: 21.016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 eLeuGluThrGlnIleGlyProProGluValAlaLeuThrThrAspGluL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150
                                                                                                                                                             568 AAAATATTTATTCCAGACATAAAATTTATAAA.....CTCTCACCAGAG 611
                                                                                                                                                                                                                    182 nValSerValLeuAsnThrLysSerAsnArgThrTrpSerGlnCysValT 199
                                                                                                                                                                                                                                                                           166 GluAspLeuProValSerMetGlnGlnIleTyrSerAsnLeuLysTyrAs 182
                                                                                                                                                                                                                                                                                                                                                                                                                                               149.ysSerIleSerValValLeuThrAlaProGluLysTrpLysArgAsnPro 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC 100
212 ThrLeuTyrCysValHisValGluSerPheValProGlyProProArgAr 228
                                                                                                                                                                                                                                                                                                                                                                                          480 ......GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 AGGCAATAGTGATACACATCTCTCCTGGAACAAAA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 197
                                                       612 ACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAAT 661
                                                                                                        34 rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUENCE CHARACTERISTICS 
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 198.00
Ratio: 0.908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to: 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479
```

			· ·
seq_documentat; seq_documentat; sequence 14, sequence 14, patent No. 5; GENERAL INFO APPLICANT A	1064 342 1114 1114 352 1140 1140 1190 1190	873 TGTGAA 290 923 AAAAGG :   297 PLYSAT 973 CTTTTT ::   310 snPheI 1014 GCTTC 327 MetSer	662 TGGTGTC :: 228 gAlaGln 711 714 erGluph 726 AATTATAG 726 AATTATAG 1         259Iles 776 TACATAT : :::: 264 eLeuphe 823 TAAAAAAG :::::: 281 ysGluLy
Ion_block: Application US/08 945511 (Commation: Iok, S1 (Iok, S1 (I	TCTATA TATCCA TATCCA GluGlu Gl	GAATTTACCTCTCCGC :::::::: rgPhePheVal TGGTCTGAGATAAA ::::::::::::::::::::::::::::::	A 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
E. E. E. E. E. E. E. E. E. E. E. E. E. E	TCGGTGCTCCAAACAGTCTGGAAACAGCCTGTGATCC     :::            :::	AGTGTGTCTTTCCTCAAAACGTTTTCCA          :	ATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA.
	CGCCTGTGATCC 1113 euArgProProG 352	AAAACGTTTTCCA 922	CAGTTGAAAATGAA. 710 ::::::::::::::::::::::::::::::::::::

```
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1 x US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-943-087-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                            298 CACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCA... 344
                                                  395 TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA 444
                                                                                                  116 TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh
                                                                                                                                                    345 GAAAAAGAAAACACTTCTTCATGGTÄTGAGGTTGACTCATTTACACCATT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                            248 AAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIOR APPLICATION DATA:
                                                                                                                                                                                                               99 laGluThrSerAspTyrGluHisGlnTyrTyrAlaLysValLysAlaIle 115
                                                                                                                                                                                                                                                                                                                    82 uAsnLysSerGluCysArgAsnIleAsnArgThrTyrCysAspLeuSerA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 CTAGTGCTCGCCGTGGGCCCATGG.....GTGTTGTCCGCAGCCGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            66 LysValThrTyrThrValGlnTyrPheIleTyrGlyGlnLysLysTrpLe 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 rGlyGly....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORMATION FOR SEQ ID NO: EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECOMMUNICATION INFORMATION ELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANDEDNESS:
DPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGTH: 553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 21.016
GluValAlaLeuThrThrAspGluL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 553
```

Se						,										
seq_name:	1190 385		1064 342		297. 973.	873 290 923	823 281	776 264	726 259	711 245	662 228	612 212	199	518 182	166	149
	AACTGA : : : : nGluSe	InGluG ATTTTT 	CCATAI	GCTTTC	PLYSAL CTTTTI CTTTTI	TGTGAL	TAAAA ::: ysGluI	TACATA	AATATA 111	erGluI	TGGTGT ::: gAlaGI	ACTACI	AAAATA     hrasn.	ATATAC       nvalse	GluAsı	AGGCAZ   :::  ysSer]
/cgn2_6/ptodata	AACTGATGTT: :::::: nGluSerLeuSe	Tuglug Tugggaa	CTATAT	CTACTT		VAATGTC	AGGAATCC :::::    LysH1sPr	ATGCAAA :::: neSerVa	TATAGAAGTCAGTGTC	heLysA	CTATAG	TATTGT	TTTATT	CTTACT	LeuPro	TAGTGA
data/1,	AC:    rArgTh	luValL luValL AACACT ::: SerGlu	CGGTGC	CCTCCA( GlyLys:	eval	AAAACT	CTGGAAAC   :::    roAlaAsn	CATGACO	AGTGTC	laLysI	TCCAGT.	CTAAAA ::: Valhis	CCAGACI   	TATCTG(   uAsnTh	GATAGTO	TACACA:
/1/1aa/5B_COMB.pep:US-08-943-087-	AACTGATGTTACAGTTCCTAATTTGAAACCACTGACTGTATAT : :::::		ICCAAAA    :::  ProGlu	GCTTTCCTACTTCCAGTCTTTAACATTAGATCCCTTAGTGATT	PTOALAGIULYSI  PTOALAGIULYSI  CTTTTTGGTCTGAAAGAGATAAAGTTTGATACTGAAATA  STILL:::   ::::   ::::    ::::	ACCCAGI	TAAAAAGGAATCCTGGAAACCATTTGTA :::::::   :::   ysGluLysHisProAlaAsnLeuIle	CTTTCA :::::: YTYrSeı	CAAAATC	CTACCTC	ACATTGI :::    sGlnCys	GTTAAAG    ::::  ValGlus	AAAATATTTATTCCAGACATAAAATTTATAAA	GAAAAAC     ::: rLysSei	GTTATGT	AGGCAATAGTGATACACATCTCTCCTGGAACAAAA.   :::    :::     ysSerIleSerValValLeuThrAlaProGluLysT
COMB.	ProAsp	: ::   ::   ::   ::	CAGTCT      Proser	ACATTA	TGATAC	GIGICI LEUI CAAGCA	GTATAA e	GTT ::: :leTyr	AGAACT	т ретгртуг	ATAAAG ::: :AlaArg	CAGCAC :: SerPheV	TTATAA : : :uValLe	TCTTCA	GGGCTT	TGGAAC
pep:US	AAACCA     LysThr	ralase Gaaaaa LyThrs	GGAAAC         GlyAsn	GATCCC      erSerL	AlaGlu AlaGlu TGAAAT	TICCIC:: :: leTyrG TCTGAT	ATGGAA	CAGTGG :::::: ArgTyr	CTATGTTC	CT	ACCACA     ThrLeu	TACTTA	A uThrTr	GGTGTA ThrTrp	TGGATG	AAAA     uLysTr
-08-94	CTGACTO	rHisLe	ACGCCT( LeuArg)	TTAGTG	Lysileva A	AAAACG      yasng	ACAAAT	CTCCAC :::    IleHis	TTAAATG	CTACCTCC       LeuPro	GTTGAA ::: Lysasp	CGTCATO	.CTCTC.	GAAGAA :::::: SerGln(	GTTTAA ::   : snLeuL	pLysAr
3-087-1		352 IncludinginginyaliysHistendiyTyrAlaSerHistenMetGlu 368 1140 ATTTTTTGGGAAAAACCTTCAAATGCTGAGAGAAAAATTATCGAGAAAAA 118        369 IlePheCysAspSerGluginAsnThrGluGlyThrSerPheThrGlnGl 385	CCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCC	GCTTTCCTACTTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATT	DLYSATGPhephevalProAlaGluLySIleValIleA  CTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAA  CTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAA	TGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCA	TAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGAC :::::::   :::   ysGluLysHisProAlaAsnLeuIle	TACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTT : :::::	AATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTA    :::::::::   IleSerIleThrValPh	CTACCTCCACCAGAA        alleupro	TGGTGTCTATAGTCCAGTACAGTTGTATAAAGACCACAGTTGAAAATGAA. :::         :::!!  gAlaGlnProSerGluLysGlnCysAlaArgThrLeuLysAspGlnSerS	ACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAAT          :::: ThrieuTyrCysValHisValGluSerPheValProGlyProProArgAr	ACATAAAATTTATAAACTCTCACCAGAG 	ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG !!!:::!! nValSerYalLeuAsnThrLysSerAsnArgThrTrpSerGinCysValT	GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC	AGGCAATAGTGATACACATCTCTCCTGGAACAAAA
. 6	1232	1 368 1189	1113	1063	310 1013	1 922 297 1 972	289	1 822 281	1775 1 264	725 . 258	. 710 s 245	r 661	611	567 199	517 182	479

```
allgnment_block:
US-09-240-675-1 x US-08-943-087-16
                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-943-087-16
                                                                                                                                                                                                            Align seg 1/1 to: US-08-943-087-16 from: 1 to: 553
                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFORWATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
TYPE: amino acid
Companyeres ainolo
                                                                                                     101 AGGTGGAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                151 ATGACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGG... 197
                                                                                                                                                                  57 CTAGTGCTCGTCGCCGTGGGCCCATGG......GTGTTGTCCGCAGCCGC 100
49 snMetLysAsnValLeuGlnTrpThrProProGluGlyLeuGlnGlyVal 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR APPLICATION DATA:
PPLICATION NUMBER: 08/803,305
TLING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE:
                                                                                                                                         LeuLeuLeuLeuAlaAlaProTrpGlyArgAlaValProCysValSe 34
                                                                    rGlyGly.....LeuProLysProAlaAsnIleThrPheLeuSerIleA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMUNICATION INFORMATION: LEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jelmberg, Anna
Adams, Robyn L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kho, Choon J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZymoGenetics, Imc.
01 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ication US/08943087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                      protein
internal
                                                                                                                                                                                                                                                                                                 198.00
0.908
50.346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOKINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theodore E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/943,087
                                                                                                                                                                                                                                                                                               Gaps: 17
Percent Identity: 21.016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96-24C1
```

1063	GCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTCATT :	!: 1014
1013 326	CTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAA ::    :::	973 310
310		297
972	TCCGCGTACAAGCATCTGATGGAAATAACACAT	923
297	LeuIleTyrGlyAsnGluPheAs	290
289 233		87. 281
872		823
281	eLeuPheSerValMetGlyTyrSerIleTyrArgTyrIleHisValGlyL	264
822		776
775	TGGGATTA	726
258	erGluPheLysAlaLysIleIlePheTrpTyrValLeuPro	245
245		228
710	TGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA.	662
661 228	ACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAAT (               :::: ::: ::: ::: ::: ::	212
611 <sup>.</sup> 211		568 199
199		182
182		166
517		480
479 165	AGGCAATAGTGATACACATCTCTCCTGGAACAAAA	149
444 149	TCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATA (	395 132
394 132	GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATT : :::    :::                       TrpGlyThrLysCysSerLysTrpAlaGluSerGlyArgPheTyrProPh :	345 116
344 115		.298 99
297 99	TCTT  : SerA	248 82
82		99
		109

ĭ	385 nGluSerLeuSerArqThrIleProProAspLysThrValIleGluTyr 401	385
32	:	1190
185	369 IlePheCysAspSerGluGluAsnThrGluGlyThrSerPheThrGlnGl 385	369
189	1140 ATTITTTGGGAAAACACTTCAAATGCTGAGAGAAAATTATCGAGAAAAA 1189	1140
868	352 inGluGluGluValLysHisLeuGlyTyrAlaSerHisLeuMetGlu 368	352
139	ATCCACT	1114
52		342
113	1064 CCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCC 1113	1064
341	327 MetSerLeuLeuGlyLysSerSerAspValSerSerLeuAsnAsp 341	327

```
Search information block:
Ouery: US-09-240-675-1
Ouery length: 1343
Database: PIR_63:*
Database sequences: 168808
Database length: 58629743
Search time (sec): 70.990000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p1r2:S490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM of: US-09-240-675-1 to: PIR_63:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Date: Jun 1, 2000 5:46 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL-frame+_n2p.model -DEV-x1p
-Q-/cgn2_l/USPTO_spool/US09240675/runat_30052000_165118_2984/app_query.fasta.1
-DB-PIR_63 -QFMT-fastan -SUFFIX-modif.rpr -GAPOP=12.000
-GAPEXT-4.000 -MINANCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 ;XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 ;XGAPEXT-0.500
-DELOP-6.000 -DELXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DCCALIGN-200 -THR_SCORE-PCt
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09240675 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lr2:B49502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1:JC4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :T191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :A4872:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : A36080
                                                                   : $51603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :T0885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :A44027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :A34157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117.50
117.50
117.50
117.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 1 190K protein human
12 1 receptor-like tyrosine kinase Eh-1
15 1 receptor tyrosine kinase Eh-1
15 1 interleukin-10 receptor mouse
15 1 interleukin-10 receptor mouse
15 1 titin, muscle - chicken (fragme
16 1 protein-tyrosine-phosphatase (
17 1 protein-tyrosine-phosphatase (
18 1 hypothetical protein F12A10.4
150 1 165K myofibrillar M-band struc
150 1 protein-tyrosine kinase (
151 1 protein-tyrosine kinase (
152 1 protein-tyrosine-phosphatase (
153 1 protein-tyrosine-phosphatase (
154 1 protein-tyrosine-phosphatase (
155 1 protein-tyrosine-phosphatase (
156 1 protein-tyrosine-phosphatase (
157 1 protein-tyrosine-phosphatase (
158 1 leukocyte antigen-related protein hypothetical protein zK617.1a (
159 1 hypothetical protein zK617.1b (
150 1 hypothetical protein zK617.1b (
150 1 hypothetical protein zK617.1b (
150 1 hypothetical protein zK617.1b (
151 1 protein - rat adhesion protein syndrome cell adhesion protein protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
151 1 protein - rat (
15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interferon receptor class II cy interferon gamma receptor beta interferon gamma receptor acces frazzled gene protein, log isc ifrazzled gene protein, log isc inegenin chicken (fragment) insulin receptor precursor interferon gamma receptor precursor interferon gamma receptor precursor interferon gamma receptor precursor interferon gamma receptor precursor in the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine receptor family II, m
cytokine receptor family class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha/beta receptor
interferon alpha receptor type
interferon alpha/beta receptor
```

piri:A34100  + 105.50 136.88 0.558 0.6791 1447 it tumor suppressor protein piri:A40091 + 105.50 140.52 0.6791 878   interleukin-3 receptor b seq_name: pir2:A32694  seq_documentation_block:     interferon alpha/beta receptor precursor - human     C;Species: Homo sapiens (man)     C;Date: 22-0un-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999     C;Accession, A33694, SJ7112     Cell 60, 255-234, 1990     A;Title: Genetic transfer of a functional human interferon alpha receptor into mon A;Reference number: A33694; MUID:90124632     A;Accession: A32694     A;Accessio	+ 107.00 140.85 0 + 106.50 141.81 0
--	--

alignment\_block: US-09-240-675-1 x A32694 Ouality: 2313.00
Ratio: 5.305
Percent Similarity: 100.000 Align seg 1/1 to: A32694 from: 1 to: 557 77 CCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTC 126 127. AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176 Length: 436 Gaps: 0 Percent Identity: 100.000 Length: ...
Gaps: 

```
1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 lAspSerPheThrProPheArgLysAlaGlnIleGlyProProGluValH
1227 GTAȚATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                   927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isLeuGluAlaGluAspLysAlaIleValIleHisIleSerProGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysLeuArgIleArgAlaGluLysGluAsnThrSerSerTrpTyrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysAspSerValMetTrpAlaLeuAspGlyLeuSerPheThrTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGATAGTGTTATGTGGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                    TTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACT
                                                                                                       ulleTyrGlulleIlePheTrpGluAsnThrSerAsnAlaGluArgLysI
                                                                                                                                         GATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAA 1176
                                                                                                                                                             GlyAlaProLysGlnSerGlyAsnThrProValIleGlnAspTyrProLe
                                                                                                                                                                                                          GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCACT 1126
                                                                                                                                                                                                                                           roProValPheAsnIleArgSerLeuSerAspSerPheHisIleTyrile
                                                                                                                                                                                                                                                             CTCCAGTCTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATC
                                                                                                                                                                                                                                                                                                          eTrpSerGluGluIleLysPheAspThrGluIleGlnAlaPheLeuLeuP
                                                                                                                                                                                                                                                                                                                                 TTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTC
                                                                                                                                                                                                                                                                                                                                                                             GlyIleTyrLeuLeuArgValGinAlaSerAspGlyAsnAsnThrSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                   GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sargasnProGlyAsnHisLeuTyrLysTrpLysGlnIleProAspCysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                snIleGluValSerValGlnAsnGlnAsnTyrValLeuLysTrpAspTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT .776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
     1276
                                                                    1226
                                                                                                       384
                                                                                                                                                                                                                                              350
                                                                                                                                                                                                                                                                               1076
                                                                                                                                                                                                                                                                                                                                                  1026
                                                                                                                                                                                                                                                                                                                                                                                    317
                                    400
                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                 334
                                                                                                                                                                                                                                                                                                                                                                                                                     976
                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
```

```
interferon alpha receptor type 1 precursor - bovine C;Species: Bos primigenius taurus (cattle) (c;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C;Accession: S27387; S3770 C;Accession: S27387; S3770 R;Mouchel-Vielh, E.; Lutfälla, G.; Mogensen, K.E.; Uze, G. FEBS lett. 313; 255-259, 1992
    alignment_block:
US-09-240-675-1 x S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: lung

A;Experimental source: lung

C;Reywords: antiviral; cytokine receptor; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

F:25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha interferon
A;Reference number: S33770; MUID:93305725
A;Accession: S33770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Specific antiviral activities of the human alpha interferons are determine A; Reference number: S27387; MUID:93076908
A; Accession: S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-421, 'V', 423-560 < LIM>
A;Cross references: EMBL:L06320; NID:g163187; PIDN:AAA02571:1; PID:g163188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:S27387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Lim, J.K.; Langer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1507.00 Length: 439
Ratio: 3.987 Gaps: 6
Percent Similarity: 86:105 Percent Identity: 64.920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-560 <MOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: $27387 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1327 CCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1507.00 Ratio: 3.987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 sSerSerValPheSerAspAlaValCysGluLysThrLysProGlyAsnT 434
                                                                                                                                                                                                                                            130 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                        230 TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 279
32 snValGluTleH1sIleILeAspAspAspAsphePheLeuLysTrpAspSer 48
                                                                                                                                                                                                                                                                                                  16 gTrpvalteuProAlaAlaSerGLyGluAlaAsnLeuLys...ProGluA
                                                                                                                                                                                                                                                                                                                                   80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTCAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ATGGTCGTCCTCGTGGCCGCGACGACCCTAGTGCTCGTCGCCCGTGGGCCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrserLys 436
                                                                                                                                                                                                                                                                                                                                                                                                   AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC 229
                                                                                                                    SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGlnIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDBK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , .
, . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417
                                                                                                                                                                                                                                                                  179
                             82
                                                                                                                         <u>გ</u>
                                                                                                                                                                                                                                                                                                            32
```

```
....1168 AGAGAAAATTATCGAGAAAAAAAACTGATGTTACAGTTCCTAATTTGAAA 1217
                                                                                                                                                                                                               1068
                                                                                                                                                                                                                                                                                               1021 TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGT. ...GATTCATTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                           971 ATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 SerArgGlyIleTyrTyrYalArgValArgAlaSerAsnGlyAsnGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 hrValTyrProGluAspLysIleTyrLysLeuSerProGluIleThrTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       571 ATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTAT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 CAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 snCysGluAsnValThrSerThrHisCysValPheProArgGluValSer 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 ePheLysLysIleProGlyAsnHisSerAspLysTrpLysGinIleProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            771 GATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTT 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     721 CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      671 TAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 GGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 TACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT...CCT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 AMATTGCGTATAAGAGCAGAAAAA...GAAAACACTTCTTCATGGTATGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 CCAAATGCAACTTTTCTTCACTCAAGCTG...AATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 GluLeuArgIleArgAlaGluGluGlyAsnAsnThrSerThrTrpTyrGl 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 hrLysCysAsnPheSerSerValGluLeuGluAsnValPheGluLysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATCCACTGATTTATGAAATTATTTTTTTGGGAAAACACTTCAAATGCTG 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspTyrProTyrGluAsnAlaThrPheGlnAlaGlnTrpLeuArgAlaPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyThrLysAspSerIleMetTrpAlaMetAspArgSerSerPheArgTy 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alHisLeuGluAlaGluAspLys&laIleIleLeuSerIleSerProPro 148
                                                                                                                                                   ValSerValGlyAlaSerGluGluSerGluAsnMetSerValAsnGlnLe 365
                                                                                                                                                                                                    ATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGA 1117
                                                                                                                                                                                                                                                    lePheProProValIleSerValLysSerValThrAspAspSerLeuHis
                                                                                                                                                                                                                                                                                                                                                             rSerPheTrpSerGluGluLysGluPheAsnThrGluMetLysThrIleI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roGluAsnIleGlnIleAsnAlaAspAsnGlnIleTyrValLeuLysTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rSerProValTyrCysIleAsnThrThrGluArgHisLysValProSerP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CysLeuLysValLysAlaGluLeuArgLeuGlnSerArgValGlyCysTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uValGluProPheValProPheLeuGluAlaGlnIleGlyProProAspV 132
                                                                                                                                                                                                                                                          348
                                                                                                                                                                                                                                                                                                          1067
                                                                                                                                                                                                                                                                                                                                                             332
                                                                                                                                                                                                                                                                                                                                                                                                              1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
```

```
C; Accession: A45283; I48423; I48424; I48425; I48426; R; Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
                                                                                   A; Status: preliminary; translated
                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 426-445 < RE6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: pir2:A45283
Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265
                                   ; Molecule type: DNA
; Residues: 473-590 < RE7>
                                                                                                                      :Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813
Accession: I48429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Mus musculus (house mouse)

Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999;

Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999;

Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999;
                                                                                                                                                                                                                                                                                                                     Residues: 397-424 <RE5>
                                                                                                                                                                                                                                                            Accession: I48428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1;
Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1;
Note: sequence extracted from NCBI backbone (NCBIN:102354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ne 148, 343-346, 1994
Title: Structure of the murine interferon alpha/beta receptor-encoding gene:
Reference number: 148423; MIID:95047447
Accession: 148423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference number: A45283; MUID:92262522
Accession: A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residues: 49 204 (KES)
Pross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 243-264 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pioss-references: EMBL:U06238; NID:g497104; PIDN:AAC01749.1; PID:g755811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 127-224 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dolecule type: DNA
Residues: 118-125 <RES>
                                                                                                                                                                                                                                                                                                                                                              tatus preliminary, translated from GB/EMBL/DDBJ 18 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   esidues: 265-375
                                                                                                                                                                                                                                                                                                                                                                                                           ross-references: EMBL:U06240, NID:g497108; PIDN:AAA65005.1; ccession: I48427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1318 CAGGAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1268 GCTGAATAAAAGCAGTGTTTTAGTGACGCTGTATGTGAGAAAACAAAAC 1317
                                                                                                                                                                                                                                                                                    SE-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roGlyAsnThrSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       luargLysValLeuGluLysArgThrAsnPheIlePheProAspLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProLeuThrValTyrCysValLysAlaArgAlaLeuIleGluAsnAspAr 415
                                                                                                                                                                                                                              preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ (:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pha/beta receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -590 <UZE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uze,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             <RE4>
                                                                                                                                                                                        A Sale of the State of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse
                                                                                      from GB/EMBL/DDBJ
                                                                                                                                                                                        STATE OF STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.; Mogensen, K.E.
                                                                                                                                                                                                                                                      ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBIP: 102357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g755810
                                                                                                                                                                                                                                                                                                                                                                                                                                PID:g510262
```

A;Introns: 177/3; 331/1 C;Keywords: cytokine receptor;

transmembrane protein

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-675-1 x A45283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 TTGCGTATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 TGGGATGGATAAATTGGATAAAATTGTCTGGGTGTÇAGAATATTACTAGTA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 AGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                   167 eArgIleTrpGlnLysSerSerSerAspLysLysThrIleAsnSerThrT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 PheArgValArgAlaGluGluGlyAsnSerThrSerSerTrpAsnGluVa
                                                                                                                                                                                                                                 627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTTGGTGTCTATAGTCC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 GlnAspGlyAsnMetTrpAlaLeuGluLysProSerPheSerTyrThrIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                            217
                                                                                                                                               677
                                                                                                                                                                                                                                                                                                                                       577 ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 hrLysCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 sAspGluAlaLysTrpLeuLysValProGluCysGlnHisThrThrThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArgThrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 snileAspValTyrileIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 ATGGTCGTCCTCGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC
                                              727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIATCTGGAAAAACTCTTCAGGTGTAGAAGAAAAGGATTGAAAATATTT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAGATAGTGTTÄTGTGGGCTTTGGÄTGGTTTAAGCTTTACÄTATAGCTT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rgLeuGluAlaGluAspLysAlaIleLeuValHisIleSerProProGly 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                   GluValLysAlaIleHisProSerLeuLysLysHisSerAsnTyrSerTh 217
                                                                                                                                                                                                                                                                               yrTyrValGluLysIleProGluLeuLeuProGluThrThrTyrCysLeu, 200
                                                                                                                             AGTACATTGTATÁAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
snLeuGlnValAspAlaGlnGlyLysSerTyrValLeuLysTrpAspTyr
                                      ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 776
                                                                                            rValGlnCysIleSerThrThrValAlaAsnLysMetProValProGlyA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1069.00
Ratio: 3.230
milarity: 75.917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 4
Percent Identity: 48.624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
     250
```

```
A:Cross-references: EMBL:U08988; NID:g571295; PID:g571296
C:Genétics:
                                                                                                                                                                           submitted to the EMBL Data Library, April 1994
A; Reference number: G06935
A; Accession: G01418
A; Status: preliminary; translated from GB/EMBL/
                                                                                                                                                                                                                                                                                                                cytokine receptor family II, member 4 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec:1996 #sequence_revision 06-Jun-1997
A;Gene: GDB:CRFB4; CRF2-4

A;Cross*references: GDB:138168; OMIM:123889

A;Map postition: '21q22'.1-21q22'.2

A;Introns: 17/1; 58/2; 111/1; 166/3; 216/1
                                                                                                                                  A; Molecule type: DNA ... A; Residues: 1-273 <LUT>
                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:G01418
                                                                                                                                                                                                                                                                       Accession: G01418 -- Lutfalla, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1224 ACTGTATATTGTGTGAAAAGCCAGAGCACACCATGGATGAAAAAGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1324 ATACCTCT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1274 TAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 erPheSer 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 roProProValIleThrValThrAlaMetSerAspThrLeuLeuValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 AAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         874 GTGAMANTGTCAMAACTACCCAGTGTGTCTTTCCTCAMAACGTTTTCCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 824. AAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 IleAlaSerAlaAspValLeuPheArgAlaGlnTrpLeuProGlyTyrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ... ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rLysSerSerSerGlySerHisSerAspLysTrpLysProIleProThrC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nLysThrSerAsnPheSerGluLysLeuCysGluLysThrArgProGlyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yLeuAsnTyrGluIleIlePheTrpGluAsnThrSerAsnThrLysIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValAsnCysGlnAspSerThrCysAsp...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rPheTrpSerGluGluLysPheIleAspSerGlnLysHisIleLeuProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrGlyThrPhePheLeuHisValGlnAlaSerGluGlyAsnHisThrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erMetGluLysAspGlyProGluPheThrLeuLysAsnLeuGlnProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrValTyrCysValGlnAlaArgVal...LeuPheArgAlaLeuLeuAs
                                                                                                                                                                             preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 17-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409
```

:

```
seq_documentation_block:
                                                                                                                                   cytokine receptor family class II protein CRF2-4 precursor - human
R; Lutfalla, G.; Gardiner, K.; Uze, Senomics 16, 366-373, 1993
                                                                                                                                                                                                                                       seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                       Species: Homo sapiens (man)
Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-240-675-1 x G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 1.704
Percent Similarity: 61.161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                               Accession: A
Lutfalla, G.
                                                                                                                                                                                                                                                                                            '212 rThrHisAspGluThrValPro 219
                                                                                                                                                                                                                                                                                                                                                                                                            196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh
                                                                                                                                                                                                                                                                                                                                                    695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 GATGGTTTA.....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 TACAC...ATCTCTCCTGGAACAAAAGATAGTGTT...ATGTGGGCTTTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 ACTICTICATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 GATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 ThralaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 snlleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 yMetValProProProGluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGAC 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eIleGlyProProGlyMetGlnValGluValLeuAspAspSerLeuHisM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisSerAspTrpValAsnIle...ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCATTCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                          P1r2:A47003
                                                           A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: G01418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 8
Percent Identity: 29.911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ខ្ល
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                                                                                                                               212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52
```

```
elignment_block:
US-09-240-675-1 x A47003 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-325 <LUT>
A;Cross-references: GB:Z17227; NID:g393378; PID:g393379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 21q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A47003; MUID: 93300510 A; Accession: A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: A new member of the cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: A47003 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh 212
                                                        645 CTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGAC
                                                                                                        179 rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu
                                                                                                                                                                595 ATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTA: 644
                                                                                                                                                                                                                      162 yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA 179
                                                                                                                                                                                                                                                                                                                                 146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl
                                                                                                                                                                                                                                                                                                                                                                              501 GATGGTTTA.....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC 544
                                                                                                                                                                                                                                                                         545 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                    129 etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 TGATACACATCTCTCCTGGAACAAAAGATAGTGTT . . ATGTGGGCTTTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 eileGlyProProGlyMetGlnValGluValLeuAlaAspSerLeuHisM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 GATTGGTCCTCCAGAAGTACATTTAGAAGCT...GAAGATAAGGCAATAG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357, ACTICTICATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 TCATTCGATTATCAAAAACTGGGATGGATAATTGGATAAAATTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 HisSerAspTrpValAsnile...ThrPheCysProValAspAspThrI1 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 erLysTyrGlyAspHisThrLeuArgValArgAlaGluPheAlaAspGlu 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 sCysMetAsnThrThrLeuThrGluCysAspPheSerSer.....LeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 ThrAlaGlnTyr.....LeuSerTyrArgIlePheGlnAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 yMetValProProGluAsnValArgMetAsnSerValAsnPheLysA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 29.911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tokine receptor gene family maps on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 325
                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129
                                                        694
                                                                                                              195
                                                                                                                                                                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: p1r2:JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Gibbs, V.C.; Pennica, D. ene 186, 97-101, 1997
ene 186, 97-101, 1997
Title: CRF2-4:isolation of cDNA clones encoding the human and mouse proteins.
Reference number: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-240-675-1 x JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: mRNA
;Residues: 1-349 <GIB>
;Cross-references: GB:U53696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: JC6311 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iterferon receptor-class II cytokine receptor - mouse
Species: Mus musculus (house mouse)
Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: JC6311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 rThrHisAspGluThrValPro 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 GAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTT 315
                                                                                                                                                                                                                                                                                                                                                                         363 TCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 GGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TCCTCAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 CAA....AAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCA 265
                                                              492 TGGGCTTTGGATGGTTTA.....AGCTTTACATATAGCTTACTTATCTG 535
                                                                                                                                                                                                                       114 yProProGluMetGlnIleGluSerLeuAlaGluSerLeuGluLeuArgP
                                                                                                                                                               463 TCTCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 rpGluValProAlaPheProLysThrAsnLeuThrPheThrAlaGlnTyr
                                                                                                                                                                                                                                                                                                                         99 GluTrpValAsnVal...ThrPheCysProValGluAspThrIleIleGl 114
                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 oProGluLysValArgMetAsnSerValAsnPheLysAsnIleLeuGlnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LeuGlyGlyPheLeuLeuValProAlaLeuGly. ........ MetIleProPr 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAACACTTCT 362
                                                                                                                                                                                                                                                                        TCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACA 462
                                                                                                                                                                                                                                                                                                                                                                                                                               yrGlyAspTyrThrValArgValArgAlaGluLeuAlaAspGluHisSer 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sArgThrAlaSerThrGlnCysAspPheSer.....HisLeuSerLysT 82
heSerAlaProGinileGi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221.50
1.582
61.404
                                                                                                                                                                 ......CCTGGAACAAAAGATAGTGTTATG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 228
Gaps: 10
Percent Identity: 28.070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                                             131
```

alignment\_block:

Percent Similarity:

Quality:

Ratio:

203.00 1.471 60.262

Percent Identity:

Length:

229 13 30.131

Align seg 1/1 to: A49947 US-09-240-675-1 x A49947

from:

,-6

332

÷

ACTICITICATGGTATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGTTGACTC

207 TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 253

.....IleAspGlySerTrpHisArgLe

297 76 49 luproSerProSerSerAsnAspProArgProValValTyrGlnValGlu

175 ACAGGAGCGATGAGTCT.....

.....GTCGGGAATGTGACT 206

49

65

125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174

32 oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG

87 TITGICCGCAGCCGCAGGTGGA.....AAAAATCTAAAATCTCC

16 LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr

32

254 G.....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT

TyrSerPhe...

uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG

335 93

382 109

93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg

```
Interferon gamma receptor beta subunit - mouse N; Alternate names: IFN-gamma R beta chain; IFN-C; Species: Mus musculus (house mouse) C; Date: 06:Oct-1994 *sequence_revision 18-Nov-
                                                                                                                                                                                                                                                                                                      R;Hemm1, S.; Bohn1, R.; Stark, G.; Di Marco, F.; Aguet, M.
Cell 76, 803-810, 1994.
A;Title: A novel member of the interferon receptor family complements functionality A;Reference number: A49947; MUID:94170381
A;Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:A49947
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                            A; Note:
                                                                                                                                                                                                                   ı; Residües :
                                                                                                                                                      Cross references: GB:S69336; NID:g545841; PIDN:AAB30165.1; PID:g545842; Experimental source: early B-cell line Y16
                                                                                                                                                                                                                                                                         Status: preliminary
                                                                                                                      Experimental source: early B-cell line Y16; Rote: sequence extracted from NCBI backbone (NCBIN:145654, NCBIP:145656)
                                                                                                                                                                                                                                                   Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A49947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 pLysAsnGlyThrAsnGluLysPheGlnValValSerProTyrAspSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 TATAAAGACCACAGTTGAAAATGAACTACCTCCA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 GlyPheLeuLeuAspGlnAsnArgThrGlyGluTrpSerGluProIleCy 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636 GCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 luValLeuArgAsnLeuGluProTrpThrThrTyrCysIleGlnValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586 ATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 s...GluArgThrGlyAsnAspGluIleThrPro
                                                                                            cytokine receptor
                                                                                                                                                                                                                      1-332 <HEMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1994 *sequence_revision 18-Nov-1994 *text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFN-gamma R species-specific cofactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
```

S

```
us-09-240-675-1 x 138500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir2:138500
                                                                                                                                                                               Align seg 1/1 to: 138500 from: 1 to: 337
                108 .....AAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       663 :GGTGTCTATAGTCCAGTACATTGTATAAAGACCACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 CCAGACATAAAATTTAT.....AAACTCTCACCAGAGACTACTTATTGT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 sTyrTrpGluLysSerGluThrGlnGlnGlnGlnValGluGlyProPheL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 alThrProGlyLysGlySerLeuVallleH1sPheSerProProPheAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 oPheGlnHisTyrGluAsnValThrValGlyProProLysAsnIleSerV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA. 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT 529
                                                                      9 LeuLeuLeuLeuGlyValPheAlaAlaAlaAlaAlaAlaAlaProProAs 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              references: EMBL:U05875; NID:g463549; PIDN:AAA16955.1; PID:g463550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProHi 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source: clone pSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1996 #sequence_revision 16-Feb-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor accessory factor-1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         '(0',65-337 <RE2>
s: EMBL:U05877; NID:g463551; PIDN:AAA16956.1; PID:g463552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.J.; Kotenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel,
                                                                                                                                                                                                                                                                                                                          50.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence of an accessory factor required for activation of MUID:94170380
                                                                                                                                                                                                                                                                                                                       Percent Identity: 22.33:
明 あいないない
```

୍ଞ : a.:	7 ATGTTCTTAAATGGGATTATACATATGCAAACATGACCTTCAAGTTC  AGGTCTTAAATGGGATTATACATATGCAAACATGACCTTCAAGTTC  AGGTCTTAAATGGGATTATACATATGCAAACATGACCTTCAAGTTC  AGGTCTTAAATGGGATTATATACAATGACATGAC	75
AGAACT	GAAAATC 9 uServalLeuAlaGlyAlaCysPhePheLeuValLeuLysTyrA	74
rLeuLe	CAGAAAATATAGAAGTCAGTGTC:	24
AATGAA ::: Alaser	1 TTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAA 1 ::	22 6
GGAAAA heArgv	3 TCTAAAAGTTAAAGCAGCACCTACCTTACGTCAT     :::   :::	: 20 : 6°
TATTG :  .   LTyrCy	9 TCCAGACATĀAAĀTTTATAAACTCTCACCAGAGACTAC ::::::    :::    :::    :::    ::: 3 ArgSerĀsnSerIleSerLeuAspAsnLeuLysProSerArgVa	57 19
TTTAT	29 TTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATA     ::::!!  78 isTyrTipGluiysGlyGlyIleGlnGlnValLysGlyP	52 17
CTTAC	9 AGATAGTGTTATGTGGGCTTTGGATGGTTTAAGGTTTACATATAGCTTAC 	16
GGAACAAA PheAspIl	35GCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGI       ::     ::     :: 49 ThrProGlyGluGlySerLeuIleIleArgPheSerSerProPhe	14 43
AA	88 CACCATTICGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAG :::   :::::::::::::::::::::::::::::::	13
ATTTA	TCATGGTATGAGGTTGACT :::    :AlaTrpValThrMetProT	34
ATAAG :::   LeuAr	OCTCAAGCTGAATGTTTATGAAG :::::!      4 GlyPheProMetAspPheAsnVal	10
erAla	5 AGAATATTACTAGTACCAAATGCAACTTTTCTTCA	8 26
GTGTC :    inCysT	3 GATGGATAATTGGATAAAATTGTĆT	23
ACTGG	3 GATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC	ښر 50 ت
AGGAGC ::: SerThr	1 ATGACAAC ::: 2 snalaGlu	4
euTyrA	5 pProLeuSerGlnLeuProAlaProGlnH1sProLysIleArgL	

seq\_documentation\_block:

Contraction of the	630 alProPheAsnArgAsnGlyMetGlyAspSerSerAlaGluIleArgVal 646
	388 CACCATTTCGCAAAGCTCAGATTGGT413
	uAlaValLeuThrGluLeuArgProHisThrAspTyrValIleSerValV 630
	rgryaraaspreutyraraa
	   luGluProThrValThrAshGlÿGluTleLeuLÿSTyrArğVálTyYTYY
	70 ATGAG
	336ATÄÄGAGCAGAAAAÄÄÄAAACÄCTTCTTCATGGT 369
	300 CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGT
•	10-
	215 CGATTATCAAAAAACTGGGATGGATAAATTGGATAAAATTGTCTGGGTGTC 264 
	174ACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATT 214     :::   :::::::
	172 GG
;	125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT 171
	102 GGTGGAAAAATCTAAAATCTCC 124                       41 447 GlyGlyLysProLeuAspSerGlyLeuGlnAlaArgLeuProSerGlnPr 463
	Align seg 1/1 to: T13822 from: 1 to: 1375
	alignment_block: US-09-240-675-1 x r13822
	alignment scores:  Quality: 129.00 Length: 622  Ratio: 0.542 Gaps: 22  Percent Similarity: 38.264 Percent Identity: 16.399
eceptor mediating	ription: may function in vivo as a receptor of component of component of compo
1	Gene: frazzled  Gene: frazzled  Map position: 2  Function:
7314.1	e type: mRNA s: 1-1375 <koi eferences: EMB g:</koi 
	A;Reference number: 217780 A;Accession: T13822 A;Status: preliminary; translated from GB/EMBL/DDBJ
n subfamily and	n. F.A.; Timpe, L.; MITCHEII, N.J.; GOOGMAN, 7-204, 1996 azzled encodes a Drosophila member of the DC
Tan I. V	ייייייייייייייייייייייייייייייייייייי

			•			
883 834 899 910			738 785 770 770 799 771	663 G 744 A 713 A 751 u 751 u 768 1	531 / 696 / 581 / 710 / 631 / 727	414 647 434 663 481 680
883 AsinLysAsinGlinHisvalThrAspAsnargHisTyrThrValSerTyrGl. 834	ACATÁTGCAAACATGACCTTTCAAGTTCAAGTGGCTCCACGCCTTTTTA 	LysGlyAspGlyProProlleTyrAspAsnIleLysThrArgAspGluGl	AGTGTCCAÀAATCAGAACTATGTTCTTAAATGG. :::::::::::::::::::::::::::::::::::	GGTGTCTATAGTCCAGTACAGTTGTATAAAGACCACAGTTGAAAATGAACT ::: Ala :::    :::      :::   ACCT :::   ASNTALLeuGluAsnAspLe ACCT :::   CCCT :::   CCACCAGAAAATATAGAAGTC	ATCTGGAAAACTCTTCAGGTGTAGAAGAAAGATTGAAAATATTTATT	LysThrPheSerSerThrProSerGluProProAsnAsnValThrLeugl  A. GCTGAAGATAAGGCAATAGTGCACACATCTCTCCTGGAACAAAAG
gHisTyrThrvalSerTyrGl AACAAATACCTGACTGTGAAA Hish Hish CAAAACGTTTTCCAAAAAGGA ::::::::	GCTCCACGCCTTTTA   ::::::     pileaspThrMetLeu	AsmīleLysThrArgAspGluGl	yArgGlyIleProAs yrHisIleLeuLysA	GTATAAAGACCACAGTTGAAAATGAACT:   :::      :::		
879 879 910 929 925	824 882 833	776 849 776	770 799 770 816 776	712 751 716 768 737 784	580 710 630 727 662 743	663 480 680 530

919 lyAlaAsnAsnIleAlaLeuHisTrpGlyProProGlnHisProGluIle 935	172 GG
902 uAspGluThrGlnValProGlyLysProlleTrplleSerileHisProG 919	614 OATGASpLeuValAlaGinileValLysSerArgPheValThrLeuSerT 631
895 Ala	
8/8 LEALAALAMETINIVALÄSIGIYSEIGIYPIOPHETHIGIUTIPASIAIG 894 663 GGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACT 712	Align seg 1/1 to: T13823 from: 1 to: 1526
TTAAAGCAGCACTACTTACGTCATGGAAAATT	alignment_block: US-09-240-675-1 x T13823
581 CAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAG 630	Percent Similarity: 38.264 Percent Identity: 16.399
LUASPATGABABACTOTOTO ACCORDANGE AND ACCARDAGABABACTOTOTO ACCORDANGE ACCARDAGABABACTOTOTO ACCORDANGE ACCARDAGABACTA ACCARDAGA ACCARDAGABACTA ACCARDAGA ACCARD	A;Cross-references: EMBL:U71002; NID:g1621116; PID:g1621117; PIDN:AAC47315.1 C;Genetics: A;Gene; frazzled A;Map position: 2
UValThrSerSerSerSerIleThrValHisTrpGluProProAlaGluG	A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A; Residues: 1-1526 < ROLL  A;
798 LysThrPheSerSerThrProSerGluProProAsnAsnValThrLeuGl 814 434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG 480	zzled encodes a Drosophila number: z17780
::	Mitchell, K.J.; Goodman, C.S.; Fri
388 CACCATTTCGCAAAGCTCAGATTGGT	frazzled gene protein, log isoform - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
764 ualavalLeuThrGluLeuArgProHisThrAspTyrVallleSerValV 781	
SerGluAsnAspSerGlyAlaAspLeuTyrHisAspSerThrAlaLeuGl	1241 AGCCAGAGCACACC 1256 
731 luGluProThrValThrAsnGlyGluIleLeuLysTyrArgValTyrTyr 747	1016 ThrMetLeuMetLeuProAsnLeuLysProTyrThrThrTyrTyrPheLy 1032
714 gAsnPheGluGlyTyrAlaArgSerHisLysGluIleTyrValLysTrpG 731 370 ATGAG	
698 ProLeuGluValSerThrGlnProGluValAsnIleAlaGlyProProAr 714 336	CTGATTTATGAAATTATTTTTTGGGAAAACA sHisThrLeuGlyGlnIleThrGlyTyrAsnIleTyrTyrThrThrAspr
681 inPheArgvalGluAlaAsnThrAsnPheGlySerGlyAlaSerSerAla 697 300CTCAAGCTGAATGTTTATGAAGAATTAAATTGCGT	GCTCCAAAACAGTCTGGAA :::::::: LeuAspGluMetAsnProP
664 SASPASPGINGINVALASNIIGGINSERLEULEUPTOGIYARGTHTTYRG 681 265 AGAATATTACTAGTACCAAATGCAACTTTTCTTCA	
648 TyrlysmetAsnAsnSerGluArgGluGlnLysmetValThrLysSerH1 664 215 CGATTATCAAAAAACTGGGATGATAAATTGGATAAAATTGTCTGGGTGTC 264	980 GTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTC 1029      :::::
631 rpValGluProLeuGlnAsnAlaGlyAspValValTyrTyrThrValTyr 647	930 ATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTG 979

seq\_documentation\_block: neogenin - chicken (frágment)

3.3 3.5

666 GTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACC 715

seq\_name: pir2:150600

C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 13-Sep-1996 A;Cross-references: EMBL:U07644; NID:g641965; PID:g641966 R;V1elmetter, J.; Kayyem, J.F.; Roman, J.M.; Dreyer, W.J.
J. Cell Biol. 127, 2009-2020, 1994
A;Title: Neogenin, an avian cell surface protein expressed during terminal neuronal A;Reference number: A55193; MUID:95105243 alignment\_block: alignment\_scores: Percent Similarity: Align seg 1/1 to: I50600 from: 1 to: 1443 US-09-240-675-1 x I50600 Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-1443 <VIE> Accession: I50600 432 lAlaThrLeuValSerThrArgPheIleArgLeuThrTrpArgThrProV 449 137 GGTCGACATCATAGATGACAACTTTATC...CTGAGGTGGAACAGG.... 179 416 LeuAlaProAlaThrThrGlyProLeuProThrAlaProArgAspValVa 432 510 ... SerSerAlaProLeuLysValAlaThr ..... GlnProGluValGl 378 GACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACA 427 328 AATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTT 377 477 rArgProGlyGluThrGlnValMetIleGlnAsnLeuMetProGluThrV 494 228 ACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAG 277 449 alserAspProGlnGlyAspAsnLeuThrTyrSerIlePheTyrThrLys 465 494 alTyrValPheArgValValAlaGlnAsnLysHisGlyHisGlyGlu... 509 278 TACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTA 590 luTyrSerPheArgValValAla.....TyrAsnLysHisGlyProGly 573 lAspValAlaGlyLeuSerTyrThrIleThrGlyLeuLysLysTyrThrG 590 516 ACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGAT 565 540 ervalThrValThrTrpGluThrProLeuSerGlyAsnGlyGluIleGln 478 AAGATAGTGTTATGTGGGCTTTG.....GATGGTTTAAGCTTT 523 nLeuProGlyProAlaProAsnIleArgAlaTyrAlaGlySerProThrS 428 TITAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAA 477 616 CTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGT 665 566 TGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTA 615 557 AsnTyrLysLeuTyrTyrMetGluLysGlyGlnAspSerGluGlnAspVa 87 TTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGA 136 GluGly... ..AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAA 227 Quality: Ratio: 127.50 0.644 47.711 ...IleAsnArgGluArgValGluAsn...ThrSe Length: 415
Gaps: 19
Percent Identity: 22.169 573 556 515 523 604 540

1. Endocrinol. 4, 235-244, 1990 1. Endocrinol. 4, 235-244, 1990 Title: The rat insulin receptor: primary structure and conservation of Reference number: A36080; MUID:90231337 Reference number: Reference mixia Molecule type: mixia Molecule t	q_name: pir2:A36080 q_documentation_block: q_documentation_block: sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin receptor precursor rat sulin rational r	AAAAACTGATGTTACAGTT  ::	1059 TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACAGCCCTGT 1108	688 ThrGluTyrAsnPheArgileAlaAlaMetThryalAsnGlyThrGlyPr 704 972TCTTTTTGGTCTGAAGAGATAAAGTTTGAFAACTACAAGCTT 1017	849 TATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGT 897	621 aAlaProGlaAsnLeuThrLeuGluAlaArgAsnSerLysSerIleMetL 638 763 TTAAATGGGATTATACATATGCAAACATGACCTTTCÁAGTTCAGTGGCTC 812	SerA
tissue-specific  500 eSerAspGiuArgArgThrTyrGlyAlaLysSerAspIleIleTyrValG 617  691 AGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGT 740  691 AGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGT 740  691 AGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGT 740  691 AGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGT 740  691 AGACCACAGAAATTAAATGAACTACTACTACATATATAGAAATTATAGAAGTCAGT 740  691 AGACCACAGAACTAAATGAACTATGTTCTTAAAATGAACTTACATA 781  690 eSerAspGiuArgAATGAAATTAGCACCTTTTAAAAAGTAGTTAGATTAGAAATTATAGATTAGATTATAAAATGAAATTATAGAAATTATAGAAATTATACATA 781  690 eSerAspGiuArgAATGAACTACCTACCACACATTATAAAAAATTAGAATTAGAAATTATAGAAATTATAGAAATTATAGAAATTATAGAAATTATAGAAATTATAAAAATGAACTATGTTCAAGTTTTAAAAAAAA	550 GTGTAGAAAGGAATGAAAATÄTTTÄTTCCAGACATAAAA 583 600 CTCTCACCAGACACTACTTATTCTCTAAAAGTTAAAGCAGCA 611:::	450 ATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTT 499 571 SerGlnThrProSerH1sProGly	350 AGAAACACTICTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCA 399 ::::::::       551GlySerAsnSerTrpThrValValAsp	241 OASPPRATGASPLEULEUGLYPHEMETLEUPHETYTLYSGLUALAPTOT 538 262 GTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCA 299      :::   538 yrGlnAsnValThrGluPheAspGlyGlnAspAlaCys550 300 CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAA 349 550	ACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCA	t_block: t_block: 40-675-1 x A36080  eg 1/1 to: A36080 frc TCAAAAAGTAGAGGTCGACATC     :::::     :::    serGlyThrLysGlyArgGlnG	alignment_scores: Quality: 127.00 Length: 474 Ratio: 0.645 Gaps: 21 Percent Similarity: 41.561 Percent Identity: 19.620

```
C;Accession: A31555:
R;Aguet, M:; Dembic, Z:; Merlin,
Cell 55, 273-280, 1988
                                                                                                                                                                                A; Title: Molecular cloning and expression of the human interferon-gamma receptor. A; Reference number: A31555; MUID:89003065 A; Accession: A31555:
                                                                                                                                                                                                                                                                                                                   interferon gamma receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-reb-1990 #sequence_revision 28-reb-1990 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                         A;Gene: GDB:IFNGR1; IFNGR
A;Cross-references: GDB:120688; OMIM:107470
                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     req_name: pir2:A31555
                                                                                                                 A;Cross-references: GB:J03143;
                                                                                                                                       Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1034 CTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTC 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1200 ACAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGC 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1300 TATGTGAGAAAACAAAACCA 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1250 ACACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTG 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1159 CAAATGCTGAGAGAAAAATTATCGAGAAA......AAAACTGATGTT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  669 LeuPheGluLeuAspTyrCysLeu.....LysGl 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                879 AATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655 ..........H1sTyrLeuValTyrTrpGluArgGlnAlaGluAspSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 ATCCTGGAAACCATTTGTATAAATGG...AAACAAATACCTGACTGTGAA
p position: 6q23-6q24

perfamily: interferon gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 841 alserAlaArgThrMetPro 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 761 LysArgArgSerLeuGluGluValGlyAsnValThrAlaThrThrProTh 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 712 SerCysProLysThrAspSerGlnIleLeuLysGluLeuGluGluSerSe 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678 yLeuLysLeuProSerArgThrTrpSerProProPheGluSerAspAspS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       929 AATTTACCTT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            777 rLeuProAspPheProAsnIleSerSerThrIle.....AlaProThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 993 .....AAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695 erGlnLysHisAsnGlnSerGluTyrAspAspSerAlaSerGluCysCys 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     792 erHisGluGluHisArgProPheGluLysValValAsnLysGluSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          825 aCysAsnGlnAspSerProGluGluArgSerGlyVal...AlaAlaTyrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    809 ValileSerGlyLeuArgHisPheThrGlyTyrArgIleGluLeuGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rPheArg...LysThrPheGluAspTyrLeuHisAsnValValPheValP 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATCCAGGATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-489, <AGD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....CTCCGCGTACAAGCAT 954
                                                                                                               NID: g184650; PIDN: AAA52731.1;
                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                          1.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ACGCCTGT 1108
                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     808
                                                                                                                 PID:g306915
  alignment_block:
US-09-240-675-1 x A31555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                      181 erGluIleGlnTyrLysIleLeuThrGlnLysGluAspAspCysAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368
                                                                                                                                                                                                                                                                                                            160 sp....
                                                                                                                                                                                                                                                                                                                                                                                                   147 sProSerValPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124.50
```

C; Keywords: cytokine receptor; transmembrane protein

Percent Identity: 22.222 Length:

to: A31555 from: 1 to: 489

86

113 rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP

roLysLeuAspIleArgLysGluGluLysGlnIleMetIleAspIle... CAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT 467

145

CCTGGAACAAAAGATAGTGTTATGTGGGCTTTTGGATGGTTTAAGCTTTAC 517 ...PheH1 147

518 ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG .....AsnGlyAspGluGlnGluValA 567

160

568 AAAATÄTTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACT .....TyrAspProGluThrThr 166 617

668 CTATACTCCAGTAC...ATTGTATAAAGACCACAGTTGAAAATGAACTAC 714

715 CTCCACCAGAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTC.. 762

1011 CAAGCTTTCCTACTTCCTCCA			TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTG
911 AAAGTTTTCCAAAAAGAATTACCTTCTCCGCTAAAAGAATCTAATG 960 670 TyrilePheArgyalArgAlayalAgaa 679 961 GAAATAACAATCTTTTTGGTCTGAAGAATAAAGTTTGATACTGAAATA 1010 961 GAAATAACAATCTTTTTGGTCTGAAGAAAAGTTTGATACTGAAATA 1010 679 laaladlyLeuSerGluTyrSerGlnAspSerGlu. AlaileGluVal 694		م نسوست	201GTGACTTTTCATTCGATTATCAAAAAACTGGGATGGATAATTGGA 246
ひょ 塩と 焼 さわご			NATION SECTION
774			Percent Similarity: 45.652 Percent Identity: 19.783
747 AATCAGAACTATGTTCTTAAATGGGAT.  1     : : :       : : :       : : :         : : :	<del></del>		emin
702GAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAA 746		PID:q407099	Status: preliminary Molecule type: mRNA Residues: 1-1451 <vin> Cross-references: EMBL:X69090; NID:g407098; PIDN:CAA48833.1; PII</vin>
677 AGTACATTGTATAAAGACCACAGTT	н	r of the sarcomeric M h	330, 1993 head domain of ti 2166; MUID:940956
627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676 :::   ::::::::::::::::::::::::::::::		4-Sep-1999	es: Homo sapiens (ma 13-Jan-1995 *sequen sion: S42167 meier, U.; Obermann,
582AGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626		· · · · · · · · · · · · · · · · · · ·	eq_name: pir2:S42167 eq_documentation_block: 90K protein - human
uAlaGlyThrGluAsnTrpGlnArg\			297 u 297
540	•		yy TIGATACTGAAATACAAGCTTTCCTACTTCCTGCAGTCTTTAACATTAGA 1046 :::      ::::     281 IleIleLeuProLysSerLeuIleSerValValArgSerAlaThrLeuGl 297 1047 T 1047
508 TAAGCTTTACA	÷		
458 ACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGGCTTTTGGATGGTT :::::::::::::::::::::::::::			897 TGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGT 946    :::
408 ATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGAT :::	1 -		847 TGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAG 896 .   :::   ::: 242 SerileLysGlySerLeuTrp
369TATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAG	:		806 GTGGCTCCACGCCTTTTAAAAAGGAATCCTGGAAACCATT846 ::::!! !!! 225 lyValThrThrGluLysSerLysGluValCysIleThrIleDheAsnSer 241
333	<del></del>		763TTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTTCA 805

266 GAATATTACTAGTACC	105 GGAAAAAATCTAAAAATCTCCTCAAAAAGTAGAGGTCGACATCATA	alignment_block: US-09-240-675-1 x 551604 Align seg 1/1 to: 551604 from: 1 to: 981	alignment_scores:  Quality: 118:00 Length: 458  Ratio: 0.602 Gaps: 21  Percent Similarity: 42.795 Percent Identity: 20.087	F;651-917/Domain: protein kinase homology <kin> F;659-667/Region: protein kinase ATP-binding motif</kin>	sterences: EMBL:568029 ne authors translated the codon G nily: protein-tyrosine kinase, re s: ATP: transmembrane protein		R: Maisonplerre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D. Oncogene 8, 3277-3288, 1993 A; Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family. Reference number: \$49015; MVID: 94067777	ine kinase Ehk-1 - rat orvegicus (Norway rat) #sequence_revision 21-Jul-1995 #:	<pre>seq_name: pir2:S51604</pre> <pre>seq_documentation_block:</pre>	1281 AGTGTTTTTAGTGACGCTGTATGTGAGAAA 1310 :::    :::     ::: 791 AlaValSerGluCysPheLysCysGluGlu 800	1231 ATTGTGTGAAAGCCAGAGCACCACCATGGATGAAAAGCTGAATAAAAGC 1280 	1181 CGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACTG	1143TTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTAT 1180	1096 GAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATT 1142   ::::: :::          :::    728 lyGlyAlaGluIleThrGlyTyrTyrValAsnTyrArgGluValIleAsp 744	:   :::      ::: :::        ::::::  711 uSerPheArgAspSerMetValLeuGlyTrpLysGlnProAspLysThrG 728
		811 TCCACGCCTTTTTAAAAGGAATCCTGGAAACCATTTGTÄTAAATGGÄAA.860 LIIIII ::: III::: II::: III:	771GATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGC 810	741 GTCCAAAATCAGAACTATGTTCTTAAATGG	720 CCAGAAAÄTATAGAAGTCAGT 740         :::       ::: 353 hrmetalaCysThrArgProProSerAlaProArgAsnAlaTleSerAsn 369	684	648 ACGTCATGGAAAATTGGTGTCTATÁGTCCAGTACAT	598 AACTCICACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTT 647	551 TGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAAATTTATA 597	501 GATGGTTTAAGCTTTACATATAGCTTACTTGGAAAAACTCTTCAGG 550	451 TAGTGATACACATCTCTCCTGGAACAAAGATAGTCTTATGTGGGCTTTG 500 :	401 AGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAA 450 ::::	351 GAAAACACTTCTTCATGGTÀTGAGGTTGACTCATTTACACCATTTCGCAA 400 :::::   :::	301 TCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAAA 350        ::: ::: 240 rgHisLeuAlaValPheProAspThrIleThrGly 251	223 eAlaLeuValSerValArgValTyrTyrLysLysCysProSerValValA 240

1. 水香香油 1.4

50	*55 YIM AIGGIDTYIVALSEIVALASNVALThIThIASDGIDALAALAPIOS 472	172
1102	1102 CGCCTGTGATCCAG	1115
472	472 erProValThrAsnValLysLysGlyLysIleAlaLysAsnSerIleSer 488	88
1116	: .	135
489	489 LeuSerTrpGlnGluProAspArgProAsnGlyIleIleLeuGluTyrGl 505	05
1136	1136 AATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTTATCGAG, 1	1184
505	505 ulleLysTyrPheGluLysAspGlnGluThrSerTyrThrIleIleLysS 522	522
1185	1185AAAAAAACTGATGTTACAGTTQCTAATTTGAAACCACTGACTGTATAT 1232	232
522	522 erLysGluThrThrIleThrAlaGluGlyLeuLysProAlaSerValTyr 538	538
1233	1233 TGTGTGAAAGCCAGAGCACACC 1256	
539	539 ValPheGlnIleArgAlaArgThr 546	

```
Database: SwissProt_38:*
Database sequences: 83857
Database length: 30454973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query: US-09-240-6
Query length: 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
Query: US-09-240-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM of: US-09-240-675-1 to: SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -Q-/cgn2_1/USFTO_spool/US09240675/runat_30052000_165119_3047/app_query.fasta.1
-DB-SW1ssFrot_38 -QFMT-fastan -SUFFIX-modif_rsp -GAPOP-12.000
-GAPEXT=4.000 -MINANCH-0:100 -LOOPCIA-0:000 -LOOPEXT-0:000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPORT-0.500
-DELOP-6.000 -DELEXT-7.000 -STAFT-1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext|-MINLEN-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAXLEN-1000000 -USER-US09240675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                issProt_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ssProt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .ssProt_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ssProt_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ssProt_38:CIC2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38:PTPD_HUMAN + 116:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38:EPA5_HUMAN + 108.00
38:I131_HUMAN + 107.00
38:I10R_HUMAN + 107.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38:MYM1_HUMAN + 1
38:EPA5_RAT + 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8:CIC2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8:DCC_MOUSE + 111.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (sec): 84.100000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _n2p.model -DEV-xlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105.50
105.50
104.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173.10
161.77
156.97 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 137.83 0.3168
135.94 0.3858
0 139.72 0.3913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161.28 0.0376
152.67 0.0476
148.19 0.0606
149.22 0.0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                          0.5497
53. 0.5888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0374
0.0374
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0860
                                                                                                                                                                                                                                                                                                                                                                                                                   1383 | 1451 | 1451 | 1451 | 1451 | 1755 | 1372 | 1372 | 1450 | 1450 | 1447 | 1037 | 1427 | 1037 | 1427 | 1382 | 1447 | 11382 | 1447 | 11382 | 1447 | 11382 | 1447 | 11382 | 1447 | 11382 | 1447 | 11382 | 1447 | 11382 | 1447 | 11382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1382 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1447 | 1
                                                                                                                                         P40189 homo sapiens (human).
P15261 mus musculus (mouse).
P08973 spinacia oleracea (s
P08973 spinacia thaliana
P56786 arabidopsis thaliana
P08875 homo sapiens (human)
P43811 haemophilus influenza
P32927 homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                  P42701 homo sapiens (human)
1 P25955 mus musculus (mouse)
1 P20241 drosophila melanogasi
1 P10586 homo sapiens (human)
1 P09976 nicotiana tabacum (d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P54757 rattus norvegicus (r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P78552 homo sapiens (human 013651 homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q61727 mus musculus (
P15208 mus musculus (
P23468 homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 rattus norvegicus (r. 5260 homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 homo sapiens (human
954 mus musculus (mouse
4289 homo sapiens (huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00 rattus norvegicus (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1756 homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2179 homo sapiens (huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )96 mus musculus (mouse
)34 homo sapiens (human
)84 homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 gallus gallus (
rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00 bos taurus
19 ovis aries
                                                             tobacco mosaic vi
                                                                                           plasmodium falcipa;
saccharomyces cerev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (mous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         norvegicus (r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SwissProt_38:CAlC_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                        EMBL; J03171; AAA52730.1;
EMBL; X60459; CAA42992.1;
PIR, A32694. A32694.
PIR; S17112; S17112.
WIM; 107450;
                                                                                                                                                                                    SIGNAL
DOMAIN
TRANSMEM
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                 Phosphorylation
                                                                                                                                                                                                                                                                Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFNAR1 OR IFNAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INR1_HUMAN
                                                                                                                                                                                                                                                                   Transmembrane;
436
457
557
220
                                                                                                                                                                          557
```

Glycoprotein; Signal;

Polymorphism;

POTENTIAL. CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

INTERFERON-ALPHA/BETA RECEPTOR CHAIN.

```
SwissProt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDIJINE; 90124632.

Uze G., Lutfalla G., Gresser I.

"Genetic transfer of a function
into mouse cells: cloning and of the cell 60:225-234(1990).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute, of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE; 92129376.

Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;

Lutfalla G., Gardiner K., Proudhon D., Vielh E., Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mullersman J., Witte M., Krishnan K., Krolewski J.;
"Direct binding to and tyrosine phosphorylation of the alpha subunit of the type I interferon receptor by pl35tyk2 tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colamonici O., Yan H., Domanski P.,
Mullersman J., Witte M., Krishnan K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15,
01-AUG-1990 (Rel. 15,
15-FEB-2000 (Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION BY TYK2. MEDLINE; 95059042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERFERON-ALPHA/BETA
                                                                                                                                                                                                                                    SUBUNITS THEMSELVES.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.
PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYRZ TYROSINE KINASE.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol 14:8133-8142(1994)
FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYLE I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYRZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SwissProt_38:INR1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         functional human interferon alpha receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.50
97.50
97.50
97.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
125
124
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Handa R., Smalley D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P06242 saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mus muscul
```

167 uLeulleTrpLysAsnSerSerGlyValGluArgIleGluAsnIleT 184	134 181-1811	101 LysLeuargileargalaciuLysciuAsminserseripTyrcluva 117 101 LysLeuargileargalaciuLysciuAsminserseripTyrcluva 117 377 TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426 111	227 AACTGGATGATAAATTGCTTATTA 276	127 AAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAAC 176	77 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTC 27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTC 27 ATGATGGTCGTCCTCCTGGGCGCGACGACCCTAGTC 27 ATGATGGTTCTCTCGCAGCGCAGGTGGAAAAA 27 CCCATGGGTGTTGTCCGCAGCGCAGGTGGAAAAA 27 CCCATGGGTGTTCTCCCGCAGCCGCAGGTGGAAAAA 28 ATGATGTTCTCCGCAGCGCAGGTGGAAAAAA 29 ATGATGTTCTCCGCAGCGCAGGTGGAAAAAA 20 ATGATGTTCTCCGCAGCGCGAGGTGGAAAAAA 21 ATGATGTTCTCCGCAGCGCGAGGTGGAAAAAA 21 ATGATGTTCTCCGCAGCGCGCAGGTGGAAAAAA 21 ATGATGTTCTCTCTCTCTGGTGTGAAAAAAAAAAAAAAA	Quality: 2313.00 Ratio: 5.305 Ratio: 5.305 Ratio: 5.305 Ratio: 100.000 Percent Id Lock: 675-1 x INR1_HUMAN 1/1 to: INR1_HUMAN from: 1	CARBOHYD 433 433 POTENTIAL.  VARIANT 168 168 'L->V CONFLICT 17 17 G->A (IN REF. 2)  SEQUENCE 557 AA; 63525 MW; 0F6744C8AlADBE73  ignment_scores:	FI CARBOHYD 81 81 POTENTIAL.  FT CARBOHYD 110 110 POTENTIAL.  FT CARBOHYD 172 172 POTENTIAL.  FT CARBOHYD 254 254 POTENTIAL.  FT CARBOHYD 313 313 POTENTIAL.  FT CARBOHYD 314 314 POTENTIAL.  FT CARBOHYD 376 POTENTIAL.  FT CARBOHYD 376 POTENTIAL.  FT CARBOHYD 416 POTENTIAL.	MOD_RES 466 466 MOD_RES 481 481 CARBOHYD 50 50 CARBOHYD 58 58
The state of the s			367. UIII 1177 TANT 1111 1384 1911 1227 GYAT	1077 GGTG 351 GLYA 1127 GATT		827 AAGG       267 sarg 877 AAAA      1	שר ביו שר ביו	627 AAAG       201 Lysv 677 AGTA      217 oval	577 A
999 (Rel. 35, Last sequence update) 997 (Rel. 35, Last annotation update)	sProt_38:INR1 sProt_38:INR1 fon_block: N STANDAI 93 (Rel. 27,	PalTyrcysVallysAlaArgAlaHisThrMctAspGlulysLeuAsnLy 417 LAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1321	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OPTOVALIA DELL'AND COLLAND DELL'AND COLLAND DELL'AND COLLAND DELL'AND COLLAND DELL'AND COLLAND DELL'AND COLLAND DELL'AND CASCACTA DELL'AND CASCACTA DELL'AND CASCACTA DELL'AND CASCACTA DELL'AND CASCACTA DELL'AND CASCACTA DELL'AND CASCACTA DELL'AND CASCACTA DELL'AND CASCACACACTA DELL'AND CASCACACACTA DELL'AND CASCACACACTA DELL'AND CASCACACACACTA DELL'AND CASCACACACACTA DELL'AND CASCACACACACACTA DELL'AND CASCACACACACACTA DELL'AND CASCACACACACACACTA DELL'AND CASCACACACACACACACACACACACACACACACACACA	SGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTT 976	AGGAATCCTGGAACCATTTGTATAAATGGAACAAATACCTGGAACAACTACTGGAACAAATCCTGGAACCAACTACTGGAACAAATCCTGGAACAACTACTGGAACAAATCCTGACAGGAACAAATCCTGACTGGAACAAATCCTGAACAACCTACTGCAACAACTACTACCAACAACCATTTCCAAAAACCTTTTCCAAAAAA		AAGÍTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676	TTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626 

```
alignment_block:
US-09-240-675-1 x INR1_BOVIN
                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DISULFID
                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: X68443; CAA48484.
EMBL: L06320; AAA02571.
PIR: S33770; S33770.
PIR: S27387; S27387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Im J.-K., Langer J.A.;

(Cloning and characterization of a bovine alpha interieron receptor., (Cloning and characterization of a bovine alpha interieron receptor., Blochim. Blophys. Acta 1173:314-319(1993).

10 FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-INCLUDING JAKS, TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouchel-Vielh E., Lutfalla G
"Specific antiviral activiti
determined at the level of r
TEBS Lett. 313:255-259(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Cl
Eutheria; Cetartiodact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
FISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. SEDLINE; 93305725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93076908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFNAR1 OR IFNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long
                                                                                            smembrane; Glycoprotein; Signal.
                                              3.987
86.105 Percent Identity: 64.920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Mammalia; actyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G., Mogensen K.E., Uze G.;
ties of the human alpha interferons are
receptor (IFNAR) structure.";
                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL:
                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                     6D76B72861E1D11 CRC64;
                                                                                                                                        16 · 16 · 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
```

Align seg 1/1

to: INR1\_BOVIN from:

6

图 医氯甲基磺胺

S Shows

921 CAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACAC 970

ACTGTGAAAAT ::              2 snCysGluAsn	GAAA GAAA GIWA GIWA GIWA GIWA GIWA GIWA	Serva TATTT ::::I rvalT rvalT GTCTA 	alglupro	CAAATGCA		O ATGGGTGTTG                         6 GTTPValLeu   6 GTTPValLeu   7 AAGTAGAGGT   7 TTPTAGAGGT   7 TTPTAGAGGT   8 TTPTAGAGGT   9 TTPTAGAGGT   10 ATGGGTGTTG   10 ATGGTGTGTG   10 ATGGTGTGTGTG   10 ATGGTGTGTG   10 ATGGTGTGTGTG   10 ATGGTGTGTGTGTGTG   10 ATGGTGTGTGTGTGGTGTG   10 ATGGTGTGTGTGTGTGGTGTGGTGTGGTGTGTGGTGGTGTG	1 MetLeuAlaL
GTCAAAACTACC     :::    ValThrSerThr	TITIANAAGE TOPS LEASING CYSTLEASING ANTOLOGISTS ANTOLOGISTS ANTOLOGISTS COAMCATGAC LITERASINALS LITERASINALS COCCESSANCE COCCESSANCE LITERASINALS FOR COCCESSANCE COCCESSANCE COCCESSANCE COCCESSANCE LITERASINALS FOR COCCESSANCE COCCESS	TIPLYSASNS PACATAAAATT HILL HASPLYSILE HAAGCAGCACT HILL HILL HAAGCAGCACT HAGGAGCACT HILL HILL HAGGAGCACT HAGGAGCACT HAGGAGCACT HILL HILL HAGGAGCACT	:::	TTTTCACTO	T - 6 - 6	TCCGCAGCCGCAG	TCCTGGGCGCGA
CAGTGTGTCTTTC :::         H1sCysValPheP	ANCASTIGAAA IIII IIII IIIII IIIIIIIIIIIIIIIII	erSerSerLeug rataaacTcTcA rataaacTcTcA riiiiiiiiiiiiii TyrLysLeuSer acTTACGTCATG acTTACGTCATG	euglualaglai GCAATAGTGAD GCAATAGTGAD 	AAGCTGAA	GACTTTTCATT          ThrPheSeral TGTCTGGGTGTC	GTGGAAAAATC	GACCCTAGTGCT       :::   uThrLeuMetLe
TCAAAACGTTTT  :::::::    OArgGluValSe	SCAACTACCTCCA SCAACTACCTCCA SUSSISSISSISSISSISSISSISSISSISSISSISSISS	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ProProAsp CTCTCC 	TTTATGAAGAA   :::   ::: alpheGluLys TCTTCATGGTA    :::     SerThTTTPTY	GATTATCAAAA          AspTyrGlnI1 AspTATTACTA  :::	ATCTCCTCA	CGTCGCCGTGGGCC         
C 920 r 298	10 120 120 120 120 120 120 120 120 120 1	. K — M — H — H — I - H — H — H — I	V 132 V 132 V 132 V 1470 V 1520 V 165	226 10 10 10 10 10 10 10 11 11 11 11 11 11	10 229 11 279	1 6 A A	oc 79

rSerPheTrpSerGluGluLysGluPheAsnThrGluMetLysThrIleI 332 ATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCC 1020

mod1f1ed

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

non-profit institutions as long as its content and this statement is not removed. Usage by an

//www.isb-sib.

.ch/announce/

and

ģ

ö

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS. TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT CONCEPTUS AT DAY 15 OF PREGNANCY.

299

315

÷

```
1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1318 CAGGAAATACCTCTAAA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     028589; 095206; 01:NOV-1997 (Rel. 35, Created) 01:NOV-1997 (Rel. 35, Last-sequence update) 01:NOV-1997 (Rel. 35, Last-sequence update) 15-FEB:2000 (Rel. 39, Last-annotation update) INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC) (INTERFERON-ALPHA/BETA RECEPTOR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                            Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 roGlyAsnThrSerLys 437
                                                                                                                                                                                                                                                                                                                                                                      TISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                    Endocrinology 138:4757-4767(1997) 4 USE IN MESSED WITE A COLUMN
                                                                                                         ribonucleic acid for ovine receptors during the estrous cycle and pregnancy.
                                                                                                                                                                                                  MEDLINE; 98006426
                                                                                                                                                                                                                                                                                             "Structure of an ovine interferon receptor and andometrium.";
                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97135690.
Kaluz S., Fisher P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Caprinae;
                                                                                                                                              Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger
                                                                                                                                                                                   Han C. S., Mathialagan
                                                                                                                                                                                                                       ISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     Mol. Endocrinol. 17:207-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gArgAsnLysGlySerSerPheSerAspThrValCysGluLysThrLysP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGAAAATTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uTyrProLeuIleTyrGluValIlePheTrpGluAsnThrSerAsnAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTG 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGA 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lePheProProValIleSerValLysSerValThrAspAspSerLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGT...GATTCATTCCAT 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACTGACTGTATATTGTGTGAAAGCCAGAGCACACACCATGGATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValSerValGlyAlaSerGluGluSerGluAsnMetSerValAsnGlnLe
                                FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEIN INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProLeuThrValTyrCysValLysAlaArgAlaLeuIleGluAsnAspAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               luArgLysValLeuGluLysArgThrAsnPheIlePheProAspLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SwissProt_38: INR1_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                   N., Klemann S.W.,
                                                                                                                                                                                                                                                                                                                                 Kaluzova M.,
TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 560
                                                                                                                                                                                                                                                                                                                                 Sheldrick E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ζ
                                                                                                                                                                                   Roberts R.M.;
                                                                                                                                                                                                                                                                                     ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                            its expression
                                                                                                                                                                                                                                                                                                                                 Flint A.P.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348
                                                       PROTEINS
```

alignment\_block:

1.10 BASE 1.100 A

US-09-240-675-1 x INR1\_SHEEP. ...

alignment\_scores:

Quality: 1503:00

\*

Percent Similarity:

3.997 Gaps: 85.649 Percent Identity:

Length: Gaps:

439 64.465 ÷.

```
888888888888888
                                                                              CARBOHYD
CARBOHYD
                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                        DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http:/
                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                          EMBL; U65978; AAB84231:1; -
                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                           DOMAIN
 SEQUENCE
                                                 CARBOHYD
                                                           CARBOHYD
                                                                     CARBOHYD
                                                                                                                     CARBOHYD
                                                                                                                               CARBOHYD
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                               EMBL; X95939; CAA65183.1;
          CONFLICT
                             CARBOHYD
                                         CARBOHYD
                                                                                                                                                                                                                                  (eceptor;
                                                                                                                                                                                                               560
                                                                                                                                                                                                                        Glycoprotein; Signal BY SIMILARITY.
                                      POTENTIAL.
POTENTIAL.
                   POTENTIAL.
S -> G (IN
          A .->
                                                                                                 POTENTIAL.
                                                                                                                                                   BY SIMILARITY
BY SIMILARITY
                                                                               POTENTIAL.
                                                                                                                     POTENTIAL.
                                                                                                                                                                       CYTOPLASMIC (POTENTIAL):
                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                               INTERFERON-ALPHA/BETA RECEPTOR
                                                                     POTENTIAL.
-> G (IN REF. 2)
-> D (IN REF. 2)
E7198A1905D4805C
 CRC64;
                                                                                                                                                                                                               ALPHA
```

```
、小心心 280、CCAAATGCAACTTTTCTTCACTCAAGCTG..., AATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                       180 AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAAC
                                                                                                                                                                                                                                                          130 AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                              230 TGGGATGGATAATTGGATAAATTGTCTGGGTGTCAGAATATTACTAGTA 279
                                                                                                              49 SerSerGluSerValArgAsnValThrPheSerAlaAspTyrGlnIleLe
                                                                                                                                                                                                     32 snyalGlulleHislleIleAspAspAspAspPheheLeuLysTrpAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                        30 ANGGINGETCCTCCTGGGCGCGACGACCCTAGTGCTCCGTCGCCCTGGGCCCC
                                       65 uGlyThrAspAsnTrpLysLysLeuProGlyCysGlnHisIleThrSerS
                                                                                                                                                                                                                                                                                          16 gTrpvalLeuProAlaAlaSerGlyGluAlaAsnLeuLysSer...GluA
                                                                                                                                                                                                                                                                                                                                     80 ATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                 1 MetLeuSerLeuLeuGlyAlaThrThrLeuMetLeuValAla...GlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: INR1_SHEEP, from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                    to: 560
                                                                                                                                                                                                                                                              179
                                                                                                                     ့်တ
                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                          32
                                                                                                                                                                                                                                                                                                                                                   129
                                                                                                                                                                                                                                                                                                                                                                                             16
                                         82
                                                                                                                                                                       229
```

```
1021 TACTTCCTCCAGTCTTTAACATTAGATCCCTTAGT...GATTCATTCCAT
                                                                                                                                                                                                                                                                                                                                                                      921 CAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571 ATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGAGACTACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 rSerValValIleTrpLysAsnSerSerSerLeuGluGluArgThrGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 TACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT...CCT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        721 CAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGG 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGAAAAATTATCGAGAAAAAAACTGATGTTACAGTTCCTAATTTGAAA
                                                                                         TTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTG
                                                                                                                 ValSerValSerAlaserGluGluSerGluAsnMetSerValAsnGlnLe 365
                                                                                                                                                       ATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGA 1117
                                                                                                                                                                                          ATCTTTTGGTCTGAAĞAĞAĞATAAĞGTTTGATACTGAAATACAAGCTTTCC 1020
                                                                                                                                                                                                                                                                                                                                   SerMetGlyIleTyrTyrValArgValArgAlaSerAsnGlyAsnGlyTh
                                                                                                                                                                                                                                                                                                                                                                                                        snCysGluAsnValThrThrThrHisCysValPheProArgAspIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGTGAAAATGTCAAAACTACCCAGTGTGTGTTTTCCTCAAAACGTTTTC 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eLeuLysLysIleProGlyLysHisSerAsnLysTrpLysGlnIleProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITAAAAAGGAATCCIGGAAACCATTIGTATAAATGGAAACAAATACCIG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roGluAsnValGlnIleAsnValAspAsnGlnAlaTyrValLeuLysTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysLeuLysValLysAlaGluLeuArgLeuGlnSerArgValGlyCysTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrValTyrProGluAspLysIleTyrLysLeuSerProGluIleThrTyr 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGGAAAGGATTGAAA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alRisLeuGluAlaGluAspLysAlaIleIleLeuSerIleSerProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uValGluProPheValProPheLeuLysAlaGlnIleGlyProProAspV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTGCGTATAAGAGCAGAAAAA...GAAAACACTTCTTCATGGTATGA
                                                                                                                                                                                                                                                                   rSerPheTrpSerGluGluLysGluPheAsnThrGluValLysProIleI
                                                                                       1167
                                                                                                                                                                                                                                                                   332
                                                                                                                                                                                                                                                                                                                                       315
                                                                                                                                                                                                                                                                                                                                                                                                          298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 115
                    1217
                                                                                                                                                                                              348
                                                                                                                                                                                                                              1067
                                                                                                                                                                                                                                                                                                                                                                       970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132
                                                        382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148
         11.57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _documentation_block:
                                                 CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                        CARBOHYD
                                                                                                                                       CARBOHYD :
                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 roGlyAsnThrSerLys 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399
                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                            DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M89641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jze G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lutfalla G.,
```

249

182

132

99

82

erLysCysAsnPheSerSerValGluLeuLysAspValPheGluLysIle

98

```
382 luargLysValLeuGluLysArgThrAspPheThrPheProAsnLeuLys
ProLeuThrValTyrCysValLysAlaArgAlaLeuIleGluAsnAspAr
                                                 CCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCACCATGGATGAAAA 1267
     415
                                                                                                     398
```

1268 GCTGAATAAAAGCAGTGTTTTAGTGACGCTGTATGTGAGAAAACAAAAC gTrpAsnLysGlySerSerTyrSerAspThrValCysGluLysThrLysP 432 1317

CAGGAAATACCTCTAAA 1334

g:

```
seq_name: SwissProt_38:INR1_MOUSE
 STANDARD;
 PRT;
590
$
```

Ol-FEB-1994 (Rel. 28, Created)
Ol-FEB-1994 (Rel. 28, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR FNAR1 OR IFNAR OR IFAR (IFN-ALPHA-REC)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Bandu M.T., Proudhon Mogensen Mammalia; Mus. X.E.;

In homospecific or heterospecific background.\*;

Proc. Matl. Acad. Sci. U.S.A. 89:4774-4778(1992).

-I FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT. PROTEINS AND IFN-R ALPHA-AND BETASUBUNITS THEMSELVES:
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS. Behavior of a cloned murine interferon alpha/beta n homospecific or heterospecific background.": receptor expressed

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). a collaboration -

AAA37890.1; IFNAR Glycoprotein; Signal. POTENTIAL:
POTENTIAL: CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY. INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN. POTENTIAL. EXTRACELLULAR (POTENTIAL). POTENTIAL. POTENTIAL 

ž

7EC6DFF370185D3A CRC64;

```
alignment_block:
us-09-240-675-1 x INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: INR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 TTGCGTATAAGAGCAGAAAAAGAAAAC...ACTTCTTCATGGTATGAGGT 376
                                                                                                                                                                                                                677 AGTACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAA 726
                                                                                                                                                                                                                                                                                                          627 AAAGTTAAAGCAGCACTACTTACGTCATGGAÁÁÁÍTTGGTGTGTATAGTCC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sAspGluAlaLysTrpLeuLysValProGluCysGlnHisThrThrThrT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrArgThrLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snIleAspValTyrIleIleAspAspAsnTyrThrLeuLysTrpSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnAspGlyAsnMetTrpAlaLeuGluLysProSerPheSerTyrThrIl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hrLysCysGluPheSerLeuLeuAspThrAsnValTyrIleLysThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTATGAAGAAATTAAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAAAC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGGTGTTGTCCGCAGCCGCAGGT&GAAAAATCTAAAATCTCCTCAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGTCGTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCGTGGGCCC 79
                                                                                                                                                                             TValGlnCysIleSerThrThrValAlaAsnLysMetProValProGlyA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                               eArgIleTrpGlnLysSerSerSerAspLysLysThrIleAsnSerThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgLeuGluAlaGluAspLysAlaIleLeuValHisIleSerProProGly 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheArgValArgAlaGluGluGlyAsnSerThrSerSerTrpAsnGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetLeuAlaValValGlyAlaAlaAlaLeuValLeuValAlaGlyAlaPr 17
                                                                                                                                                                                                                                                                    GluValLysAlaIleHisProSerLeuLysLysHisSerAsnTyrSerTh
                                                                                                                                                                                                                                                                                                                                                             yrTyrValGluLysIlePröGluLeuLeuProGluThrThrTyrCysLeu
                                                                                                                                                                                                                                                                                                                                                                                     ATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA
                                                                                                                                 ATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTAT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTATCTGGAAAAACTCTTCAGGTGTÁGAAGAAAGGATTGAAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleAlaSerAlaAspValLeuPheArgAlaGlnTrpLeuProGlyTyrSe 267
                                            ...ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTT 823
                                                                                      snLeuGlnValAspAlaGlnGlyLysSerTyrValLeuLysTrpAspTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1069.00
3.230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 436
Gaps: 4
Percent Identity: 48.624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436
                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                                                          626
                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100
                                                                                         250
```

```
REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: SwissProt_38:CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1324 ATACCTCT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block:
CRF4_HUMAN STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1224 ACTGTATATTGTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAA 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1024 TICCICCAGICITTAACATTAGATCCCTTAGIGATICATTCCATAICTAT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1274 TAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAA 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1074 ATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 ThrValTyrCysValGlnAlaArgVal...LeuPheArgAlaLeuLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 ValAsnCysGlnAspSerThrCysAsp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                974 TTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTAC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ThrGlyThrPhePheLeuHisValGlnAlaSerGluGlyAsnHisThrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924 AAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATC 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 YSAlaAsnValGlnThrThrHisCysValPheSerGlnAspThrValTyr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            874 GIGAAAATGICAAAACIACCCAGIGIGICTITCCTCAAAACGIIITCCAA 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 rLysSerSerGlySerHisSerAspLysTrpLysProIleProThrC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       824 AAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACT 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            018334;
01FEB:1995 (Rel. 31, Created)
01-FEB:1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-FETAL BRAIN,
MEDLINE: 93300510.
                                                                                                                                                                                                                                     "A new member of the cytokine receptor gene family maps on chromosome lates than 35 kb from IFNAR.".
                                                                                                                                                                                                                                                                                                                                                      Lutfalla G., Gardiner K., Uze G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLysThrSerAsnPheSerGluLysLeuCysGluLysThrArgProGlyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yLeuAsnTyrGluIleIlePheTrpGluAsnThrSerAsnThrLysIleS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGATTTATGAAATTATTTTTTTGGGAAAACACTTCAAATGCTGAGAGAA 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roProProValIleThrValThrAlaMetSerAspThrLeuLeuValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         erMetGluLysAspGlyProGluPheThrLeuLysAsnLeuGlnProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rPheTrpSerGluGluLysPheIleAspSerGlnLysH1sIleLeuProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .G1 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426
```

SEQUENCE FROM N.A.

MEDLINE; 96054036.

Lutfalla G., McInnis M.G., Antonarak
"Structure of the human CRFB4 gene:
neighbor.";
Mcl. Evol. 41:338-344(1995).

Antonarakis S.E.,

Uze G.; with its

IFNAR

ij

comparison

Genomics 16:366-373(1993).

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 HisSerAspTrpValAsnIle ... ThrPheCysProValAspAspThrIl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1 x CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 60.268
                                      357 ACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCA 406
                                                                                                                 310 ATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAA...AAAGAAAAC 35
                                                                                                                                                                                                      260 GTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                160 TTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                               123 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z17227; CAA78933.1;
EMBL; U08988; AAA86872.1;
EMBL; A47003; A47003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch
                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                      36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCT......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                         sCysMetAsnThrThrLeuThrGluCysAspPheSerSer....LeuS 80
                                                                                                                                                                                                                                        ThrAlaGinTyr.....LeuSerTyrArgIlePheGlnAspLy 65
                                                                                                                                                                                                                                                                                   TCATTCGATTATCAAAAACTGGGATGGATAATTGGGATAAAATTGTCTGG 259
                                                                                                                                                                                                                                                                                                                                                                                                             yMetValProProCluAsnValArgMetAsnSerValAsnPheLysA 36
                                                                              erLysTyrGlyAspH1sThrLeuArgValArgAlaGluPheAlaAspGlu
                                                                                                                                                                                                                                                                                                                                snIleLeuGlnTrpGluSerProAlaPhéAlaLysGlyAsnLeuThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuGl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRF4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .228.50
1.693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37011 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 29.911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC: (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66706C79F8514B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR CLASS-II CRF2-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                52
            の、在すののとはない上の
```

```
seq_name: SwissProt_38:INGS_HUMAN
                                                212 rThrHisAspGluThrValPro 219
                                                                                                                  695 CACAGTTGAAAATGAACTACCT 716
                                                                                                                                                                     196 ProAspArgAsnLysAlaGlyGluTrpSerGluProValCysGluGlnTh
                                                                                                                                                                                                                                                                                    179 rgAsnLeuGluProTrpThrThrTyrCysValGlnValArgGlyPheLeu
                                                                                                                                                                                                                                                                                                                                          595 ATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTA 644
                                                                                                                                                                                                                                                                                                                                                                                                      162 yThrAspGluLysPheGlnIleThrProGlnTyrAspPheGluValLeuA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 GATGGTTTA.....AGCTTTACATATAGCTTACTTATCTGGAAAAACTC
                                                                                                                                                                                                                                 645 CTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                545 TTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LysAsnValTyrAsnSerTrpThrTyrAsnValGlnTyrTrpLysAsnGl 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 etArgPheLeuAlaProLysIleGluAsnGluTyrGluThrTrpThrMet 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454 TGATACACATCTCCTGGAACAAAAGATAGTGTT...ATGTGGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 eIleGlyProProGlyMetGlnValGluValLeuAlaAspSerLeuHisM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 GATTGGTCCTCCAGAAGTACATTTAGAAGCT...GAAGATAAGGCAATAG
                                                                                                                                                                        212
                                                                                                                                                                                                                                    694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453
```

```
documentation_block:
                                                                                                                                                                                                                                                              01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
101-NOY-1997 (Rel. 35, Last annotation update)
1NTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).
1FNGR2 OR IFRGT1.
1FNGR2 OR IFRGT1.
Homo sapiens (Human)
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                    Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                              TISSUE-LUNG FIBROBLAST;
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Emanuel S.L., Schwartz B., Miki T., Pestka S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 AA
```

"Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor.",

Cell\_76:793-802(1994).

CELL\_76

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).

(See http://www.isb-sib.ch/announce/

¥B.

Transmembrane; Glycoprotein; Signal; Repeat

1. 15 50 1.

529 TTATCTGGAAAAA	388-CACCATT  133 lnHisTy  435	87 hrGlnil 300 104 GlyPheP 141 AGCACAA 116 9AlaGlu		108	Align seg 1/1 t 60 GTGCTCGT :::   :: 9 LeuLeuLe	alignment_block: US-09-240-675-1	alignment_scores:     Quality:     Ratio:     Percent Similarity:	FT CARBOHYD FT CARBOHYD FT CARBOHYD FT CARBOHYD FT CARBOHYD FT CARBOHYD FT VARIANT FT VARIANT FT SEQUENCE	ET SIGNAL ET CHAIN ET TOMAIN ET TRANSMEM ET DOMAIN ET CARBOHYD
CICI	388-CACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACAATTTAGAA.  133 lnHlsTyrArgAsnValThrValdlyProFroGluAsnIleGluVal 133 lnHlsTyrArgAsnValThrValdlyProFroGluAsnIleGluVal 1435	hrGinileThrAlaThrGluCysAspPheThrAlaAlaSerProSerAla	ArgProvalValTyrArgValGlnPheLySTyrThrAspSerLys  GATGGATAATTGGATAAAATTGTCT		g 1/1 to: INGS_HUMAN from: 1 to: 337  GTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGA:   ::: ::           :::   ::: :::    ::: ::	x INGS_HUMAN	155.50 1.030 50.333 Percent	85 PO 110 PO 137 PO 219 PO 231 PO 64 R 64 R 7F	1 .27 POTENTIAL. 28 337 INTERFERON-( 28 247 EXTRACELLUL) 248 268 POTENTIAL. 249 337 CYTOPLASMIC 56 56 POTENTIAL:
		uCysaspheThrAlaAlaSerProSerAla 103 ArGTTATGAAGAAATTAAATTGGGTATAAG 340       snVal	yrThrAspSerLys73 yrThrAspSerLys73 GGGTGTC 264 SerIleGlyValAsnCysT 87 TTCA: 299	GTAGAĞGTCGACATCATAG 150 ProLysileArgLeuTyrA 42 ProLysileArgLeuTyrA 42 ProLysileArgCeaGC 182	to: 337 CCGCAGCCGCAGGTGGA 107 ::         !aAlaAlaAlaProProAs 25	•	Length: 300 Gaps: 14 Identity: 22.333	TENTIAL. TENTIAL. TENTIAL. TENTIAL. TENTIAL. 1800. 1800. 1800. 1800. 1800.	POTENTIAL. INTERFERON-GAMMA RECEPTOR BETA CHAIN. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). POTENTIAL.
192	1.63 (1.1 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2 1.2	03 10 16 187 187	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	3 3 5 6	<b>77</b>				TA CHAIN.
DR.	88888888888	88888888	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	R C C C S C C C C C C C C C C C C C C C	seq_n seq_d ID	• ,			

	nme: SwissProt_38:INSR_RAT	Ħ.
806 292	157 ATGTTCTTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTTCAG 806 	757 276
756 276	756 uServalLeuAlaGlyAlaCysPhePheLeuValLeuLysTyrArgGlyL 276	.59
743 259	11 CTACCTCCACCAGAAAATATAGAAGTCAGTGTC	11
710 242	61 TTGGTGTCTATAGTCCAĞTACATTGTATAAAGACCACAGTTGAAAATGAA 710	26
660 226	23 TCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAA 660     :::   :::                  09 sLeuGlnValGlnAlaGlnLeuLeuTrpAsnLysSerAsnIlePheArgV 226	09
622 209	79 TCCAGACATAAAATTTAT:AAACTCTCACCAGAGACTACTTATTG 622 :::::!!! 93 ArgSerAsnSerIleSerLeuAspAsnLeuLysProSerArgValTyrCy 209	93

Rattus noivegicus (Rat). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammali Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. Goldstein B.J., Dudley A.L.;
"The rat insulin receptor: primary structure and conservation of tissue-specific alternative messenger RNA splicing.";
Mol. Endocrinol. 4:235-244(1990). SEQUENCE FROM N.A. MEDLINE: 90231337. 15127: p97681; 11-APR-1990 (Rel. 14, Created). 11-PRR-1990 (Rel. 14, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR). numentation\_block: STANDARD; PRT; 1383. AA. Mammalia;

PARTIAL SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
L1u y Tam Tam Tam

Liu Y., Tam J.W.O.;
Submitted, (MAY-1997). to the EMBL/GenBank/DDBJ databases.
Submitted, (MAY-1997). to the EMBL/GenBank/DDBJ databases.
FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A TYROSINE-PROTEIN
FUNCTION: ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

```
alignment_scores:
Quality:
                                                                                                   alignment_block:
US-09-240-675-1
472 SerGlyThrLysGlyArgGlnGluArg. AsnAspIleAlaLeuLysThrA 488
                                                                    Align seg 1/1
                                                                                                                                                Ratio:
Percent Similarity:
                               125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                  to: INSR_RAT
                                                                                                * INSR_RAT
                                                                                                                                                               127.00
0.645
                                                                                                                                                41.561
                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED
                                                                                                                                                Percent Identity: 19.620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSULIN RECEPTOR, ALPHA-SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOSPHORYLATION (AUTO-).
MPORTANT FOR BIOLOGICAL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMOVED IN MATURE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
                                                                  to: 1383
                                                                                                                                                                                                                                        M (IN REF. 2).
4B919566902A944A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE
                                                                                                                         1.0E01...13:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BETA-SUBUNIT
```

929 678	879 669	650 655	634 782	691 617, 741	600	500 584	550	500 581	450 571	400 560	350 551	550	300	262	243 521	505	488 225
AATTTACCTT  :::      yLeuLysLeuProS	AATGTCAAAACT	nGlyAs ATCCTC				• •			•						* * *	- · · · · · · · · · · · · · · · · · · ·	
ი ∙	AATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGG	1 1	AshSerSerSerGinileIeLedLySTrpLystroProSerAspProAs TGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGA	AGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGT	GTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAA	CTCTCACCAGAGACTACTTATTGTCTAAAAGGTTAAAGGAGGACTACTTAC    ::	GTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAA	GGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAG       taiggly	ATAGTGATACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGGTTT	AAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCA	AGAAAACACTTCTTCATGGTATGAGGTTGAC ::::::::       		yrGlnAsnValThrGluPheAspGlyGlnAspAlaCys	ACT	OASPPheArgAspLeuLeuGlyPheMetLeuPheTyrLysGluAlaProT	:::    :::::    ArgThrSerPheAspLysIleLeuLeuArgTrpGluProTyrTrpProPr	
CT :: rArgThrTrpSerProProPh	TTTCCTCAAAAC	2 : :	LysTrpLysPro	CTCCACCAGAAA	TGTCTATAGTCC	CTAAAAGTTAAAG	TTTATTCCAGAC	CTTACTTATCT	ACAAAAGATAG	TACATTTAGAA	AGGTTGACTCAT		SlyGlnAspAla ATTAAATTCCC	AGTACCAAA	TGGA:	ıLeuArgTrpGlı	::: AsmGluLeuLeu
TCCGCGTACAAGCAT:::::   	GTTTTCCAAAAAG	AAACAAATACCTGACTGTGAA	ProSerAspero	ATATAGAAGTCAGT	ATTGGTGTCTATAGTCCAGTACATTGTATAA	TTAÄAGCAGCACTACTTAC [-      .  : : : : : : : : : : : : : : : :	CATAAAATTTATA	GAAAAACTCTTC	IGTTATGTGGGCTTT	GAAGCTGAAGATAAGGCA :::::::    ArgSerAsnAspProLys	TCATTTACACCATTTCGCA	, national color	Cys	.AGTACCAAATGCAACTTTTCTTCA	TGGATAAAATTGTCTGGGT::::           ::: PheTyrLysGluAlaProT	uProTyrTrpPro	LyspheSerPhe
AT 954  -   ps 695	GG 928		AS 650 GA 831	GT 740 11 er 633	AA 690 :: 1G 617	AC 649		:AG 549	TT 499  Me 581	3CA 449 3ys 570	3CA 399	550		rca 299	3GT 261 roT 538		Tie 504

```
seq_name: SwissProt_38:INGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1300 TATGTGAGAAAACAAAACCA 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1250 ACACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1200 ACAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1159 CARATGCTGAGAGAAAATTATCGAGAAA......AAAACTGATGTT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1109 GATCCAGGATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             761 LysArgArgSerLeuGluGluValGlyAsnValThrAlaThrThrProTh 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              993 .....AAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 erGlnLysHisAsnGlnSerGluTyrAspAspSerAlaSerGluCysCys 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         955 CTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Mětázoa; Chórdata; Craniata;
Eutheria; Primatés; Catarrhini; Hominida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           809 ValileSerGlyLeuArgHisPheThrGlyTyrArgIleGluLeuGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. SALES SECUENCE SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFNGR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rél. 14, Created)
01-APR-1990 (Rél. 14, Cast sequence update)
15-JUL-1999 (Rél. 38, Last amotation update)
INTERFERON-GAMÁA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).
INVERT
Walter M.R., Windsor W.T.,
Zauodny P.J., Narula S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INGR_HUMAN
                                                                                                             MEDLINE;
                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
                                                                                                                                                                                                                                                                                                         Stueber:D., Friedlein®A., Fountoulakis M., Lahm H.-W., 
*Alignment of distilfide bonds of the extracellular dome 
interferon; gamma: receptor and investigation of their ro 
idological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFIDE BONDS, PARTIAL SEQUENCE, GEDLINE; 93183911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular cloning and expression of the human interferon-gamma
                                                                                                                                                                                                                                                               ochemistry .32:2423-2430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erHisGluGluHisArgProPheGluLysValValAsnLysGluSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roArgLysThrSerSerGlyAsnGlyAlaGluAspThrArgProSerArg 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAACAG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerCysProLysThrAspSerGlnIleLeuLysGluLeuGluGluSerSe 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aCysAsnGlnAspSerProGluGluArgSerGlyVal...AlaAlaTyrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rPheArg...LysThrPheGluAspTyrLeuHisAsnValValPheValP 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alSerAlaArgThrMetPro 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rLeuProAspPheProAsnIleSerSerThrIle.....AlaProThrS
                                                                                                                  95342235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                              Nagabhushan T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 489 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              raniata; Vertebrata; Mammalia;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i,
                    Lundell D.J., Lunn C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGCCTGT
                                                                                                                                                                                                                                                                                                                                                                  role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garotta
                                                                                                                                                                                                                                                                                                                                                                                                                      the
```

```
Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A., Winkler F.K., Robinson J.A.; "Neutralizing epitopes on the extracellular interferon gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 376:230-235(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Crystal structure of a complex between soluble high-affinity receptor.";
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
EMBL; J03143; AAA52731.1; -.
                                                           or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFNgammaR) alpha-chain characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Biol. 273:882-897(1997).
- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTOR'S BIND ONE
                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN:
PYM: PHOSPHORYLATED AT SER/THR RESIDUES.
SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERFERON-GAMMA DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crystal structure of the A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stuart F., Henke C., Bridges A., Williams G., Birch A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fab-IFNgammaR1-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interferon-gamma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homolog
complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its
```

```
alignment_scores:
                                                                                                                                                                             alignment_block:
                                                                                                                                                          US-09-240-675-1 x INGR HUMAN
                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                   Percent Similarity:
130 aagtagaggtcgacatcatagatgacaactttatcctgaggtggaacagg
                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                      DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                         33 GTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCCGTGGGCCCATG
                                     17 aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrA
                                                                               1 MethlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl
                                                                                                                                                                                                                                                         0 18 6 TO TO 8 8 TO
                                                            GGTGTTGTCCGCAGCC...GCAGGTGGAAAAAATCTAAAATCTCCTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1JRH; 25-MAR-98
                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                  Ratio:
                                                                                                                                 ်
(၆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Glycoprotein; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain;
                                                                                                                                      INGR_HUMAN from: 1
                                                                                                                                                                                                    0.666
53.276
                                                                                                                                                                                                                              124.50
                                                                                                                                                                                                                                                                                54404
                                                                                                                                                                                                                                                             3D-structure.
                                                                                                                                                                                               Length: 351
Gaps: 16
Percent Identity: 22:222
                                                                                                                                                                                                                                                                              WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                  POTENTIAL...
                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                         DCF9E574D8F47400 CRC64;
                                                                                                                                                                                                                                                           v postavna.
                                                                                                                                        to: 489
                                                                                                                                                          .
                                                                                                                                                                                  CONTRACTOR OF THE SALE OF SALES
                                                                                                                                                         351
                                                                                                                                                                                                           ,
                                                                                                                                                          1
              179
                                                               129
                                      ω
A
                                                                                                                                                                                                                                      Ç.
   es
R
Gar
Car
```

180 AGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCATTCGATTATCAAAA 226

34 snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr

50

(190

KD CONNECTIN-

Mammalia;

```
251 lValAlaAlaLeuLeuPheLeuValLeuSerLeuValPheIleCysP
                                                                                                                                                                                                                                                            897 TGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGT
             281. IleIleLeuProLysSerLeuIleSérValValArgSerAlaThrLeuGl
                                                         997 TTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGA 1046
                                                                                                                                                 947 ACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGT
                                                                                                                                                                                                                                                                                                                                                            847 TGTATAAATGGAAACAAATÄCCTGACTGTGAAAATGTCÄÄAAACTACCCAG 896
                                                                                                                                                                                                                                                                                                                                                                                                           225 lyvalThrThrGluLysSerLysGluvalCysIleThrIlePheAsnSer 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 sValSerAlaGluGlyValLeuHisVal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 AAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACT 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 AAATTGCGTATAAGAGCA.....GAAAAAGAAAACACTTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                618 TATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGT 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 ......GlnIleMetProGlnValProValPheThrValGluValLysAs
                                                                                                                                                                                                                                                                                                           GTGGCTCCACGCCTTTTTAAAAAAGGAATCCTGGAAACCATT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....TTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTTCA 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleGlnCysGlnLeuAlaIleProValSerSerLeuAsnSerGlnTyrCy 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTC.. 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erGluIleGlnTyrLysTlèLeuThrGlnLysGluAspAspCysAspGlu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTATAGTCCAGTAC...ATTGTATAAAGACCACAGTTGAAAATGAACTAC 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysTyrIleArgValTyrAsnVal.TyrValArgMetAsnGly.....S 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roLysLeuAspIleArgLysGluGluLysGlnIleMetIleAspIle... 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATGAGGTTGACTCATTTACACCATTTCGCAAAAGCTCAGATTGGTCCTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TrpValArgValLysAlaArgValGlyGlnLysGlu.....SerAlaTy 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1sH1sTyrCysAsnIleSerAspH1sValGlyAspProSerAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP
                                                                                                          ......TyrlleLysLysIleAsnProLeuLysGluLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .AsnGlyAspGluGlnGluValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...TyrAspProGluThrThr 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 17 17 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297
                                                                                                                                                         996
                                                                                                                                                                                                                                                            946
                                                                                                                                                                                                                                                                                                                                                                                                                                                               846
                                                                                                          280
                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
  Ratio:
                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: SwissProt_38:MYM1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 u 297
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 603508; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vinkemeier U., Obermann W., Weber K., Fuerst D.O.;
"The globular head domain of titin extends into the center of the sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron microscopy of two titin associated proteins."

J. Cell Sci. 106:319-330(1993).
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
MYOMESIN 1 (190 KD TITIN-ASSOCIATED PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYM1_HUMAN
P52179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-SKELETAL MUSCLE; MEDLINE; 94095665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mmunogiobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATED PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: MAJOR COMPONENT OF THE VERTEBRATE MYOFIBRILLAR M BAND BINDS MYOSIN, TITIN, AND LIGHT MEROMYOSIN. THIS BINDING IS DOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPENDENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                          AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain; Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
     123.50
0.588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to license@isb-sib.ch).
                                                                                                                               162452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is not removed. Usarro
                                                                                                                                                                         FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                         IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                        FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                 G-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT: 1451 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA TANDEM REPEATS
Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thick filament; Repeat.
```

TYPE-III.

460

CRC64

alignment\_block: US-09-240-675-1 x MYM1\_HUMAN Align seg 1/1 to: MYM1\_HUMAN Percent Similarity: 45.652 Percent Identity: 19.783 153 GACAACTTTATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAAT... 404 olleLeuGlyTyrPheIleAspLysCysGluValGlyThrAspSerTrp. 420 507 euSerValThrGluAlaThrArgSerTyrValValLeuSerTrpLysPro 523 508 TAAGCTTTACA......TATAGCTTACTTATCTGGAAA... 539 477 LeuLysSerPro.....LeuSerThrLeuAspTrpThrValIleVa 369 .....TATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAG 407 443 rTyrIlePheArgValArgAlaValAsnLysMetGlyIleGlyPheProS 460 333 .....CGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGG::.. 368 427 ProValLysPheAlaArgPheProValThrGlyLeuIleGluGlyArgSe 297 TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTG...... 421 .....SerGlnCysAsnAspThr 426 247 TAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCT 296 201 .... GTGACTTTTTCATTCGATTATCAAAAAACTGGGATGGATAATTGGA 246 388 AspTyrIleIleIleSerTrpLysGlnProAlaValAspGlyGlySerPr 582 ....AGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTA 626 540 uAlaGlyThrGluAsnTrpGlnArgValAsnThrGluLeuProValLysS 557 524. ProGlyGlnArgGlyHisGluGlyIleMetTyrPheValGluLysCysGl-540 540 ..... AACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTA 577 490 lThrGluGluFroSerGluGlyIleValProGlyProProThrAspl 507 458 ACACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTT 460 erArgValSerGluAlaValAlaAlaLeuAspProAlaGluLysAlaArg 603.ysAlaProGlyLysIleIleProSerArgAsnThrAspThrSerVal... 618 574 ArgValArgCys.....SerAsnSerAlaGlyValGlyGluPr 586 627 AAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCC 676 557 erProArgPheAlaLeuPheAspLeuAlaGluGlyLysSerTyrCysPhe 573 702 ..... GARAATGAACTACCTCCACCAGAAATATAGAAGTCAGTGTCCAA 746 ATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGAT AGTACATTGTATAAAGACCACAGTT... oSerGluAlaThrGluValThrValValGlyAspLySLeuAspIleProL 603 .... ValValSerTrpGluGluSerLysAspAlaLysGluLe 631 .TATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCC 813 332 701 490 476 443 404 507 457

R 8 8				49	<i>Q</i>		S		'	ያ ጸ	seq_d	seq_n		<sub></sub> .		ല	•••		, µ	•	<b>.</b>		i j				Ø			
SEQUENCE STRAIN-S MEDLINE;	Oncoger	"Ehk-1 and Ehk-2 kinase family wi	MEDLINE	SEQUENC STRAIN-	Eutheria; Rodentia	Eukaryo	EPHAS OR EXHL OR EHK-1	EPHRIN	01-0CT-199	P54757; 01-0CT-19	PAS	ame: Sw	791 Ala	281 AGT	774 YrG	231 ATT	.181 CGA ::: 758 lAr	745 G1y	1143	1096 GAA   -     196  -	711 uSe	٠ ،	;	679 laA	961 GAA	911 AAA 670	60	861 CAA	814 ACGCC ::: 648 roCys	٠.
SPRAGUE-DAV 5; 95206467.	ie 8:32	family	jerre	TRAIN-SPRAGUE-DAWLEY	a; Rod	norveg	R EKH1	TYPE-A	1996	. 966T	100	Swisspro	ValSer	GITTIT	InPheG	ATTGTGTGAAAGCCAGAGCACACAC	GAGAAAAAAACTG	yValPro		ACACGC	ATCCCTTAGTG:     :::    uSerPheArgA	ALAALA	CAAGCTTTCCTACTTCCTCCA.	aAlaGlyLeu	AAATAACAC	CGTTTT		CAAATACCTO	S	
N.A. E-DAWLEY 6467.	ú	: D	: 3	N.A. E-DAWLE	. ••	∵ 😄	OR EHR	A RECEPTOR	Rel. 34	(Rel: 34	block: STANDARD	t_38:EP	ValSerGluCysPheLysC	AGTGACG	::::: lnvalAJ	AAGCCAG	AACTGAT :::: uAla	roGlyLys <sup>1</sup>	TTT	CTGTGAT		TEALAR	TACTIC	Sej-	CATCTTI	CAAAAA	Chrcysh	ACTGTG	. >	•
Η,	3(1993)	two novel		; TIS		(Kat).	11	5 5 6		rea	JARD;	A5_RAT	heLysc	CTGTAT	aAlaMe	AGCACA	GTTACAGTTC ::: TyrLysileS	TrpArg.	TTTTGGGAAAACACTTC	CCAGGA	MetVal	Soldor	CTCCA.	rGluTyrSe	TTGGTC	GGAATT	ThrCysH1sGlyLeuValThrG	AAAATG	GAATCC :      nAsnPr	
ISSUE-BRAIN	•	lve	E .	SUE-BRA	ciurognathi;	ta; Cr	TOMON HOMON			g ;	PRT		ysGluG	GTGAGA	tAsnMe	CACCATO	GTTCCT/ ::: Ileser/		ACACTTO	TTATCCI     rTyrVal	ATCTATA ::: LeuGly1	erpropi		erGlnAsp	TGAAGAG	TACCTTCTCCG	euValT	TCAAAAC	TGGP OValLys	
AIN;		ruct	K., Yan	NIN;	, Murid	niata	TO TOOL	OR (EC 2.	ice updat		100		lu 800	AA 1310	yrGinPheGinValAlaAlaMetAsnMetAlaGlyLe	ATGGATGAAAAGCTGAATAAAAGC	GAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCACTGACTG		AAATGC	AAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTATT  :::::       yGlyAlaGluIleThrGlyTyrTyrValAsnTyrArgGluValIle	AICCCTTROTGATTCATTCCATATCTATATCGGTGCTCCAAAACAG :   :::      ::: ::: USerPheArgAspSerMetValLeuGlyTrpLysGlnProAspLys	erProProcysAsplieThrcysLeug		pSerGlu	ATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATA	AAACGITTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG    ::::     :::   TyrIlePheArgValArgAlaValAsnA	uGlyGlnS	CTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCC	GGAAACCAT :::    LysThrHis	
:	-	es and i	ပ္သ		ae;	Vertebr		)  - 	÷ (*)		5 AA.			•.T	uGly	AAGCTG	AACCAC    ysGlua	:::   :::     :: GluAlaAsnValLysAlaVa	aaatgctgagagaaaaattat	TATGAA     ArgGlu	CTCCAA      InProa	priern	GTCTTTAAC	:	TTTGAT	GCGTACAAG      :::   rgValArgA	nser	GIGIGI	TTGTATAAATGGAAA ::: ArgPhe	
i fi		rece	os G.D		rinae;	ata		12)						•	AlaPro	AATAAA	ACTGACTGTAT	  Lysal	AAAAAT	ATTATT:::	SpLysTh	гсузце	TAACAT	AlaIleGluVa	ACTGAA	AGCATCTGATG :    :::: gAlaValAsnA		CTTTCC	AAATGGA	
		-0			Rattu	Mamma l	٠.	(TYROSINE		•	,	•			Ser 79	AGC 128	TAT 12	:: ava 75	H	T 114     eAsp 744	TCTG 109	) ⊢		Val 694	ATA 101	ATG 960 ::: snA 679		TCA 910	659	
, I	٠.	express				lia;		NE-PROT		٠			•		.ŏ	.080	30	ěi.	.80	4 2	. 80 3		5	Ā	10	v 0	ý	.0		1
	· ·:	yros:						OTEI					• •																	

RAS Taylor-V., Pfarr S., Miescher G.C., Honegger P., Breitschopf H.,

```
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ONIB AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00790; RECEPTOR TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X78689; CAA55357.1;
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00069; pkinase; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lassmann H., Steck A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression and developmental regulation of Ehk-1, a neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A1, -A2, -A3, -A4 AND -A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Alternative splicing
                    ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF_2; UNKNOWN_1
                                                                                                                                                                                       621 --
                                                                                                                                                                                                                                                                                                           358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -A3, -A4 AND -A5
                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARI
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                            SPLICED FORMS).
VCRPGTFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR
RESDPPTMACTR -> G (IN SPLICED FORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                               RPPSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCK
                                                                                                                                                                                                                                                                                                                                            GRRRTQGRGGG ->'DADGPRAQASWCHARR (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN TYPE-A RECEPTOR 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
                                           (IN REF. 2).
(IN REF. 2).
(IN REF. 2).
(IN REF. 2).
(IN REF. 2).
(IN REF. 2).
                                                                                                                                                                                  CGRASSLCAVAHPSLIW -> R (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FALSE_NEG.
                                                                                                                                                                                                                        SDLSPGTROYVSVNVTTNOAA -> T
                                                                                                                                                                                                                                               ECGGHVRYLPQQIGLKNTSVMMADPLAHTNY
                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN THE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
      (1) 五個·清
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
        .
            ., (2, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
741 GTCCAAAATCAGAACTATGTTCTTAAATGG
                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio
```

```
US-09-240-675-1 x EPA5_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: EPA5_RAT
                                                                                                                                                                                                 648 ACGTCATGGAAAATTGGTGTGTGTATAGTCCAGTACAT.....
                                                                                                                                                                                                                                                                             598 AACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTT
                                                                                                                                                                                                                                                                                                                                                            551 TGTAGAAGAAAGGATTGAAAATATT, TATTCCAGACATAAAATTTATA
353 hrMetAlaCysThrArgProProSerAlaProArgAsnAlaIleSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 GATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 euval......prolleglyLysCysMetCys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 TAGTGATACACATCTCCTCGGAACAAAAGATAGTGTTATGTGGGCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 AlaAspSerSerGlnLeuLeuGluValSerGlySerCysValAsnHisSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 snThrGluValArgAspValGlyProLeuSerLysLysGlyPheTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 aAspGluSerPheThrGluLeuAspLeuGlyAspArgValMetLysLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 GGAAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 GAATATTACTAGTACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 AlaPheGlnAspValGly...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 GlyArgAsnIleLysAspAsnGlnTyrIleLysIleAspThrIleAlaAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 eAlaLeuValSerValArgValTyrTyrLysLysCysProSerValValA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 GATGACAACTTT.....
                                                                 rSerCysValCysGluLysAspTyrPheArgArgGluSerAspProProT
                                                                                                                                                                                                                                                                                                                 yTyrGluGluLysAsnGlyThrCysGlnValCysArgProGlyPhePheL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rValThrAspAspProProLysMetH1sCysSerAlaGluGlyGluTrpL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAA 450
                                                                                                                                                                                                                                         ysAlaSerProHisSerGlnThrCysSerLysCysProPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgHisLeuAlaValPheProAsp...........ThrIleThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATTATCAAAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGGAGCGATGAGTCTGTCGGGAATGTGACT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAGCTGAATGTTTATGAÄGAAATTAAATTGCGTÄTAAGAGCAGAAAAA
                                                                                                                  ..TGTATAAAGACCACAGTTGAAAATGAACTACCTCCA.....719
                                                                                                                                                             0.602
42.795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
                                      ...CCAGAAATATAGAAGTCAGT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....AlaCysIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATGCAACTTTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....ATCCTGAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458
21
20.087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTCATTC
                                                                                                                                                                                                                                                                                                                                                                                                           .LysAlaGl
369
                                                                                                                                                                                                                                                                                                                          313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                            353
                                                                                                                                                                                                     683
                                                                                                                                                                                                                                             326
                                                                                                                                                                                                                                                                                    647
                                                                                                                                                                                                                                                                                                                                                                                                         296
                                                                                                                                                                                                                                                                                                                                                                                                                                                 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198
```

```
CCCERREREROSS
                                                                                                                                                                                                                                                                                                                            seq_name: SwissProt_38:I10R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1011 CAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGATCCCTTAGTGATTC 1060
                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 yGlyGlyLysAspValSerTyrTyrIleLeuCysLysLysCysAsn...S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          961 GAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 erHisAlaGlyValCysGluGluCysGlyGlyHisValArg......
                                         HO A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.; "A receptor for interleukin 10 is related to interferon receptors Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                            15-JUL-1998
15-DEC-1998
                                                                                          EDLINE; 94068585.
                                                                                                                                                                                            L10RA OR IL10R.
                                                                                                                                                                                                             NTERLEUKIN-10 RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                        5-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                        OR_MOUSE
                                                                                                                                                                                                                                                                                                                                                         ValPheGlnIleArgAlaArgThr 546
                                                                                                                                                                                                                                                                                                                                                                                             TGTGTGAAAGCCAGAGCACACACC 1256
                                                                                                                                                                                                                                                                                                                                                                                                                           erLysGluThrThrIleThrAlaGluGlyLeuLysProAlaSerValTyr 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCCATATCTATATCGGT......GCTCCAAAACAGTCTGGAAACA 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....GATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAsnGluThrSerValPheLeuGluTrpIleProProAlaAspThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ulleLysTyrPheGluLysAspGlnGluThrSerTyrThrIleIleLysS 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuSerTrpGlnGluProAspArgProAsnGlyIleIleLeuGluTyrGl 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCCTGTGATCCAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluAla..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isThrAsnTyrThrPhe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nGlnIleGlyLeuLysAsnThrSerValMetMetAlaAspProLeuAlaH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAA 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAG. 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erProValThrAsnValLysLysGlyLysIleAlaLysAsnSerIleSer 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yThrArgGlnTyrValSerValAsnValThrThrAsnGlnAlaAlaProS
                              FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
                                                                                                                                                                                                                          (Rel. 37, Last sequence update) (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....GATTATCCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . ValAsnGlyValSerAspLeuSerProGl
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....TyrLeuProGl
                                                                                                                                                                                                    tion update)
                                                                                                                                                                                                                                                                                        575 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGATTTATGA 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...... 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .GluIle 443
FAMILY OF RECEPTORS - 5 & -
                                                                                                                                            Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
                                                          receptors.
                                                                                                                                         5.7% tr
    a);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-240-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (eceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEM
                                                                                                                                                                                                                                                                                                                                    ValAlaLeu...
                                                                                                                                                                                                                                                                                                                                                                                             leLeuH1sTrpLysProIleProAsnGlnSerGluSerThrTyrTyrGlu
```

```
between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                      EMBL; L12120; AAA16156.1; -. MGD; MGI:96538; IL10RA.
                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-s:
                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                          requires a
238
575 AA;
  64248 MW;
                                                                                                                                                                                                                                                               Glycoprotein; Signal.
                           POTENTIAL
                                                               POTENTIAL
                                                                                         POTENTIAL.
                                                                                                             POTENTIAL.
                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                               INTERLEUKIN-10 RECEPTOR. EXTRACELLULAR (POTENTIAL
                                             POTENTIAL
                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                               POTENTIAL
  820B9CD576F686B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                        .
Сh
                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                   as its content
                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
```

Percent Similarity: Ratio: x I10R\_MOUSE 117.50 0.691 43.702 Gaps: Percent Identity: 20.308

Align seg 1/1 to: I10R\_MOUSE from: 1 6 575

113 TCTAÂAATCTĆĆTCAÁAAAGTAGAGGTCGACATCATAGATGACAACTTTA 162 63 CTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAA 25 uLeuProSerProSerTyrValTrpPheGluAlaArgPhePheGlnH1sI 42 TCCTGAGGTGG.... LeuValThrIleSerSerLeuSerLeuGluPheIleAlaTyrGlyThrGl **AACAGGAGCGATGAGTCTGTCGGGAAT** 200 25

251 ATTOTOTOGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTTCAC 300 LysGlnTyrGlyAsnSerThrTrpAsnAs 71

301 TCAAGCTGAATGTTTATGAAGAA... 71 pileHisileCysArgLysAlaGlnAlaLeuSerCysAspLeuThrThrP 88 .ATTAAATTGCGTATAAGA 341

342 GCA: GAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCA...TT 385 heThrLeuAspLeuTyrH1sArgSerTyrGlyTyrArgAlaArgValArg 104

105 AlavalAspAsnSerGlnTyrSerAsnTrpThrThrThrGluThrArgPh 121 TACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAG 435

...ValAspGluValIleLeu CTGAAGATAAGGCAATAGTGATACACATCTCCCTGGAACAAAAGATAGT ThrValAspSer 132 485

```
ROCORED TO A Be
                                                                                                                                                                                                                                                                      _name: SwissProt_38:INSR_MOUSE
                                                                                                                                                                                                                                         documentation_block:
                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INSULIN RECEPTOR PRECURSOR (EC 2.7.1.112) (IR)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 snProLeuCysProGluThrProAspAlaIleHisIleValAspLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       813 CACGCCTTTTAAAAAGGAATCCTGGAAACATTTGTATAAATGGAAACA
                                                                                                                                                                                                                                                                                                                       334 erGlnPheLeuLeuPro 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133
                                                                                                                                                                                                                  INSR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
                                                                                                                                                                                                                                                                                                                                                                  AAGCTTTCCTACTTCCT 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAA 964
                                                                                                                                                                                                                                                                                                                                                                                                            rThrAspSerGlyPheGlySerGlyLysProSerLeuGlnThrGluGluS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValPheProLysValSerLeuGluLeuArgAspSerValLeuHisGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erMetLeuLeuPheCysGlyIleLeuValCysLeuValLeuGlnTrp...
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAACACATCT...TTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATAC 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sLeuProThrValLeuValPheLysLysProHisAspPhePheProAlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTCTTAAATGGGATTATACATATGCAAACATGACCTTTCAAGTT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAACTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACATAAAATTTATAAACTCTCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oArgProThrIleThrProAlaGlyAspGluTyrGluGlnValPheLysA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              snLysAlaGluTrpSerGluGluGlnCysLeuLeuI]eThrThrGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yValArgLysPheCysValLysValLeuProArgLeuGluSerArgIleA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spleuArgValTyrLysIleSerIleArgLysPheSerGluLeuLysAsn 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValThrLeuLysAlaMetAspGlyIleIleTyrGlyThrIleHisProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....Acttattgtctaaaagttaaagcagcactacttacgtcatgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaThrLysArgValLysGlnGluThrPheThrLeuThrValProIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......CCAGAGACT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .TyrileArgHisProGly.....Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......PheThrValThrAsnLeuSerIleLeuValIleS 245
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                           1372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....CAGTGGCTC
                 Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614
      5. 19 Th 5.23
                                                                                                                                                                                                                                                                                                                                                                                                                                     R HSSP; P06213; IIRK

R HSSP; P06213; IIRK

R MGD MGI96575; INSR

R PRINTS; PR00001; FRNTYPEIII.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00239; RECEPTOR_TYR_KINASE_DOM; 1.

R PROSITE; PS00239; RECEPTOR_TYR_KINASE_DOM; 1.

R PFAM; PF00041; fn3; 1.

R PFAM; PF00069; Pkinase; 1.

R PFAM; PF00069; Pkinase; 1.

R PFAM; PF00757; Furin-like; 1.

R PFAM; PF00130; Recept_domain 1.

R PFAM; PF01030; Recept_domain 1.

R Tansferase, Tyrosine-protein kinase; Receptor; Transmembrane;

Glycoprotein; ATP-binding; Phosphorylation; Signal; Repeat.
                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-3' FROM N.A.

MEDILINE; 9009938.

Sibley E., Kastelic T., Kelly T.J., Lane M.D.;

"Characterization of the mouse insulin receptor gen

Proc. Natl. Acad. Sci. U.S.A. 86:9732-9736(1999).

1- FUNCTION: THIS RECEPTOR BINDS INSULIN AND HAS A
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J05149; AAA39318.1; -.
EMBL; M28869; AAA39319.1; -.
PIR; A34157; A34157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a copyren the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                            DOMAIN .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flores-Riveros J.R., Sibley E., Kaste Substrate phosphorylation catalyzed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase. Kinetic correlation to autophosphorylation of in the beta subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS, CONTRIBUTE TO THE FORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264:21557-21572(1989).
                                                                                                                                                                                                                                                                                          1372 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                           152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                      INSULIN RECEPTOR, ALPHA-SUBUNIT REMOVED IN MATURE FORM.
INSULIN RECEPTOR, BETA-SUBUNIT.
                                                                                                                                                                                                                                                                                                                              INSULIN RECEPTOR, BETA-SUBUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute. There are no resutions as long as its content is not removed. Usage by an
                                                                                                                                                                                                                  FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                  BY SIMILARITY: AUTO-).
PHOSPHORYLATION (AUTO-).
IMPORTANT FOR BIOLOGICAL ACTIVITY
                                                                                                    BY SIMILARITY
                                                        POTENTIAL.
                                                                            INTERCHAIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kastelic T.,
lyzed by the
                                                                                                                                                                                     (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSULIN AND HAS A TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib
                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
```

way

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: INSR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-1 x INSR_MOUSE
600 CTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTTAC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                    539 yrGlnAsnValThrGluPheAspGlyGlnAspAlaCys.......551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 GTCAGAATATTACT.....AGTACCAAATGCAACTTTTCTTCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506 ArgThrSerPheAspLysIleLeuLeuArgTrpGluProTyrTrpProPr 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 AAAACTGGGATGGATAAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           489 snGlyAspGlnAlaSerCysGluAsnGluLeuLeuLysPheSerPheIle 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 ACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                                                                                                                                                                                                                                                                        561 ......IleAspProProGln......ArgSerAsnAspProLys 571
                                                                                                                                                                                                                                                                                                                                                                                     350 AGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGAAAA, 349
                                                                                                                               582 tArgGly.....
                                                                                                                                                             500 GGATGGTTTAAGCTTTACATATAGCTTACTTATCTGGAAAAACTCTTCAG 549
                                                                                                                                                                                              450 ATAGTGATACACATCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTT 499
                                                                                                                                                                                                                                                                                                                          400 AAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522 oAspPheArgAspLeuLeuGlyPheMetLeuPheTyrLysGluAlaProT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551
                                                                                               GTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATAAA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117.00
0.603
41.991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGATAAATTGTCTGGGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424
541
635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155639
                                                                                                               584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 462
Gaps: 21
Percent Identity: 19.697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ĭ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1DA2A0BB74618964 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
                                                         584
   は、日本のなりのできます。
seq_documentation_block:
prp__HUMAN STANDARD; PRT; 1912 AA
AC p23468;
pr 01-NOV-1991 (Rel. 20, Created)
pr 01-NOV-1996 (Rel. 34, Last sequence update)
                                                                                                         seq_name: Swissprot_38: PTPD_HUMAN
                                                                                                                                                                                                                        810 IleGluLeuGlnAlaCygAsnGlnAspSerProAspGluArgCysSerVa
                                                                                                                                                                                                                                            1236, GTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAAAAGCAGTGT 1285
                                                                                                                                                                                      1286 TITTAGTGACGCTGTATGTGAGAAAACAAAACCA 1319
                                                                                                                                                                                                                                                                                                                                                                                                         1145 TTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAA ...... 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101 ACCCCTGTCATCCAGGATTATCCACTGATTTATGAAATTÄTTTT 1144
                                                                                                                                                                                                                                                                                                  793 snLysGluSerLeuvalIleSerGlyLeuArgHisPheThrGlyTyrArg 809
                                                                                                                                                                                                                                                                                                                                            1188 ... AĂĂĂCTGĂTGTTACAGTTCCTĂĂTTTGĂĂĂCCACTGACTGTĂTĂTTGT 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1084 CAMANCAGTCT.....
                                                                                                                                                                                                                                                                                                                                                                           778 1 Septembes GlifflightsargpropheGluLysvalvalA 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1034 CITTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTC 1083
                                                                                                                                                   826 1. AlaAlaTyrvalSerAlaArgThrMetPro 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                   762 AlaThrThrLeuThrLeuProAspPheProAsnValSerSerThrIleVa 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    832 ATCCTGGAAACCATTTGTATAAATGG...AAACAAATACCTGACTGTGAA 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             618 lnThrAspAlaThrAsnProSerValProLeuAspProIleSerValSer 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             929 AATTTACCTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 AsnSerSerSerGlnIleIleLeuLysTrpLysProProSerAspProAs 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691 AGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 eSerAspGluArgArgThrTyrGlyAlaLysSerAspIleIleTyrValG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650 GTCATGGAAA....ATTGGTGTCTATAGTCCAGTACATTGTATAA 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    585 LeuLysProTrpThrGlnTyrAlaIlePheValLysThrLeuValThrPh 601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              729 rPheArg...LysThrPheGluAspTyrLeuHisAsnValValPheValP 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          713 SerCysProLysThrAspSerGlnIleLeuLysGluLeuGluGluSerSe 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   696 erGlnLysHisAsnGlnSerGluTyrAspAspSerAlaSerGluCysCys 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 955 CTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             679 YLeuLysLeuProSerArgThrTrpSerProProPheGluSerAspAspS 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670 LeuPheGluLeuAspTyrCysLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 AATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGG 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651 nGlyAsnIleThr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               782 TGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGA 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       741 GTCCAAAATCAGAACTATGTTCTTAAATGG......GATTATACATA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roArgProSerArgLysArgArgSerLeuGluGluValGlyAsnValThr 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..........AAGTTTGATACTGAAATACAAGCTTTCCTACTTCCAGT 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......HisTyrLeuValTyrTrpGluArgGlnAlaGluAspSerGlu 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....CTCCGCGTACAAGCAT 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....LysG1 679
                                                             1912 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             992
```

The control of the co

1. The state of th

Ç, .... .

```
REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L38929; AAC41749.1; -
EMBL; X54133; CAA38068.1; -
PIR; S12052; S12052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright.
between the Swiss Institute of Bioi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 95204468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression of alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine phosphatas
                                                                                                                                                                                                                                                                                                                     RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :yrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural diversity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 91006018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 390-1912 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolecular characterization of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pulido R., Krueger N.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE FOUND IN DIFFERENT
TISSUES DUE TO ALTERNATIVE SPLICING.
PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
FROM THE TRANSMEMBRANE SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P18052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270:6722-6728(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                    .
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             informatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Early 159 and old secure of the old by
                                                                                                                                                                                                                                                                                                                                                                                                                 ) Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELLULAR REGION TYPIC OF A CAM FAMILY (3 IG-
OWED BY 8 FIBRONECTIN TYPE III-LIKE DOMAINS)
REGION COMPOSED OF TWO PTPASE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN TYROSINE PHOSPHATE + H(2)0 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito H.;
                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR" (POTENTIAL).
                                                                                                                                 BRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane protein-tyrosine
                                                                                                                                                                                                                        CE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     It is produced through a collaboration informatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of human receptor-like protein
                                                                                                                                                                                            C2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                              icing. . Apple
                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                         TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito H
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its content
                                                                                                                                                                                                                                                                                                                                                                      PHOSPHATASE DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAINS),
出す。13日 Anna 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 way
```

		.:.						_
	6 CRC64;	3AE8CBCD32182E26 CRC64	MW; 3AE8	214759	AA;	1912	SEQUENCE	SO
CLEAVAGI	REDUCTION IN	5-FOLD REDU	R->A: 2.	ω	1178	1178	MUTAGEN	Ŧ
ORM).	BRAIN ISOFORM	(IN FETAL B	MISSING	7	113	609	VARSPLIC	ij
	ISOFORM).	(IN KIDNEY	MISSING	ω,	78	775	VARSPLIC	4
	ISOFORM).	(IN KIDNEY	MISSING		22	226	VARSPLIC	Ţ
	ISOFORM).	(IN KIDNEY	MISSING		18	181	VARSPLIC	FT
		٢	POTENTIAL	~	83	832	CARBOHYD	H
	a :		POTENTIAL	-	724	724	CARBOHYD	FT
			POTENTIAL		. 299	299	CARBOHYD	H
			POTENTIAL	-	25	254	CARBOHYD	H
	<u>د</u>	(POTENTIAL	CLEAVAGE	ω	117	1175	SITE	H
		ARITY.	BY SIMILARITY		184	1844	ACT_SITE	Ţ
			BY SIMILARITY	ω.	155	1553	ACT_SITE	Ŧ
•	PHOSPHATASE	į,	PROTEIN-TYROSINE		1912	1619	DOMAIN.	ŦΤ
•	PHOSPHATASE	(A)	PROTEIN-TYROSINI		1618	1375	DOMAIN	FT
	H	TIN TYPE-II	FIBRONECTIN	7	113	1020	DOMAIN	FT

## Percent Similarity: 116.00 0.768 52.982 Percen

US-09-240-675-1 x PTPD\_HUMAN

Align seg 1/1 to: PTPD\_HUMAN irom:

537 AAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAG 583         :::::::::::::::::::::::::::::
537 AAAAACTCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAG 583          ::::::::::::::::::::::::::::

1025

502 ProLeuSerSerAspIleGlnValIleThrGlnThrGlyValProGlyGl 518

inLysThrTyrSerValLysValLeuAlaPheThrSerIleGlyAspGly 501

AAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCT 974 HisAsnValAlaAspSerGlnIleThrThrIleGlyAsnLeuValProG

485

468 924

TTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACT 102

875 TGAAAATGICAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAA

825 AAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTG 874

CCTTTCAAGTTCAGTGGCTCCACGCCTTTTTA 824

rThrIleLeuValGlnTrpLysG 440

yGlnIleGlnGlyTyrArgValTyrTyr 455

1233

```
1125 CTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1327 CCTCT 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1277 AAGCAGTGTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAATA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1222 TGACTGTATAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 hrSer 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 gIleThrIleGluProGlyThrSerTyrArgLeuGlnGlyLeuLysProA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545 AlaAsnTyrGluLeuValTyrLysAspGlyGluHisGlyGluGluGlnAr 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535 erTrpThrProProArgSer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               595 AlaSerThrAlaGluIleSerAlaArgThrMetGlnSerLys.....Pr 609
                                                                                                                              EMBL; D11474; BAA02033.1;
PIR; A44027; A44027.
HSSP; P56276; lTLK
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archos
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus
                                                                                                                                                                                                                                                                                                                                                                                                    -1- DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE CONTENT IS GRADUALLY INCREASED THROUGHOUT THE OVO DEVELOPMEN REACHED ITS PEAK AFTER HATCHING.
-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -I- TISSUE SPECIFICITY: IS EXPRESSED IN PECTORALIS AND CARDIAC MUSCLE
-I- DEVELOPMENTAL STAGE: CAN BE DETECTED BY DAY 10-13 IN OVO, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.lsb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PROTEIN, STRIATED MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-JUN-1994 (Rel. 29, Last sequence update)
5-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete primary structure and tissue expression of chicken actoralis M-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSUE-EMBRYONIC PECTORALIS MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oSerAlaProProGlnAspIleSerCys....
                                                                                                                                                                                                                         send an' email' to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snSerLeuTyrTyrPheArgLeuAlaAlaArgSerProGlnGlyLeuGly 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATT...ATCGAGAAAAAACTGATGTTACAGTTCCTAATTTGAAACCAC 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....TGTGTGAAAGCCAGAGCACACACCATGGATGAAAAGCTGAATAA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iol: Chem. 267:20302-20310(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_38:MPSF_CHICK
                                                                                     PF0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yanagisawa M., Imamura M., Kasuya Y., Sakurai T.
Repeat; Immunoglobulin domain.

Repeat; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::
=
                                                                                                                                                                                                                                                                                           institutions as
                                                                                                                                                 · .
                                                                                                                                                                                                                                                   is not removed. O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1450 AA
                                                                                                                                        .ThrSerProSerSerT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..... 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspThrIle 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE OVO DEVELOPMENT AND
                                                                                                                                                                                                                                                                                       its content
                                                                                                                                                             . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    봈
                   おいているとない
                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-240-675-1 x MPSF_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: MPSF_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                  507
                                                                                                                                                                                                                                                                                  483 AGTGTTATGTGGGCTTTGGATGGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                               457 rargyalSerGluProvalAlaAlaLeuAspProvalAspLeuGluArgT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 TCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGAT.....AAGG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 ....GlnCysAsnAspAlaProValLysIleCysLysTyrProValThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                              491 Asp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 AACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 lyLeuTyrGluGlyArgSerTyrIlePheArgValArgAla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 TACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412 ValGlyLeuGluAsnTrpVal....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 ATGAGTCTGTCGGGAAT.....GTGACTTTTTCATTCGATTATCAAAAA
                                                                                                                                                                                                                                                                                                                                      474 hrGlnThrValHisValAspGluGlyArgLysIleValIleSerLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 AATTG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 GGTC...GACATCATAGATGACAACTTTATCCTGAGGTGGAACAGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 LeuIleAlaGlyAlaProGly.....
                                                                520 spProProValProArgGlyArgGluProLeuThrTyrPheIleGluLys
                                                                                                             538 AAAAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 TTGTCCGCAGCCGCAGGTGGAAAAATCTAAAATCTCCTCCAAAAAGTAGA 136
                                                                                                                                                 rAsnValHisAlaSerGluIleSerLysThrTyrValValLeuSerTrpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             snThrThrSerGlnAsnProValIleGlyTyrPheValAspLysCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sCysHisAspAlaAsnArgAspTyrValIleValThrTrpLysProProA
                                                                                                                                                                                                                                                                                                                                                                        CANTAGTGATACACATCTCTCCTGGA......ACAAAAGAT
                       .TCTTCAGGTGTAGAAGAAAGGATTGAAAATATTTATTCC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115.00
0.618
43.765
                                                                                                                                                                                                                                         LeuGluGlyAspileGlnileProGlyProProTh 503
                                                                                                                                                                                          TTAAGCTTTACATATAGCTTACTTATCTGGA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ValAsnSerAlaGlyIleSerArgProSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRONECTIN TYPE-III:
FIBRONECTIN TYPE-III:
IG-LIKE C2-TYPE DOMAIN:
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...CGTATAAGAGCAGAAAAAGAA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....AlaProMetAspValLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 to: 1450
```

434

327

418

520

542

490

506

457

447

183

378

411

227 395

```
seq_name: SwissProt_38:TYO3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1097 AAACACGCCTGTGATCCAGGATTAT 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1012 AAGCITICCTACTICCTCCAGTCTIT.....AACATTAGATCCCTTAGT 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 693
                            TISSUE-BRAIN;
                                                                                                                                 Rattus norvegicus (Rat), distribus (Rattus norvegicus (Rat), de la constanta (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norvegicus (Rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           924 AAAGGA...ATTTACCTTCTCCGCGTACAAGCATCTGATGGA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            633 TyrileAspTyrSerValValGlySerAsnGlnTrp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              774 TATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 616 alvalValGlnTrpAspLysProLysHisGluGluAsnLeuTyrGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537
                                                                                                                  Eutheria; Rodentia;
                                                                                                                                                                                                                                                                   TYROSINE-PROTEIN KINASE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            824 AAAAAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  553 lLysSerProArgTyrAlaValPheAspLeuAlaGluGlyLysProTyrV 570
                                                                                                                                                                                                                                                                                                                                                      -OCT-1996 (Rel: 34) Created) The Sald of the Live Live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlyGluGlnTyr[lePheArgValLysAlaValAsnAlaValGlyPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alPheArgVal.....LeuSerAlaAsnLysHisGlyIleSer 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yGlySerProlleLeuGlyTyrTyr, 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysAspGlyHisSerMetThrLeuGlyTrpLysAlaProLysTyrSerGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eSerGluAsnSerGlnGluSerGluAlaIleLys......valG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTCATTCCATATCTATATCGGT.....GCTCCAAAACAGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lnAlaAlaLeuThrCysProSerTyrProHisGlyIleThrLeuLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . AATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AsnTyrAsnArg......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ......GluProAlaAsnHis......LysProIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lProSerAlaProGlyArgValValAlaThrArgAsnThrLysThrSerV 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .CCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAAT.....CAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspProSerGluIleThrGluProIleGlnProGlnAspIleValValVa 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTAT 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerMetValGlySerGlySerTrpGlnArgValAsnAlaGlnValAlaVa 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACATAAAATTTATAAACTCTCACCAGAGACTACTTATT 621
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD; PRT; 880 AA.
                                                                                                           Chordata; Cran
Sciurognathi;
                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                             TYRO3 PRECURSOR (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheValValHisGlyLeuGlu
                                                                                                              Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Commence of the first of the
                                                                                                              Murinae;
                                                                                                                                                                                                                                                                                                                      1, 4 . 3 . 1. . . . .
                                                                                                           Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          773
      110-1100-10-10-1
            The second of
                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                          US-09-240=675-1 x TY03_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an
```

```
PROSITE; PS00107; PROTEIN_KINASE, PROSITE; PS00109; PROTEIN_KINASE, PROSITE; PS50011; PROTEIN_KINASE, PFAM; PF00041; fn3; 2.

PFAM; PF00047; fg; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor tyrosine kinase
J. Biochem. 117:1267-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D37880; BAA07119.1; - HSSP; P11362; 1FGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no wamodified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohashi K., Honda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular cloning and in situ localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTI
IN THE CENTRAL NERVOUS SYSTEM.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              email to license@isb-sib.ch)
  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :1267-1275(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ichinomiya N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosine-protein kinase; ATP-binding;
  ž
                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                       FIBRONECTIN TYPE-III: FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Bioinformatics
                                                                                                                POTENTIAL.
                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYROSINE-PROTEIN KINASE RECEPTOR TYRO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura
E86AAE5FA5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mizuno K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain
                                                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTICULARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
```

γ: /113.50 γ: / 0 7. 45.634

Percent Identity: 22.254 AS A TATABLE TORNER TO TO SOLD SOLD

Length:

Align seg'1/1 to: TYO3\_RAT from: 1 'to: 880; ' 0.840 F.Ob. 3.

15 LeuLeuLeuAlaGlyLeuAlaSerLeuLeuLeuProGly...... GTCGTCCTCGTGGGCGCGACGACCCTAGTGCTCGTCGCCCGTGGGCCCCATG 82 27

GGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAG 132

(b) (b) (c) (c)

MEDLINE; 96104999.

942	3 CCAGTGTGTCTTTCCTCAAAAGGTTTTCCAAAAAGGAATTTACCTTCTCCC	
271	258GluTrpGluAlaLeuAlaValValValProValProProPh	25
892	TGTATAAATGGAAACAAATACCTGACTGTGAAAAATGTCAAAACTAC	82
257	ercysThrvalGlavalAlaHisAla	24
842	CCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAAC	79
792	GGGATTATACATATGCAAACATGA	75
230	laAlaProPheAsnIleThrValThrThrIleSerSerSerAs	21
754	CCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAA	71
213	PIPATCIAINAICCMAINAITIBINI MANANCACANA I BANANAI BANCIA.	21.0
213	gProAlaileIleArgLeuGlnAla	205
: 663	TACTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTG	19
205	ThrGluPheSerCysGluAlaHisAsnileLysGlyLeuAlaThrSerAr	189
613	AATTTATAAACTCTCACCAGAGAC	56
563 188	4 TTACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGG ::: '[   :::  ]       :::     ' '' :::     5 erSerProSerValLeuAsnValThrGlyValThrGlnArg	51 17
	(ePheTrpTrpArgGlyProThrLysValGlyGlyProAlas	15
513	9 AGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCT	47
. Un	6 PheGlnLeuSerCysGluAlaValGlyProProGluPr	14
478	9 TTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAA	42
4		
428	TTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACAT	ω
383	8 AAGAGCAGAAAAACACTTCTCATGGTATGAGGTGAACTCA 8	111
117	3 GlyLeuTyrTrpCysGlnValLysAspGlyGluGluThrLysIle	10
337	AACTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTAT	288
102		87
287	T TAATTIGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGC	238
86		74
237	GAATGTGACTTTTTCATTCGATTATCAAAAAACTGGGATGG	197
74	AAANATORAMAA IIAALUTANOOTORRAMOORAUGATORAGIUTOUU 	59
, ,		: :
146	TAGAGGTCGACATC :::  ::: otmbryalsercinglycingrovalizationagoryaldingly	133
12		22
:		

- 271 eThrCysLeuLeu...ArgAsnLeuAlaProAlaThrAsnTyrSerLeuA 287 943 GCGTACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATA 992

138.27

7 0.5158 0.5224 0.5732

Q9y2h

O61210 caenorhabditis

```
sp_rodent:062682
sp_mamma1:077773
sp_rodent:054711
sp_rodent:088307
                                                                                    sp_invertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_vertebrate:Q9YHW0 + sp_roden+.oc**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
Query: US-09-240-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database sequences:
Database length: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -0-/cgn2_1/USFTO_spoo1/US09240675/runat_30052000_165119_3020/app_query
-DB-SFTREMBL_12 -QFMT-fastan -SUFFIX-mod1f.rspt -GAPOP-12.000
-CAPEXT-4.000 -MIMARCH-0.100 -LOOPCI--0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPEXT-7.000 -YGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ery length: 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAXLEN-1000000 -USER-US09240675 -NCPU-6 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE
ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-
                                                                                                                                                                  rodent:Q63155
                                                                                                                                   human:060468
                                                                                                                                                   human:060469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jun 1, 2000 6:02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                             13.50 155.44

+ 113.00 150.13 0 60

113.50 149.51 0.1319 60

.0 + 113.00 139.56 0.1336 6f

.51 + 113.00 138.51 0.1342 7

.113.00 158.26 0.1268 7

.113.00 158.26 0.1268 7

.113.50 149.53 0.1537 7

.1150 149.53 0.1537 7

.11,50 149.53 0.1537 7

.11,50 149.53 0.1530 0.227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŗ
                                          0.215
4 0.2228
4 0.228
0.2688
0.2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -THR_SCORE-pct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  software,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  version 4.5,
077773
054711
088307
Q9y6n7
                                                                                           Q63155 rattus norvegicus (rat

Q66469 homo sapiens (human).

Q60468 homo sapiens (human).

Q60468 homo sapiens (human).

Q95209 oryctolagus cuniculus;

1 Q18094 caenorhabditis elegan
                                          Q62682 rattus norvegicus (rat
077773 sus scrofa (pig). volt
                                                                             homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:

ID Q9YHW0 PRELIMINA
AC Q9YHW0;

PT 01-MAY-1999 (TrEMBLICE
DT 01-MAY-1999 (TrEMBLICE
DT 01-MAY-1999 (TREMBLICE
DT 01-MAY-1999 (TREMBLICE
DT 01-MAY-1999 (TREMBLICE
DE INTERPERON ALPHA/BETA
GN IFNAR1.
OS Gallus gallus (Chicke
OC Eukaryota; Metazoa; C
OC Neognathae; Galliform
RN [1]
RP SEQUENCE FROM N.A.
P SEQUENCE-LIVER;
BR 1 TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_invertebrate: 009165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_invertebrate:0612
                                                                             97
                                                                                                                                                                                                                                                                                                                                                                                                                                     62 GCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EBOUL J., GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240-675-1 x Q9YHW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   569 AA;
```

```
seq_name: sp_vertebrate:Q9YHW0
                                         REBOUL J., GARDINER K., MONNERON D., "Comparative genomic analysis of the receptor gene cluster."; Genome Res. 0:0-0(1999).
EMBL, AF082664; AAD13669.1; -.
                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniat
Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TIEMBLIE1: 10, Created)
01-MAY-1999 (TIEMBLIE1: 10, Last sequence update)
01-MAY-1999 (TIEMBLIE1: 10, Last annotation update)
INTERFERON ALPHA/BETA RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
  64055 MW;
                                                                                                                                                                                                                                                          Craniata;
F99BC099 CRC32;
                                                                                                              UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                 Phasianinae;
                                                                                                                                                                                                                                                     Vertebrata; Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ξ
                                                                                                                                                                                                                                 Gallus
```

Align seg 1/1 to: Q9YHW0 from: 2.384 63.736 Percent Identity: 37.363 . 6

112 ATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTT 31, snLeuLysSerProGlnAspIleGlnValTyrAlaValAsnThrAsnPhe .....ArgCysCysAlaGlyGlnThrA 47 161 31

48 ThrLeuMetTrpAsnTyrThrGlyAspGlyThr. . AsnValThrPheSe 162 ATCCTGAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTC 63 211

8 A Transport TAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCT 296

, 297 TCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGAGCAGA 346 ysGluLeuSerGlyCysGlnAsnValSerHisThrGluCysAspPheSer SerAlaIleThrAlaTyrTyrAspThrHisHisIleArgIleArgAlaGl 113 96

AAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCAT 393 130

TTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAGAT 443

```
1067 TATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGG 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1258 TGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGTATGTGAG 1307
                                                                                                                                                                                                                                                                                                                                               1117 ATTATCCACTGATTTATGAAATTATTTTTTGGGAAAACACTTCAAATGCT 1166
                                                                                                                                   1208 TAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCACACCA 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 spAsnSerSerAsnVal...GluLysValArgSerIleLeuProIleAsp 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 sMetTrp...LeuIleSerValPhePheLysTyrAsnValValIleTrpA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 yrGluIleAlaGlnIleGlyProProGluIleAlaLeuGlnSerIleAsn 146
                                                                                                                                                                                                                                                                               374 euTyrAspPheSerTyrGlnIleLeuTyrTrpLysAsnSerSerAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 erryssercysteuserrysaspyalGluvalaspproprovalThrasn 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  967 ACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCT 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        832 ATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAAAT 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 leLysThrThrArgLysValAsnAspLeuLeuCysProThrAsnValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               688 TARAGACCACAGTTGAA...AATGAACTACCTCCACCAGAAAATATAGAA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 aThrValProLeuGluAspLysGlyGlyLeuPheSerProIleHisCysI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 ValileAsnAspLeuAlaProGluThrThrTyrCysLeuLysValGlnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                588 AAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 GlyAlaIleLysIleAsnIleSerProProGluAlaAsnGlnValArgLy 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 AAGGCAATAGTGATACACATCTCCTGGAACAAAAGATAGTGTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        917 TTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 IleThrSerMetLysCysAsnLeuSerSerVallleLysProThrSer.. 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 euTyrAspAspTyrSerSerLysTrpGlnLysValSerGlyCysGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 nGluHisValThrTyrThrValGlnTyrLeuThrGlyTyrLeuLysAsnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      783 .GCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGA 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 ValPheAlaLeuAsnMetLysPheTyrLeuLeuTrpAspAsnHisTyrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    735 GTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGATTATACATAT.. 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rAspLeuAlaProSerThrLeuTyrCysValLysValGlnAla..... 422
                                                                                                                                                                                        GluGluGluValLysMetLysGluThrLysGlnThrIleAlaThrValSe 407
                                                                                                                                                                                                                                                                                                                                                                                             sileLysileThrProProGlyGlyProGlyAsnLysileMetSerAspL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluIleGlyProProAspValLysValAspIleSerAspValLeuLeuH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCAAAACTACCCAGTGT......GTCTTTCCTCAAAACGT 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .........AlaSerTyrTyrPheArgValGlnAlaMetAsnGluTyrS
                                                                                                                                                                                                                                                                                                390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      488
122 rLeuAlaGluSerLeuHisLeuArgPheSerAlaPro...GlnIleGluA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_rodent:061190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-240-675-1 x Q61190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SORRERRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                   90 rgAlaGluLeuAlaAspGluHisSerGluTrp...ValAsnValThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1308 AAAACAAAACCAGGA 1322
                                                      1049 CCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAA 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         711 CTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGT
                                                                                                                                                    999 GATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGATC 1048
                                                                                                                                                                                                                                                                  949 AAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTT 998
                                                                                                                                                                                                                                                                                                                                                                       899 TGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           761 TCTTAAATGGGAT:....TATACATATGCAAACATGACCTTTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seg
01-NOV-1999 (TrEMBLrel. 12, Last ann
CYTOKINE RECEPTOR FAMILY 2, MEMBER 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 GlyThrAlaGlyGly 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 heSerGluAlaTyrAsnLysSerSerAspPheSerArgGluGluCysIle 438
                                                                                                             106 CysProValGluAspThrIleIleGlyProProGluMetGlnIleGluSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U53696; AAC53062.1; ... MGD; MGI:109380; I110rb. PFAM; PFO0041; fn3; 1. SEQUENCE 349 AA; 39774 MW;
                                                                                                                                                                                                                                                                                                              74 SASpPhe...SerHisLeuSerLysTyrGlyAspTyrThrValArgValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIBBS V.C., PENNICA D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 97199375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                   58. SerTyrArgSerPheGlnAspHisCysLysArgThrAlaSerThrGlnCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 IleProProGluLysValArgMetAsnSerValAsnPheLysAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sene 186:97-101(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRF2-4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L10RB OR CRFB4 OR CRF2-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATGGAAACAAATACCTGAC...TGTGAAAATGTCAAAACTACCCAGTG 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laGlnTyr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTAT, 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eLeuGlnTrpGluValProAlaPheProLysThrAsnLeuThrPheThrA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolation of cDNA clones encoding the human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 061190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222.50
1.660
62.617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 214
Gaps: 9
Percent Identity: 26.168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4AC1802A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......Glu 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AA
```

37.

760

108

122

105

7 - 50 mg

.....GTCGGGAATGTGACT 206

49

32

65

```
seq_documentation_block:
Align seg 1/1 to: Q63953 from: 1
                                                                                                                 Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1184
                                                                                                                                                                                                                                                                                                                       EMBL; U69596;
EMBL; U69596;
EMBL; U69597;
EMBL; U69598;
EMBL; S69336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1137 ...ATTATTTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGA 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1284 GTTTTTAGTGACGCTGTATGTGAGAAAACAAAACCAGGAAAT 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 ArgValGlnTyrTrpLysAsnGlyThrAsnGluLysPheGlnValValSe 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Genomic organization and promoter analysis of the gene ifngr2 encoding the second chain of the mouse interferon gamma recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 GluTrpSerGluProIleCysGluArgThr.....GlyAsn 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unctionality of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMMI S., BOHNI R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A. EDLINE; 94170381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NOV-1996 (TrEMBLrel.
-NOV-1996 (TrEMBLrel.
-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TERFERON GAMMA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 76:803-810(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysIleGlnValGlnGlyPheLeuLeuAspGln....AsnArgThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGTGAAAGCCAGAGCACACCATGGATGAAAAGCTGAATAAAAGCAGT 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snGluProGluThrTrpThrLeuLysAsnIleTyrAspSerTrpAlaTyr 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rProTyrAspSerGluValLeuArgAsnLeuGluProTrpThrThrTyrC
                                                                                                                                                                                                                                                                                                    MGI:107654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rodent:Q63953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97128072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEMBIC.
                                                       x Q63953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHEE S., MUTHUKUMARAN G., LEMBO D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., STARK G:, DI MARCO F., AGUET M.; f the interferon receptor family complements
                                                                                                                                                                                                                                                        37471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
                                                                                                                                                                                                                 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01, Last sequence update)
12, Last annotation updat
                                                                                                                 Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INTERFERON GAMMA RECEPTOR BETA SUBUNIT)
                                                                                                                                                                                                                   シャン・シャナ ひあいさい
                                                                                                                                                                                                                                                   OBF24E9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      いきには著いむるで
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation
                                                                                                                                                                                                                                                                                                                                                     ......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interieron-gamma receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
                                                                                                                    13
30.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DONNELLY R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
                                                                                                                                                                                                                                                                                                                                     seq_name: sp_vertebrate:09YGC8
                                                                                                                                                    Q9YGC8;
Q1-MAY-1999 (TIEMBLIEL 10, C
01-MAY-1999 (TIEMBLIEL 10, L
01-MAY-1999 (TIEMBLIEL 10, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              624 CTAAAAGTTAAAGCAGCACTA CTTACGTCATGGAAAATT
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                                                           663 .GGTGTCTATAGTCCAGTACATTGTATAAAGACCACA 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 ysSerAsnSerIleValLeuGlyAsnLeuLysProTyrArgValTyrCys 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 ATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAA...GTACATT
                                                                                                                 Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 GATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGCTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 TAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ValArgAlaLysArgGlyAsnLeuThrSerLysTrpValGlyLeuGluPr 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336 ATAAGAGCAGAAAAAGAAAAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 sTyrTrpGluLysSerGluThrGlnGlnGlnGlnValGluGlyProPheL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 G....TCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGA 174
                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 lyGlyGlyArgLeuLysLeuPheProHisProPheThrValPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 uLeuGluProAsnCysThrAspIleThrGluThrLysCysAspLeuThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 TyrSerPhe
                                                                                                                                                                                                                                                                                                                                                                     sGlyLeuLeuSerAsnValSerCysHisGluThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....ValpheHisGlyAlaThrPheGlnTyrLeuValH1 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     luProSerProSerSerAsnAspProArgProValValTyrGlnValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oLeuAsnProArgLeuHisLeuTyrAsnAspGluGlnIleLeuThrTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oPheGlnHisTyrGluAsnValThrValGlyProProLysAsnIleSerV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGGAGCGATGAGTCT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuGlnThrGluAlaGlnLeuIleLeuLysAsnLysLysIleArgProH1 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGlyAlaAlaAlaSerSerProAspSerPheSerGlnLeuAlaAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTCATTCGATTATCAAAAAACTGGGATGGAT...AATTGGATAAAATT 25:
                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....IleAspGlySerTrpHisArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . AAACTCTCACCAGAGACTACTTATTGT
                                                                                                                                                                              Last sequence up
```

579

529

623 188

662

ACTTCTTCATGGTATGAGGTTGACTC

382

93

.297

109

429

143

to: 332

genomic

analysis of

UZE G., LUTFALLA G.; interferon/interleukin-10

Gallus.

Archosauria; Aves;

PRT;

341 AA.

update)

SABBER

PRELIMINARY;

PRT;

918 AA.

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: 09YGC8 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-240-675-1 x Q9YGC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1072 ATATCGGTGCTCCA. .... ... AAACAGTCTGGAAACACGCCTGTGATC 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1301 ATGTGAGAAAACA 1313
                                                                                                                                                    1251 CACACCATGGATGAAAAGCTGAATAAAAGCAGTGTTTTTAGTGACGCTGT 1300
                                                                                                                                                                                                                                                                                                                                                   1160 AAATGCTGAGAGAAAAATTATCGAG:.....AAAAAAACTGATGTTA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 spPheThrGlyProAlaAlaAspArgGluHisAspLysTrpSerLeuLys 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        734 AGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGAT...... 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         684 TGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 0:0-0(1999).
EMBL; AF082667; AAD13678.1;
EMBL; AF082666; AAD13671.1;
                                                                                                                                                                                                                                                                                                                                                                                               150 GlnTyTTyrGlySerTrpTleTyrArgTleLeuTyTTrpLysLysGlySe 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                972 TCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            922 AAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 TGAAAATGTCAAAACTACCCAGTGT:::GTCTTTCCTCAAAACGTTTTCC 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              825 AMANGGAATCCTGGAMACCATTTGTATAMATGGAMACAMATACCTGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          775 ATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTA 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 rThrAsnLeuAsnValThrGluCysAspValSerSerLeuSerValTyr. 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 LysGlnAsnPheAsnAsn.....ValTh 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 alargLysGlyAsnLeuSerTyrThrValGlnAlaLysSerIlePhePro 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 CysLeuLeuCysValSerGlyIleValProLysProArgAsnAlaAr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 .....GlyAlaTyrValLeuArgValArgThrGluTrpGluAspGluHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gIleSetSerValAsnPheArgSerValLeuLeuTrpAspProProGlyV 45
uCysGlugInThr 216
                                                                                                                                                                                                                                                  CAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCA 1250
                                                                                                                                                                                                                                                                                              rAsn.....LysLysValileHisileAspThrLysHisAsnSerGluI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGATTAT...CCACTGATTTATGAAATTATTTTTTGGGAAAACACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eGlyProProSerValAsnValLysSerGluSerGlyThrLeuHisValA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerAspTrpAla:..ValValArgPheLysProMetAlaAspThrValIl
                                                                                                                                                                                                  leLeuSerGinLeuGluProTrpThrIleTyrCysIleGinValGinGly 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                   .....VallleProGluTrpAsnLysThrGlyGluArgSerGlnGluLe 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 189:50
: 1.469
: 58:371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 27.149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .
          1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7433D364 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: sp_vertebrate:09W6U9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-240-675-1 x Q9W6U9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
               324 Shanna yalThrThrGluAspLysPro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9W6U9;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
GLYCOPROTEIN 130 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEISSEN M., HELLER S., PENNICA D., ERNSBERGER U., ROHRER H.; "The specification of sympathetic neurotransmitter phenotype depends on gp130 cytokine receptor signaling."; Development 125:4791-4801(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 TAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGG...AACAGG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 ......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 TrpValGluAlaAlaAsnAlaLeuGlyLysAlaGluSerAspHisLeuVa 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          609M60
                                                                                                                                            368 GTATGAGGTTGACTCATTTACACCATTTCGCAAAAGCTCAGATTGGTCCTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-EMBRYONIC HEART PRIMARY CULTURE (E7, E8).
                                                                                                                                                                                                            301
                                                                                                                                                                                                                                             330 TTGCGTATAAGAGCAGAAAAAGAAAAC.....ACTTCTTCATG 367
                                                                                                                                                                                                                                                                                              284 roArgThrSerPheSerIleGlnGlyLeuArgProTyrThrGluTyrVal 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 TGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 IleSerThrValValMetGluLeuLysPheAsnIleArgTyrArgIleSe 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 AGCGATGAGTCTGTCGGGAATGTGACTTTTCATTCGATTATCAAAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 alAsnSerGlyIleLeuProThrValLeuLysLeuSerTrpGluAsnGln 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 lPheAspProIleGluIleValLysProProProProArgAsnLeuSerV 235
                                                          418 CAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT 467
                                                                                                                                                                                                                                                                                                                                                      280 CCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAA 329
                                                                                                                                                                                                                                                                                                                                                                                                    268 rSerAspThrAsnTrpMetGluValProPro...GluAspThrAlaSerP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ011688; CAB42084.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 TGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAAT.....
```

Quality: Ratio:

138.50 0.656 46.374

Length: 455
Gaps: 24
Percent Identity: 20.220

918 AA;

26 POTENTIAL. 102495 MW; 9DC128C3 CRC32;

to: Q9W6U9

from: 1

to: 918

..CTAAAATCTCCTCAA......AAAG

132

113

229

99026068.

; Archosauria; Aves; Gallus.

PheSerIleArgCysMetLysGluAspGlyValGlyPheTrpSerAspTr 317

pSerGlu..

.....GluGlnIleGly....

323

330

```
1192 CTGATGTTACAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAAA 124
                                                                                                                                                                                                                                                                                                                                                                                  1054 GTGATTCATTCCATATC.......TATATCGGTGCTCCAAAACAG 1091
             579 hrGluTyrThrLeuSerSerLeuThrSerAspThrLeuTyrThrValArg
                                                                                                                                                                                                                                   552 AsnGly......PhelleArgSerTyrThrlleLeuTyrLysThrVa
                                                                                                                                                                                                                                                                                                 .092 TCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTAT 1141
                                                                                                                                                                                                                                                                                                                                          535 lyLysAlaGluAlayalLeuThrTrpAsnHisLeuThrValAspGluGln 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972 TCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCT 102
                                                                                                                                            565 lAspGlyAsnGluThrAlaValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 IleThrGluTrpGlnThrGluProGly.....AsnIle......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 yrVallleGluTrpCys.....LeuMetSerAsnSerSerAspCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696 ACAGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGTGTCCA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 646 TTACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACC 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 luAlaAsnGlyValIleLeuGlnTyrGluValThrIleArgAlaLysPro 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 CCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGC....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 494 ysCysTyrLeuIleThrValTyrProLeuPheAlaAspGlyGlnGlySer 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        746 AAATCAGAACTATGTTCTTAAATGGGATTATACATATGCAAACATGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 alalaHisasnargValGlyAla...SerProProSerValLeuLeuIle 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 ProLeuSerHisProProSerArgTyrAsnValThrThrThrSerLeuTh 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 .....SerLysGlyProThrIleTrpArgThrIleAspValSerProSe 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                   uGlnGlnGlyArgProSerLysGlyProThrValGlnThrLysLysValG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sAspGlyLysLeuTrpValGlyTrpThrAlaProAsnAsnValLeuLysT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGATTGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCA.... 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rProAlaPheTrpIleValArgLeuMetTrpLysAlaLeuGluProPheG
                                                                                                                                                                                             TTTTTGGGAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGAAAAAA 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..ATTTACCTTCTCCGCGTACAAGCA.....TCTGATGGAAATAACACA 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGTATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCA 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCAT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProSerSerAsnSerLysAlaProValLysAsnIleArgThrLeuProLy 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCTTCAGGTGTA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .CCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTAC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnSerValLysAlaTyrLe 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGTCTTTAACATTAGATCCCTTA 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....GAAGAA 560
                                                                                                                                            : ValAspProSerLysT
                                                                                                                                            579
                                                                                                                                                                                                                                                565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512
                  Percent Similarity: 52.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allgnment_block:
US-09-240-675-1 x 014936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: sp_human:Q14936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: 014936
                                                                                                                                                          34 snValThrIleGluSerTyrAsnMetAsnProIleValTyrTrpGluTyr 50
                                                                                                                                                                                                                                                                 17 aGluMetGlyThrAlaAspLeuGlyProSerSerValProThrProThrA 34
                                                                                                                                                                                                                                                                                                                 📜 83 GGTGTTGTCCGCAGCC. . . GCAGGTGGAAAAAATCTAAAATCTCCTCCTCAAA 129
227 AACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                33 GTCGTCCTCCTGGGCGCGACGACCCTAGTGCTCGTCGCCCTTGGGCCCATG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1242 GCCAGAGCACACACC 1256
                                                                                                            180 AGCGATGAGTCTGTCGGGAATGTG...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  596 MetMetAlaTyrThr 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBirel. 01, Last sequence update) 01-NOV-1998 (TrEMBirel. 08, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaLeuLeuPheLeuLeuProLeuValMetGlnGlyValSerArgAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell 55:273-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 89003065.
AGUET M., DEMBIC Z., MERLIN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MERLIN G., VAN DEK LEEDE .
BANNWARTH W., ROMQUIN N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                        51 .....GlnIleMetProGlnValProValPheThrValGluValLysAs
                                                                                                                                                                                                                130, AAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGTGGAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular cloning and expression of the human interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  munogenetics 45:413-421(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The gene for the ligand binding chain of the human interferon gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAN DER LEEDE B.-J.M., MCKUNE K., KNEZEVIC R., ROMQUIN N., VIEGAS-PEQUIGNOT E., KIEFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 22.000
                                                                                                            ACTITITCATICGATIATCAAAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EBC99D1F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  を  
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                        65
                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGUET M.,
```

1022 ACTTCCT... 511 Gly : . . . .

```
seq_documentation_block:
ID 09YHV9 PRELIMINARY; PRT;
AC 09YHV9;
DT 01-MAY-1999 (TrEMBLrel: 10 ) Created)
                                                                                                                                                        seq_name: sp_vertebrate:Q9YHVS
                                                                                                                                                                                                                                                                              1000 ATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGAT 1047
                                                                                                                                                                                                            277 IleLeuProLysSerLeuIleSerValValArgSerAlaThrLeuGlu 292
                                                                                                                                                                                                                                                                                                                                                                                                    950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 erGluIleGlnTyrLysIleLeuThrGlnLysGluAspAspCysAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668 CTATAGTCCAGTAC...ATTGTATAAAGACCACAGTTGAAAATGAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 TATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 sp...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       568 AAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 sProSerValPheVal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 ATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 CCTGGAACAAAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTAC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 rAlaLysSerGluGluPheAlaValCysArgAspGlyLysIleGlyProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 GTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                            258 uValPheIleCysPheTyrIleLysLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900 GTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACA 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 IleLysGlySerLeuTrpIleProValValAlaAlaLeuValLeuSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      850 ATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGT 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 alThrThrGluLysSerLysGluValCysIleThrIlepheAsnSerSer 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      809 GCTCCACGCCTTTTAAAAAGGAATCCTGGAAACCATT.....TGT 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 sSerAlaGluGlyValLeuHisVal......TrpGlyV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            765 AAAT.....GGGATTATACATATGCAAACATGACCTTTCAAGTTCAGTG 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 IleGlnCysGlnLeuAlaIleProValSerSerLeuAsnSerGlnTyrCy 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            715 CTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTT 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 CysTyrIleArgValTyrAsnVal.TyrValArgMetAsnGly.....S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 AAATTGCGTATAAGAGCA......GAAAAAGAAAACACTTCTTCATG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 GTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 TrpValArgValLysAlaArgValGlyGlnLysGlu......SerAlaTy 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 isHisTyrCysAsnIleSerAspHisValGlyAspProSerAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 nTyrGlyValLysAsnSerGluTrpIleAspAlaCysIleAsnIleSerH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roLysLeuAspIleArgLysGluGluLysGlnIleMetIleAspIle... 145
                                                                                                                                                                                                                                                                                                                                                                                                AGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTG 999
                                                                                                                                                                                                                                                                                                                                     .IleAsnProLeuLysGluLysSerIle 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AsnGlyAspGluGlnGluValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....TyrAspProGluThrThr 166
                                                                    508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
```

```
S A DR REFERENCE OF THE RESERVE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                  382 CATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q9YHV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-240-675-1 x Q9YHV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                 108 rphevalGlyThrGluvalpheAsnSerSerLeuLeuHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 .....ATCCTGAGGTGGAAC...AGGAGCGATGAGTCTGTCGGG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 AATCTCCTCAAAAAGTA.....GAGGTCGACATCATAGATGACAACTTT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 0:0-0(1999).
EMBL; AF082665; AAD13670.1;
HSSP; P13726; ITFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REBOUL J., GARDINER K., MONNERON "Comparative genomic analysis of receptor gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TREMBLrel. 10, Last sequence update) 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
477 .....AAAGATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACAT 519
                                                                      138 SerSerCysValHisCysIleAsnIleThrIleLysLeuProProThrH1 154
                                                                                                                                     432 GAAGCTGAAGATAAGGCAATAGTGATACACATCTCT...CCTGGAACA... 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 TCTTCACTCAAGCTGAATGTTTATGAAGAA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFNAR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERFERON ALPHA/BETA RECEPTOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 GGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 rTyrArgValLeuTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 ysIleProArgGluProProAspAsnLeuGlnMetThrSerAsnAsnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 ATGGTCGTCCTGGGCGCGACG.....ACCCTAGTGCTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 ThraspaspPheGlnValValSerAspGluTyrSerAlaPheValGlnSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 rpLysIleAlaLysGlnCysSerArgIleValGlnProPheCysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 | Serile ..... LeuCysAlaAlaCysTyrSerSerLeuSerGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 CGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGGAAAAAATCTAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetGluThrLeuMetGlyGlyProLeuArgPheTyrGlnLeuValPheVa 17
                                                                                                                                                                                                        PheSerProLeuSerGluThrPheLeuGlyProProGluPheAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnHisIleLeuSerTrpArgAlaHisSerAspProThrValProThrTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.567
46.016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .57049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 502
Gaps: 29
Percent Identity: 21.116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2DC4E498 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UZE G., LUTFALLA G.;
interferon/interleukin-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerHisSerAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31
```

154 sleuArglysAsnGlyLysLeu

.L 162

```
388 tAspAlaGluGlu...........GluLysAspThrAspSerGluLeu....
                                                                                                                                                                                                                                                                                                                                                                                            342 eValArgArgAlaProGlnSerSerAspThrSerProValPheValGlnH 359
                                                                                    1160 AMATGCTGAGAGAAAAATTATCGAGAAAAAAACTGATGTTACAGTTCCTA 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038 AACATTAGATCCCTTAGTGATTCATTCCATATCTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 SerValGluIleIleTyr: LysGluValLysLysLys................ 310
                                                                                                                                                                                                            1113 ... CAGGATTATCCACTGATTTATGAAATTATTTTTTTGGGAAAACACTTC 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1077 ....... GGTGCTCCAAAACAGTCTGGAAACACGCCTGTGATC: ::::: 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     938 TCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTGGTCTGAAG 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            570 AATATTTATTCCAGACATAAA....
                                                                                                                                                          376 ProAspAspGlyProGluValPheGlu
                                                                                                                                                                                                                                                                        359 isserThrSerSerThrCysAspGlySerSerSerTrpValSerGlnAsn 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                988 AGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTCCAGTCTTT 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         888 ACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAAGGAATTTACCT 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757 ATGTTCTTAAATGGGATTATACATATGCAAAC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 TGAACTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACT 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657 AAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 ervalmetvalThrAlaSerLeuÁsnLysHisSerIleProSerAlaTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 AAGTT.....AAAGCAGCACTACTTACGTCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 oPheSerIleValIleGluGluLeuTyrProAsnArgAsnTyrCysValS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 ThrValGlyGluGluHisLysArgSerProGluLysValThrGluGluPr 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 euSerLeuPheAspIleTyrAsnLysValAsnTyrGluIleThrLeuArg 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 hrLysMetPheSerTyrLeuProPheThrPheGluCysGluGluIleThr 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            789 ....ATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTAAAAAGGAATCC 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 ATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGATTGAA 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spAspSerAspAspSerGluSerAspAlaMet......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAAACCATTTGTATAAATGGAAACAAATACCTGAC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yr......TyrGlyIleThrIleAlaGlyAlaIleCysPheSerIle 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .GlyGlyTyrIleLeuHisLysLysSerLeuProAspThrLeuValPheT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....ATTTATAAACTCTCACCAGAGACTACTTATTGTCTAA 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....AlaGluGlySerValGlyAlaValSerSerGluA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....SerAsnHisAspTyrThrArgArgAspIl 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....CysIleThrThrAsp.....
                                                                                                                                                GluAsnGluMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...SerValAlaGluLysAspT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....TGTGAAAATGTCAAA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..... 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...872
                                                                                                                                                                                                                                                                                                                                1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                  400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    656
SEGRET 360 TOTTCATGGTATGAGGTTGACTCATTTACACCATTTCGCAAAGCTCAGAT 409
```

```
alignment_block:
US-09-240-675-1 x P97798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 130.00
Ratio: 0.637
Percent Similarity: 49.157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: P97798 from: 1 to: 1493 ,...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eq_name: sp_rodent:P97798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                     __523 nProGlyGluMetGlnValThrIleGlnAsnLeuMetProAlaThrValT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 TIGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCTCAAAAAGTAGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1248 GCACAC 1253
540 yrllePhe..
                                                                                                                                                                                                 228 ACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAG 277
                                                                                                                                                                                                                                                                                                                                               178. GGAGCGATGAGTCTGCGGAATGTGACTTTTTCATTCGATTATCAAAAA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y09535; CAA70727.1; -. HSSP; P02751; lTTG. MGD; MGI:1097159; Neol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 SerAsn 418
                                                  310 ATGTTTATGAAGAATTAAATTGCGTATAAGAGCAGAAAAAAGAAAACACT 359
                                                                                                                                                                                                                                                                                                         494 laSerAspProHisGlyAspAsnLeuThrTyrSerValPheTyrThrLys 510
                                                                                                                                                                                                                                                                                                                                                                                                       477. 1AlaSerLeuValSerThrArgPheIleLysLeuThrTrpArgThrProA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 GGTCGACATCATAGATGACAACTTTATC...CTGAGGTGGAAC......A 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 LeualarroalaThrThrGlyProLeuProSeralaProArgAspValVa 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00041; fn3; 6.
PFAM; PF00047; 1; 4.
PRINTS; PR00014; FNITYPEIII.
SEQUENCE 1493.AA; 163159 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 ..LeuSerProLeuSerLysValAsnCysThrTyrSerLeuArgSerArg 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EELING S.L., GAD J.M., COOPER H.M.; Mouse Neogenin, a DCC-like molecule, has four splice variants and is expressed widely in the adult mouse and during embryogenesis."; ncogene 15:691-700(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                   ......ACCAAATGCAACTTTTCTTCACTCAAGCTGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 415
Gaps: 20
Percent Identity: 21.446
LysValMetAlaGlnAsaLysHisGly 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.
12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98F26676 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATATTGTGTGAAAGCCAGA 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
```

```
1206 CCTAATTTGAAACCACTGACTGTATATTGTGTGAAAGCCAGAGCA 1250
                                                                                                                                                                                                                 1159 CAAATGCTGAGAGA...AAAATTATCGAGAAAAAAACTGATGTTACAGTT 1205
                                                                                                                                                                                                                                                                                                                                                             1109 GATCCAGGATTATCCACTGATTTATGAAATTATTTTTTTGGGAAAACACTT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1059 TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGÄÄACACGCCTGT 1108
828 GluAsnLeuAspProSerSerHisTyrVallleThrLeuLysAla 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629 lyLeuLysLysTyrThrGluTyrSerPheArgValValAla.....Tyr 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 yrAlaThrSerProThrSerIleThrValThrTrpGluThrProLeuSer 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 ....GlnProGluValGlnLeuProGlyProAlaProAsnIleArgAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  767 hrArgValProGluValProSerSerLeuHisValArgProLeuValThr 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 uSerAspValProSerAlaAlaProGlnAsnLeuSerLeuGluValArgA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 AsnLysHisGlyProGlyValSerThrGlnAspValAlaValArgThrLe 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 AACTCTCACCAGAGACTACTTATTGTCTAAAAGTTAAAGCAGCACTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596 GlyAsnGlyGluIleGlnAsnTyrLysLeuTyrTyrMetGluLysGlyTh 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 ...GATGGTTTAAGCTTACATATAGCTTACTTATCTGGAAAAACTCTTC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552 SerGly...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786 AAC.....ATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTAAA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTTTTGGTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTT 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrGluTyrAsnPheArgValAlaAlaLeuThrValAsnGlyThrGlyPr 750
                                                                                                                                                                                                                                                                                                                                                                                                                                         SerIle...ValValSerTrpThrProProGluAsnGlnAsnIle...Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATÄÄCÄCÄ.... 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  snSerLysSerIleValIleHisTrpGlnProProSerSerThrThrGln 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGTCATGGAAAATTGGTGTCTATAGTCCAGTACATTGTATAAAGACCAC 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rAspLysGluGlnAspIleAspValSerSerHisSerTyrThrIleAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTGTAGAAGAAAGGATTGAAAATATTTATTCCAGACATAAAATTTATA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACATCTCTCCTGGAACAAAAGATAGTGTTATGTGGGCTTTG...... 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oAlaThrAspTrpLeuSerAlaGluThrPheGluSerAspLeuAspGluT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCAAAAA 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sSerAspValThrGluThrLeuValThrGlyThrGlnLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAATCCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTG 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnGlyGlnIleThrGlyTyrLysIleArgTyrArgLysAlaSerArgLy 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTTGAAAATGAACTACCTCCACCAGAAAATATAGAAGTCAGTGTCCAAA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTCCTCCAGAAGTACATTTAGAAGCTGAAGATAAGGCAATAGTGATAC
                                                                                                                                                                                                                                                                                     lvalArgGlyTyrAlaIleGlyTyrGlyIle.....GlySerP 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCTACTTCCTCCAGTC.....TTTAACATTAGATCCCTTAGTGAT 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AT...CAGAACTATGTTCTTAAATGG......GATTATACATATGCA 785
                                                                                                                                            roHisAlaGlnThrIleLysValAspTyrLysGlnArgTyrTyrThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....SerGlnLeuIle.....GluGlyLeuAspArgGly 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .GluSerSerAlaProLeuArgValGluThr..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459
                                                                                                                                                827
                                                                                                                                                                                                                                                                                                                                                                                                                                         798
       r.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_invertebrate: 094537
```

```
alignment_block:
US-09-240-675-1 x Q94537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
563 gAsnPheGluGlyTyrAlaArgSerHisLysGluIleTyrValLysTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q94537 from: 1
                                                                                                                                                                                                                                                                                                      215 CGATTATCAAAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1997
01-FEB-1997
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                   497 TyrLysMetAsnAsnSerGluArgGluGlnLysMetValThrLysSerH1 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 TCANANAGTAGAGGTCGACATCATAGATGACAACTTTATC...CTGAGGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                              480 rpvalGluProLeuGlnAsnAlaGlyAspValValTyrTyrThrValTyr 496
                                                                                                                                                                                                                                                                 513 SASPASPGINGINValAsnIleGInSerLeuLeuProGlyArgThrTyrG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 OATGASPLEUVAIAJAGINIJEVAILYSSETATGPheValThrLeuSerT 480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 GGTGGAAAAATCTAAAATCT.....
                                                                                                                                                                                      530 lnPheArgValGluAlaAsnThrAsnPheGlySerGlyAlaSerSerAla 546
                                                                                                                                                                                                                           265 AGAATATTACTAGTACCAAATGCAACTTTTCTTCA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 GG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 GlyGlyLysProLeuAspSerGlyLeuGlnAlaArgLeuProSerGlnPr 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00041; fn3; PFAM; PF00047; 1g; PRINTS; PR00014; FN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U71001; AAC4731
FLYBASE; FBGn0011592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JAN L.Y., JAN Y.N.;
"frazzled encodes a Drosophila member of the DCC immunoglobulin subfamily and is required for CNS and motor axon guidance."; Cell 87:197-204(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster: (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAZZLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KOLODZIEJ P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                       ProLeuGluValSerThrGlnProGluValAsnIleAlaGlyProProAr 563
                                                                                                                                           ...CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGT......
                                                                                                                                                                                                                                                                                                                                                                               AACAGGAGCGATGAGTGTGTGGGGAATGTGACTTTTTCATT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97015076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TIEMBLIEL 02, Created)
(TIEMBLIEL 02, Last sequence update)
(TIEMBLIEL 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                              ....ATAAGAGCAGAAAAAGAAAACACTTCTTCATGGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIMPE L., MITCHELL K.J., GOODMAN C.S., FRIED S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129.00
0.542
38.264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENTYPEIII.
NA; 151692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ф
6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43806DBC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      622
22
16.399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .... 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :
റ്റ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insecta;
                                                                                                                                             335
                                                                                                                                                                                                                               299
                         580
```

r	824	777 ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACGCCTTTTTA	7
	866	849 uProValAspAlaProThrProLeuGluValProValGlyLeuArgAlaI	φ
	776	776	7:
	849	833 LysGlyAspGlyProProlleTyrAspAsnIleLysThrArgAspGluGl	. 00
	776	776	7
	. 832	816 snLeuGluSerAsnMetAspTyrValValSerLeuArgAlaArgAsnVal	œ
		771	7
	816	799 pGluAsnThrIleGluLeuLysGluThrGluArgTyrHisIleLeuLysA	7.
	770	770	7:
	770	795 LYSILEArgAsnTyrValLeuGlyTrpGlyArgGlyIleProAs	7
•		•	. 2
	768	betarurern var brogryphsbro	3
	•	ACCT	
	1,		. 7
		GGTGTCTATAGTCCAGTACATTGTA	0
	662	631 : TANAGCAGCACTACTT	7. 6
	727		. 2
		מי מי מייחית מיית מי	<u>بر</u>
	580	531 ATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGAAAGATTTATTC	on 01
	695	680 luaspargasnGlyGlnIleThrGlyTyrLysIleArgTyrArgLys	<u>۾</u>
		ooo avarrii serserserserserser recht vanhren polariopioalaging	4 6
٠.		434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG	n . 4-
		:::	ે જ્ઞ:.
			٠ ـــ
	646		<u>ور</u> و
		UALAVALLeuThro	
	•		·ω
	613	SerGluAsnAspSerGlyAlaAspLeuTyrH1sAspSerThrAlaLeuGl	5
:	374		ω
•	596	580 luGluProThrValThrAsnGlyGluIleLeuLysTyrArgValTyrTyr	<u>u</u>
	374	370 ATCAG	w

8			•						•		
1032 1032		1156 999	1125 982	1080 966	1030 , 959	980 942	930 926	910	834 899	883 883	866 
AGCCAGAGCACACC 1250   :::::!  :::    SValGlnAlaArgThr 1037  . sp   nvertebrate:004538	ACTGATGTTACAGTTCC		CTGATTTATGAAAATATTTTTTTGGGAAAACA 1155     :::   :::	GCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCA 1124	CAGTCTTTAACATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGT 1079	GTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCTC 1029	ATTTACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACATCTTTTTG 979     ::	ATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGTTTTCCCAAAAAGGA 929	CCTGGAAACCATTTGTATAAATGGAAACAAATACCTGACTGTGAAA    :::::    :::::::::::::::::::::::	AAAAGGAAT  ::::::       ASDLVSASGGINHISVS  ThraspaspargHisTvrThvVs  SprTvrG	TII :::::: :::::
						•					

RRRRRRRRR RRCCCC seq\_documentation\_block: Drosophila melanogaster (Fruit fly) Bukāryotā; Metazor; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. RAZZLED. PORT IN LAND l-FEB-1997 (TrEMBLrel. 02, Created) 1-FEB-1997 (TrEMBLrel. 02, Last sequence update) 1-NOV-1999 (TrEMBLrel. 12, Last annotation update) PRELIMINARY; CANDADADADADA MINING AND THE PERSON WAS A STREET OF THE PERSON WAS ASSESSED.

	530 846	481 ATAGTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACATATAGGTTACTT :::::       :::::
	480	A GCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAG
	433	14 CITCCAGARAT SCHOOL STATES COLUMN TO THE C
	413	88 CACCATTCGCAAAGCTCAGATTGGT
•	387 781	
	764	re:
	374 747	ATGAG      uGluProThrValThrAsnGlyGluIleLeuLysTyrArgYalTyrTyr
	369 731	ATAAGAGCAGAAAAAGAAAAGAAAACACTTCTTCATGGT    ::::      gAsnPheGluGlyTyrAlaArgSerHisLysGluIleTyrValLysTrpG
	335 714	300CTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGT
	,299 697	SerSerAla
	264	re – circ
	214	174AACAGGAGCGATGAGTCTGTCGGGAATGTGACTTTTTCATT
	173 647	Туг
	171 631	TCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATCCTGAGGT
	12 <b>4</b> 61 <b>4</b>	ਜੂ=8
	:	Allgn seg 1/1 to: Q94538 from: 1 to: 1526
•		lignment_block: US-09-240-675-1 x Q94538
		lignment_scores: Quality: 129.00 Length: 622 Ratio: 0.542 Gaps: 22 Percent Similarity: 38.264 Percent Identity: 16.399
		R PRINTS; PRO0014; FNTYPEIII. Q SEQUENCE 1526 AA; 168787 MW; F17B1EC9 CRC32;

ATATCTATATCGGT 1079 ::::: luvalThrValArg 1116	1030 CAGTCITTAACATTAGATCCCTTAGTGATTCATTCCA
CTITCCIACTICCTC 1029	980 GTCTGAAGAGATAAAGTTTGATACTGAAATACAAGCTTTCCTACTTCCT 
AACACATCTITTTG 979	930 ATTTACCTTCCCCCGTACAACATCTGATGGAAATAACACATCTTTTTG
TCAAAACGITTTCCAAAAAGGA 929, :::::::::::::::::::::::::::::::::::	880 ATGTCAAAACTACCCAGTGTGTCTTTCCTCAAAACGT   :::: 1061 snThrThrAspLeuAsnCysMettle;::AsnAspLe
GGAPACAATACCTGACTGTGAAA,879	834CCTGGABACCATTTGTATAAATGGAAACAAATA     :::::    ::::: 1050 yileThrGlySerAsnArgTyrArgTyr
B33. ThrvalSerTyrGl .1050	GlnHisValThrAspAsnArgHisTy;
TGGCTCCACGCCTTTTTA 824	777ACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCACG
yLeuArgAlaI 1	1000 uProValAspAlaProThrProLeuGluValProValGl
	vekratterkar
mh=1==1==1==1==========================	
rgAlaArgAsnVal 983	771GATTAT
rHisIleLeuLysA 967	950 pGluAsnThrIleGluLeuLySGluThrGluArgTyr
77	
ArgGlyIleProAs 950	738 AGTGTCCAAAATCAGAACTATGTTCTTAAATGG ::::::::::::::::::::::::::::::::
AAAATATAGAAGTC 737 :::::    ::: :InHisProGluIle 935	717
eSerIleHisProG 919	
716	713 ACCT
GTTGAAAATGAACT 712 :::      :::   LeuGluAsnAspLe 902	663 GGTGTCTATAGTCCAGTACATTGTATAAAGACCACAGTT :::   ::: 895 Ala
ACGTCATGGAAAATT 662     :::   ::: roPheThrGluTrpAsnArg 894	878 lealaalaMetThrValAsnGlySerGlyProPheTh
uTyrGlnValLysI 87	61 gTyrPheGluLeuSerAsnLeuAspArgAsnAlaGl
AlaAsnileAr 861	ysSerThrPro
GAAAATATTTATTC 580	531 ATCTGGAAAAACCTTCAGGTGTAGAAGAAAGGATTGAAAATAT

```
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: sp_vertebrate:090610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-675-1 x 090610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: 090610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1133 SHISThrLeuGlyGlnIleThrGlyTyrAsnIleTyrTyrThrThrAspT 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1117 LeuAspGluMetAsnProProThrValIleValGlnTrpIleProProLy 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1080 GCTCCAAAACAGTCTGGAAACACGCCTGTGATCCAGGATTATCCA....
                                        228 ACTGGGATGGATAAATTGGATAAAATTGTCTGGGTGTCAGAATATTACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                       449 alSerAspProGlnGlyAspAsnLeuThrTyrSerIlePheTyrThrLys 465
                                                                                                                                                                                                                                180 ... AGCGATGAGTCTGTCGGGAATGTGACTTTTTCATTCGATTATCAAAAA 227
                                                                                                                                                                                                                                                                                                      432 lalaThrLeuValSerThrArgPheIleArgLeuThrTrpArgThrProv 449
                                                                                                                                                                                                                                                                                                                                                                               137 GGTCGACATCATAGATGACAACTTTATC...CTGAGGTGGAACAGG....179
                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 LeualaProalaThrThrGlyProLeuProThralaProargaspvalva-432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U07644; AAC59662.1; -
HSSP; P80362; IWTL.
FFAM; PF00041; fn3; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIELMETTER J., ROMAN J.M., DREYER W.J.;
"Neogenin, an avian cell surface protein expressed during terminal neuronal differentiation, is closely related to the human tumor suppressor molecule deleted in colorectal cancer.";
J. Cell Biol. 127:2009-2020(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gailus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 TTGTCCGCAGCCGCAGGTGGAAAAAATCTAAAATCTCCCTCAAAAAGTAGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEOGENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLINE; 95105243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NOV-1996 (TIEMBLrel. 01, Created)
-NOV-1996 (TIEMBLrel. 01, Last sequence of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGATGTTACAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGAA 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |::::::|||:::|||
sValGlnAlaArgThr 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrThrLysArgAspArgAspTrpSerValGluAlaPheAlaGlyGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCAGAGCACACCC 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrMetLeuMetLeuProAsnLeµLysProTyrThrThrTyrTyrPheLy 118:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ......CTGATTTATGAAATTATTTTTTGGGAAAACA 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: "0.644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1443 AA; 158050 MW; 270877DC, CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGHORN; TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1. to: 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 22,169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ということはのがない
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1166
                                                             できるなぜすびゃく かし知し
1059 TCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGGAAACACGCCTGT 1108
                                                                                                                                                                                                                                                                                                                                                                                                                    900 CLOWERS AND STREET OF THE STREET OF THE STREET OF STREET TO 972 ....TCTTTTTGGTCTGAAAGAGAGAGATAAAGTTTGATACTGAAAAGAGAAAGCTT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        588 ThrGluTyrAsnPheArgilleAlaAlaMetThrValAsnGlyThrGlyPr 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 YTYTLYSTICATGTYTATGLYSVALSCTATGLYSSCTASEVALTHTCLUS 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           646 ...... ClyThrHisSerGlyGinTleThrG1 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              638 euHisTipGlnProProProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            763 TTAAÄTGGGATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTC 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590 luTyrSerPheArgValValAla....TyrAsnLysHisGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 CTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 TGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557 AsnTyrLysLeuTyrTyrMetGluLysGlyGlnAspSerGluGlnAspVa 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 GACTCATTTACACCATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACA 427
                                                                                                                                                                                   721 erArgValProGluValProSerSerLeuHisValArgProLeuValThr 737
                                                                                                                                                                                                                                                                                                                                               704 oAlaThrAspTrpValSerAlaGluThrPheGluSerAspLeuAspGluS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     813 CACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTG 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  621 aAlaProGlnAsnLeuThrLeuGluAlaArgAsnSerLysSerIleMetL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 TCCACCAGAAAATATAGAAGTCAGTGTCCAAAAT...CAGAACTATGTTC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         605 ValSerThrGlnAspValValValArgThrLeuSerAspValProSerAl 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           666 GTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573 lAspValAlaGlyLeuSerTyrThrIleThrGlyLeuLysLysTyrThrG 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 TITAGAAGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 ACATATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGAT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 erValThrValThrTrpGluThrProLeuSerGlyAsnGlyGluIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478 AAGATAGTGTTATGTGGGCTTTG......GATGGTTTAAGCTTT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 nLeuProGlyProAlaProAsnIleArgAlaTyrAlaGlySerProThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 alTyrValPheArgValValAlaGlnAsnLysHisGlyHisGlyGlu...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 AATTGCGTATAAGAGCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  477 rArgProGlyGluThrGlnValMetIleGlnAsnLeuMetProGluThrV 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 TACCAAATGCAACTTTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTACTTCCTCCAGTC......TTTAACATTAGATCCCTTAGTGAT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....TACCTTCTCCGCGTACAAGCATCTGATGGAAATAACACA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerSerAlaProLeuLysValAlaThr.....GlnProGluValGI 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATAAATGGAAACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGT 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CI TRACKER OF THE HOSPITALISM
```

604 665 556

540

509

645

少人等等 文分五次節 是多典的是教

等落分分為一審 分替於行

55500

721 1017 SO DE RETERENTE DE RECORDE DE RETERENTE DE R

93

683

528

\$\text{0.00} \text{0.00} \text

```
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: sp_human:Q92859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-240-675-1 x Q92859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
486 gValGluAsnThrSerHisProGlyGluMetGlnValThrIleGlnAsnL 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1230 TATTGTGTG 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1095 GGAAACACGCCT...GTGATCCAGGATTATCCACTGATTTATGAAATTAT 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1057 ATTCATTCCATATCTATATCGGTGCTCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1142 TTTTTGG.....GAAAACACTTCAAATGCTGAGAGAAAAATTATCGAGA 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1186 AAAAAACTGATGTTACAGTTCCTAAT...
                                            242 TIGGATAAAATIGICIGGGIGTCAGAATATTACTAGTACCAAATGCAACT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381 ValCysval 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 GlyValAlaProAspValLeuLysGluAsnValLeuGlyTyrArg...Le 347
                                                                                                 470 AspleuThrTyrSerValPheTyrThrLysGluGlyIleAlaArgGluAr 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 hrLysAlaAsnLeuThrThrTrpAsnProI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 uGluTrpIleGlnAspAsnValThrGlnGlyGluMetIleValGlnAspT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 lnAsnIleHisValIleGlnArgAspProGlyLeuValLeuGluTrpGlu 331
                                                                                                                                           198 AATGTGACTTTTCATTCGATTATCAAAAAACTGGGATG......GATAA 241
                                                                                                                                                                                                      453 rgPheIleLysLeuThrTrpArgThrProAlaSerAspProHisGlyAsp 469
                                                                                                                                                                                                                                                                                                                        436
                                                                                                                                                                                                                                                                                                                                                                           107 AAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACA 156
                                                                                                                                                                                                                                                                                                                                                                                                                          425 LeuIleIleLeuGluHisAlaPro......AlaThrThrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Incogene 0:0-0(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 CTAGTGCTCGTCGCCGTGGGCCCATGGGTGTTGTCCGCAGCCGCAGGTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QUENCE FROM N.A.
                                                                                                                                                                                                                                          ACTITATO...CTGAGGTGGAAC:::...AGGAGCGATGAGTCTGTCGGG 197
                                                                                                                                                                                                                                                                                                          yProLeuProSerAlaProArgAspValValAlaSerLeuValSerThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EB-1997 (TrEMBLrel. 02, Created)
EB-1997 (TrEMBLrel. 02, Last sequence update)
OV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: Q92859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17263.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOOK A.T., BIGNER S.H., FEARON E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159958 MW; OAB7247E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High Titles with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 20.665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 to: 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGAAACCACTGACTGTA... 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1461 AA
                                                                                                                                                                                                                                                                                                             453
                                                                                                                                                                                                                                                                                                                                                                                                                                436
  でするこのとのあのとのうだった
```

راق	762
AAACACGCCTGTGATCCAGGATTATCCA	1091
7.1	1041 747
0 ATACTGAAATACAAGCTTTCCTACTTCCTCCAGTC; Ada	1000 730
9. TGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTG, 9	P - 5
9 CAAAACGITITCCAAA 7 GluGlyLeuAspArgG	697
9. AACAAATACCIGACTGTGAAAAATGTCAAAAACTACCAGTGTGTCTTTCCT.90 11:::::::::::::::::::::::::::::::::::	859 690
9 GCTCCACGCCTTTTAA 	809 673
7 ProhlaProhlaThrGlnAsnGlyGlnIleThrGlyTyrL	657
TAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTAAATGGGAT	730 640
0 ACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATA 729 	680 623
O GTTAAAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAGT, 679 	630
O CCAGACATAAAATTTATAAACTCTCACCAGAGACTACTTATTGTCTAAAA 629 :::	580 592
O TATCTGGAAAAACTCTTCAGGTGTAGAAAGAAAGGATTGAAAATATTTI 5 rTyrMetGluLysGlyThrAspLysGluGlnAspValAspValSerSe	530 575
2 TGGGCTTTGGATGGTT     :::   9 TrpGluThrProValSerGlyAsnGlyG	492 559
2 ATAAGGCAAT :: 2 laProAsnLe	542
ATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAG 4  :::	392 527
CTTCATGG   :::  erGly	342 515
3 euwerproAlaThrWalTyrTiePhe	503
	292

```
alignment_scores: 0uality: 122.50 Quality: 0.581 Ratio: 0.581 Percent Similarity: 50.119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: 000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-675-1 x 000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eq_name: sp_human:000340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1141 TTTTTTGGGAAAACACTTCAAATGCTGAĞAĞA...AÄÄÄTTATCGAĞAÄA 1187
292 TTTCTTCACTCAAGCTGAATGTTTATGAAGAAATTAAATTGCGTATAAGA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   807 eThrLeuLysAla 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     791 GlnArgTyrThrIleGluAsnLeuAspProSerSerHisTyrValIl 807
                                                                                                         486 gValGluAsnThrSerHisProGlyGluMetGlnValThrIleGlnAsnL 503
                                                                                                                                                                                                                                                                                                                470 AsnLeuThrTyrSerValPheTyrThrLysGluGlyIleAlaArgGluAr 486
                                                                                                                                                                                                                                                                                                                                                                                                   198 AATGTGACTTTTCATTCGATTATCAAAAAACTGGGGATG.....GATAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 rgPheileLysLeuThrTrpArgThrProAlaSerAspProHisGlyAsp 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 ACTITATC...CTGAGGTGGAAC.....AGGAGCGATGAGTCTGTCGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 LeuilelleLeuGluHisAlaPro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
                                                                                                                                                                                                                  242 TTGGATAAAATTGTCTGGGTGTCAGAATATTACTAGTACCAAATGCAACT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 yProLeuProSerAlaProArgAspValValAlaSerLeuValSerThrA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AAAAAATCTAAAATCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 CTAGTGCTCGCCGTGGGCCCCATGGGTGTTGTCCGCAGCCGCAGGTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Senomics 41:414-421(1997)
EMBL; U72391; AAC51287.1;
HSSP; P02751; LTTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELMETTER J., CHENG X.N., MISKEVICH F., LANE R.P., YAMAKAWA K., ORENBERG J.R., DREYER W.J.;
Molecular characterization of human neogenin, a DCC-related protein, modethe mapping of its gene (NEO1) to chromosomal position 15q22.3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLINE; 97312699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAAGCCAGAGCA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0014; FNTYPEIII.
1461 AA; 160015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 421
Gaps: 20
Percent Identity: 20.665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaThrThrG1 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9D5AE1C4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1461 AA
                A STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA
```

	•
A 1140 . 777	.091 GTCTGGAAACACGCCTGTGATCCAGGATTATCCACTGATTTATGAAATTA ::::         :::            762 uAsnGlnAsnIleValValArgGlyTyrAlaIleGlyTyrGlyIle.
A 1090 1,762	1041 ATTAGATCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACA :::
C 1040 S 746	1000 AȚACTGAAATACAAGCTTTCCTACȚTCCTCCAGTCTTTAAC 
G 999 G 730	959 TGGAAATAACACATCTTTTTGGTCTGAAGAGATAAAGTTTG    :::
A 958 h 713	909 CHANACGTTTTCCAAAAAGGAATTTACCTTCTCCGCGTACAAGCATCTGA 95
T 908	859 AACAAATACCTGACTGTGAAAATGTCAAAACTACCCAGTGTGTCTTTCC
A 858	809 GCTCCACGCCTTTTTAAAAAGGAATCCTGGAAACCATTTGTATAAATGG
G 808 9 673	774
. 773	730 TAGAAGTCAGTGTCCAAAAATCAGAACTATGTTCTTAAATGGGAT::::::::::::::::::::::::::
A 729	680 ACATTGTATAAAGACCACAGTTGAAAATGAACTACCTCCACCAGAAAATA :::::::::    623 PValAlavalArgThrieuSerAspValProSerAlaAlaProGlnAsni
T 679	630 GTTANAGCAGCACTACTTACGTCATGGAAAATTGGTGTCTATAGTCCAGT
9 608	580 CCAGACATAAAATTTATAAACTCTCACCAGAGAGACTACTTATTGTCTAAAA :::
T 579	530 TATCTGGAAAAACTCTTCAGGTGTAGAAGAAAAGGATTGAAAATATTTAT 575 rTyrMetGluLysGlyThraspLysGluGlnaspValAspValSerSer
T 529 Y 575	TGGGCTTTGGATGGTTTAAGGTTTACATATAGCTTACA     :::    :::    :::    :::    :::      TrpGluThrProValSerGlyAsnGlyGluIleGlnAsnTyrLysLeuT
G 491	Α.: Ç.
G 441	392 ATTTCGCAAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGAAGCTGAAG  :::    ::    ::    :::    :::    :::    :::    ::    ::    :::    :::    :::
C 391	342 GCAGAAAAAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACAC    ::::::::::::::::::::::::::::::::
t 514	::: ArgValme

1141 TTTTTTGGGAAAACACTTCAAATGCTGAGAGA...AAAATTATCGAGAAA 1187

```
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-240-675-1 x Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block:
Q91562 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 TCTCCTCAAAAAGTAGAGGTCGACATCATAGATGACAACTTTATC...CT
  506 snGlu
                                    349 AAGAAAACACTTCTTCATGGTATGAGGTTGACTCATTTACACCATTTCGC
                                                                                                                     314 T....
                                                                                                                                                                481 GlnProIle...
                                                                                                                                                                                                                                                                                                                                                                        167 GAGGTGGAACAGGAGCGATGAGTCTGTCGGGAATGTG...ACTTTTTCAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                   431 AlaProArgAspValValProValLeuValSerSerArgPheValArgLe 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                       264 CAGAATATTACTAGTACCAAATGCAACTTTTCTTCACTCAAGCTGAATGT 313
                                                                                                                                                                                                                                              464 alTyrPheSerLysGlnGlyValGlnArgGluArgAlaValAsnThrSer
                                                                                                                                                                                                                                                                                         214 TCGATTATCAAAAAACTGGGATGGATAATTGGATAAAATTGTCTGGGTGT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the nervous system of developing Xenopus embryos."; Dev. Biol. 166:654-655(1994).
EMBL; U10986; AAA70168.1; -.
HSSP; P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEAM; PE00041; fn3; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDLINE; 95113183.

"IERCEALL W.E., REALE M.A., CANDIA A.F., WRIGHT C.V., CHO K.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-NOV-1996 (TIEMBLIE1.
1-NOV-1996 (TIEMBLIE1.
1-NOV-1999 (TIEMBLIE1.
DMOR SUPPRESSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eThrLeuLysAla 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMAGCCAGAGCA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnArgTyrTyrThrIleGluAsnLeuAspProSerSerHisTyrValIl 807
                                                                                                                                                                                                                                                                                                                                   uSerTrpArgProProValGluSerLysGlyAsnIleGlnThrTyrThrV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..........GlySerProHisAlaGlnThrIleLysValAspTyrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_vertebrate:Q91562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1427 AA; 156533 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117.50
0.596
47.017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNTYPEIII
                                                                                                                                                            TATGAAGAAATTAAATTGCGTATAAGAGCAGAAA 348
TrpGlyProGlyGluSerSerGlnGluValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01, Created)
01, Last sequence update)
12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E50B7475 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
22.196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                480
                                                                                                                                                                                                                                                                                                                                                                                                                                                            166
                                       398
                                                                                                                                                                                                                                                                                                                                   464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 790
        7.650....GlySerProTyrAlaGluThrValArgValAspSerLysGlnArg
                                                                                                                                                                                                                             1047 TCCCTTAGTGATTCATTCCATATCTATATCGGTGCTCCAAAACAGTCTGG
                                                      1147 GGGAAAACACTTCAAATGCTGAGAGA...AAAATTATCGAGAAAAAACT 1193
                                                                                                                           719 spleuAspGluSerGlnValProAspGlnProSerSerLeuHisValArg
                                                                                                                                                                                                                                                                                                                                                                                         965 TAACACATCTTTTTGGTCTGAAGAGATAAAGTTTGATACT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                686 LeuGluLysGlySerGlnTyrSerPheGlnValAlaAlaMetThrValAs
                                                                                                                                                                                    736 ProLeuThrThrSerIle...IleMetSerTrpThrProProLeuAsnPr
                                                                                                                                                                                                                                                                                                                                                    702 nGlyThrGlyProSerSerAspTrpTyrThrAlaGluThrProGluAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             921 ... CAAAAAGGAATT... TACCTTCTCCGCGTACAAGCATCTGATGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669 lyGluLeuGluThrLeuGluProAsnAsnLeuTrpTyrLeuPheThrGly 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   766 AATGGGATTATACATATGCAAACATGACCTTTCAAGTTCAGTGGCTCCAC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            624 aMetProGlnAsnValSerLeuGluValAlaAsn..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 erValLeuIleSerTrpAspProProAlaTyrAlaAsnGlyProValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 GTGTTATGTGGGCTTTGGATGGTTTAAGCTTTACA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AGCTGAAGATAAGGCAATAGTGATACACATCTCTCCTGGAACAAAAGATA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 ValValThrGlnProGluLeuGlnValProGlyProValGluAsnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       851 TARATGGARACARATACCTGACTGTGARARTGTCARARCTACC..... 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              716 TCCACCAGAAAATATAGAAGTCAGTGTCCAAAATCAGAACTATGTTCTTA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          608 ValSerSerGluGluHisThrValValThrLeuSerAspValProSerAl 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   666 GTCTATAGTCCAGTACATTGTATAAAGACCACAGTTGAAAATGAACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593 luTyrSerIleArgValLeuAla.....TyrAsnArgTyrGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616 CTTATTGTCTAAAAGTTAAAGCAGCACTACTTACGTCATGGAAAATTGGT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 eGluValAspGlyIleValTyrArgLeuGluGlyLeuArgLysPheThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    566 TGAAAATATTTATTCCAGACATAAAATTTATAAACTCTCACCAGAGACTA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             560 GlyTyrArgLeuPheCysAlaGluThrPheSerGlyArgGluGlnAsnIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 ... TATAGCTTACTTATCTGGAAAAACTCTTCAGGTGTAGAAGAAAGGAT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 ..
                                                                                               oAsnIle...ValValArgGlyTyrIleIleGlyTyrGlyVal.....
                                                                                                                                                                                                                                                                                                         .....GAAATACAAGCTTTCCTACTTCCTCCAGTCTTTAACATTAGA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....CAGTGTGTCTTTCCTCAAAACGTTTTC........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....LeuProProProGlyThrGlnAsnGlyPheIleThrGlyTy 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....SerArgSerIleLysValSerTrp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .... AAAGCTCAGATTGGTCCTCCAGAAGTACATTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....ValValSerThrAlaPro......ThrS 543
                                                                                                                                          1146
                                                                                                                                                                                                                                                                                                                                                                                             1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635
                                                                                                                                                                                    751
                                                                                                                                                                                                                             1096
                                                                                                                                                                                                                                                                                                                                                      719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         669
                                                                                                 764
                                                                                                                                                                                                                                                                                                                                                                                                                                      702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559
```

1194 GATGTTACAGTTCCTAATTTGAAACCACTGACTGTATATTGTGTGTAAAGC 1243
:::::: ||||||:::|||
780 TyrTyrSerIleGluAsnLeuGluProSerSerHisTyrValIleSerLe 796

1244 CAGAGCA 1250 :::||| 796 uLysAla 798

ments in